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Marker-trait-sensor association in a multi-parent advanced generation intercross (MAGIC) population in barley *(Hordeum vulgare* ssp. *vulgare*)

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„*Prepare for awesomeness*“

(Kung Fu Panda)

ABSTRACT

The objective of the present study was to identify quantitative trait loci (QTL) for yield, yield components and water content in leaves as measured with the THz-sensor in a MAGIC population derived from eight different parents, the so called “founder of the German barley breeding”. The MAGIC double haploid (DH)-lines were genotyped with the Illumina 9K iSelect chip from TraitGenetics, Germany. Phenotypic values for 534 MAGIC DH-lines were scored in two consecutive years in an augmented designed pot experiment in a polytunnel under two different water conditions - well watered and terminal drought.

QTL detection was carried out in SAS 9.2 with multi-locus analysis and cross validation which included marker, line nested in the marker genotype, treatment and their interaction. Epistatic interactions were calculated using the same program, including marker*marker interaction among others. Two mapping approaches were conducted, using either binary SNP marker data (BA), or haplotype information (HA) from each parent gained with R/mpMap.

The QTL analysis of the DH-lines resulted in 108 putative QTL, 35 out of them mapped simultaneously with both approaches, four out of them with marker*treatment interaction allele effects. When the two approaches were compared, a greater power of allelic effect was detected with the HA. The best contributing parent could directly be assigned and multiple mean comparisons calculated. With this information, QTL QTkw.MAGIC.HA-2H.a could be identified as an improving QTL for thousand kernel weight under terminal drought conditions. The remaining allele effects for marker*treatment interaction did not differ significantly between the parental allelic mean determined with the haplotype approach. In comparison, the binary approach was able to map the allelic effects to smaller genetic intervals. Thus both mapping approaches have their advantages and disadvantages when applied to a multi-parent population, and therefore should be used in conjunction with each other when analysing this type of population. The results of epistatic interaction emphasised the importance of interaction between genomic regions in the characteristic value of agronomic traits. For the trait days to heading a reduction by 7.2 days was investigated by interaction between two regions. The genomic region on 5H, 206.4 cM was significantly involved, furthermore the marker sequence matched with that of a predicted protein sequence that regulates the phyto hormone auxin, which is involved in plant growth. Thus the present study demonstrates that the established MAGIC barley population is an important genetic resource and will be an ideal mapping population in which to investigate both, inheritance and interactions between gene regions.

ZUSAMMENFASSUNG

Im vorliegenden Projekt steht die Identifizierung von QTL bezüglich des Ertrags, Ertragskomponenten und für den Wassergehalt von Blättern, ermittel mit dem THz-Sensor, in einer acht Eltern MAGIC Population im Vordergrund. Dafür wurden 534 DH-Linien der MAGIC Population mit dem 9k iSelect chip von TraitGenetics, Germany, genotypisiert. Die Phänotypisierung erfolgte in zwei aufeinanderfolgenden Jahren in zwei Bewässerungsstufen - ausreichende Bewässerung und zeitlich begrenzter Wasserstress, in Topfversuchen in einem Folientunnel. Die QTL Kartierung wurde mit Hilfe von SAS 9.2 mit einer multi-locus Analyse und cross validation mit den Faktoren Marker, Bewässerung, DH-Linie genestet im Markergenotyp, und den entsprechenden Interaktionen durchgeführt. Epistatische Effekte wurden mit dem gleichen Modell unter Berücksichtigung der Marker*Marker Interaktion berechnet. Zwei unterschiedliche Auswertemethoden wurden zur QTL Kartierung verwendet, ein binäres Auswertesystem (BA) und die Haplotypeninformationen (HA) der acht Eltern ermittelt durch das Programm R/mpMap.

Die QTL Kartierung mit beiden Auswertemethoden detektierte 108 putative QTL, davon 35 mit beiden Auswertemethoden, vier davon mit einer Marker*Bewässerung-Interaktion. Im Vergleich der Auswertemethoden konnte mit dem HA ein stärkerer Alleleffekt ermittelt werden, die allelischen Mittelwerte der Eltern berechnet, und dadurch Mittelwertvergleiche aller Eltern in allen Bewässerungsstufen berechnet werden. Mit Hilfe dieser Information konnte das QTL QTkw.MAGIC.HA-2H.a gemappt werden, welches ein vorteilhaftes Allel bezüglich Tausendkornzahl unter Trockenstress aufweist. Die restlichen allelischen Mittelwerte der Eltern aller QTL mit Marker*Bewässerung-Interaktion waren nicht signifikant zueinander. Mit dem BA konnte der genetische Effekt im Vergleich zu HA in ein kleineres genetisches Intervall gemappt werden. Beide Auswertemethoden haben Vor- und Nachteile, und sollten in einer Vielelternpopulation gemeinsam angewendet werden. Die Ergebnisse aus der Analyse der epistatischen Effekte hebt die Bedeutung dieses Phänomens zur Merkmalsausprägung von agronomischen Merkmalen hervor. Für den Blühzeitpunkt konnte eine Reduktion um 7,2 Tage im Zusammenspiel zweier Genorte berechnet werden. Dabei spielt die genomische Region auf 5H, 206,4cM eine wichtige Rolle, weiterhin stimmte die Markersequenz in dieser Region mit einer Sequenz für ein „predicted protein“ überein, welches Auxin reguliert, ein wichtiges Phytohormon im Pflanzenwachstum. Die vorliegende Arbeit demonstriert, dass MAGIC Populationen eine wichtige genetische Ressource bilden, um Vererbung und Interaktionen von Genregionen zu ermitteln.

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1. Introduction

Global agriculture is and will be facing declining water availability, a reduction in arable land, competition between the cultivation of bio fuel, feedstock or food, and strongly increasing demand for harvested products (Tardieu, 2012). Predictions of climate change indicate an increased variability of rainfall in the next 40 years and an increased risk of high temperature (IPCC) that will cause appreciable limitations of yield due to abiotic stresses (Brisson et al., 2010; Tebaldi and Lobell, 2008). Cereal grain yields alone must increase by at least 70% before 2050. Rice demand has already exceeded supply for the years 2007 and 2008 (Furbank et al., 2009). To face this problem it is necessary to develop crops that are tolerant to drought. Unfortunately, drought is made complex by variations in its severity, duration, and timing. The responses to drought are complex; therefore drought tolerance is a complex trait. Barley is a genetically wide adapted crop species and model crop, which is known to be drought tolerant, with established genomic resources and is suitable for mapping of complex traits. Bi-parental crosses are grateful when used for individual traits, like resistances to abiotic stresses. But when it comes to identify the genetic control of complex multigenic traits like yield, and especially in complex environments like drought stress, there is a need to move from 'purpose-build' bi-parental populations to those with a broader genetic and phenotypic base (Huang et al., 2012). Therefore, a more complex breeding design was formed and the barley MAGIC population, derived from eight German barley landraces/cultivar, was established.

Understanding how to maximise water use efficiency of cultivated plants is a promising strategy to remedy the above mentioned global water shortages (Hadjiloucas et al., 2002). Measuring the water content of plants invasively would be a major gain in the overcoming of high-throughput phenotyping of plants. This can be perfectly addressed with the terahertz (THz) spectroscopy, whereas point measurements on leaves can determine the water content of leaves.

Adding it all together, the MAGIC population, the established genotyping facility with 7800 SNP data points and the use of the THz-sensor to measure water content leads to the main objective of this work, the detection of favourable allele effects for yield and yield component and water content in plants under terminal drought stress.

1.1 *Hordeum vulgare* ssp. *vulgare* (Barley)

Barley (*Hordeum vulgare* L.) belongs to the tribe of Triticeae in the family of grass, Poaceae, representing the largest family of monocotyledonous plants. The genus *Hordeum* contains 32 species and 45 taxa, including diploid, polyploid, perennial and annual types, distributed throughout the world (Bothmer et al., 2003).

Barley is one of the first crop domesticated, approximately 7500 B.C.E. as archaeological remains emphasize. It is assumed that the domestication of barley took place from two-rowed wild barley *(Hordeum vulgare ssp. spontaneum*, in the following written as *Hordeum spontaneum*) in the Near East, the Fertile Crescent. Wild barley is still broadly distributed in these regions. But there are ongoing debates among researchers about the evidence of multiple barley domestication sites (Molina-Cano et al., 2005; Tanno et al., 2002).

Barley is one of the most important cereal crop species in food production. It is ranking fifth in the world after wheat, maize, rice and soya in terms of acreage (FAO 2010, http://faostat.fao.org). Approximately 75% of global production is used for animal livestock feed, 20% is malted for use in alcoholic and non-alcoholic beverages, and 5% as use in human food products (Blake et al., 2011). Barley is widely adapted to different environmental conditions, and is more stress tolerant to cold, drought, alkalinity and salinity then its close relative wheat (Nevo et al., 2012).

1.2 Barley genetics

Barley is a diploid, self-pollinating, highly homozygous crop with a high degree of inbreeding. Compared with the plant models *Arabidopsis* (135 Mb) and rice (430 Mb) the genome of barley is very large, but with 7 chromosomes (2n=14) it is one of the smallest genome regarding the tribe of Triticeae, turning barley into a highly investigated model for classical genetics, with genetic and genomic resources being established over the last years (Stein et al., 2007). These contain geographically diverse elite varieties, landraces and wild accessions, a comprehensive number of well-characterized genetic stocks and mutant collections (Caldwell et al., 2004), containing alleles that could ameliorate the effect of climate change (Lundqvist et al., 1996). Large numbers of expressed sequence tags (EST) have been developed, providing resources for microarray design that in turn establish routine functional genomics (Close et al., 2004; Druka et al., 2006). Several (high density) maps based upon different genetic marker techniques were published over the last decade (Close et al., 2009; Potokina et al., 2008; Ramsay et al., 2000; Stein et al., 2007; Varshney et al., 2007; Wenzl et al., 2006). The same sequences were used to develop and implement high-throughput single nucleotide polymorphism (SNP) genotyping and to construct the first high-density gene map (Close et al., 2009), containing 2,943 SNP loci in 975 marker bins covering a genetic distance of 1099 cM. This technology enables to dissect genetically agronomical important traits (Wang et al., 2010; Wang et al., 2012). Recently genotyping by sequencing (GBS) has been developed as a tool for association studies and genomics-assisted breeding, being able to detect and locate thousands of SNPs on the genome.

A major step towards understanding and exploitation of these resources mentioned above and the amount of genetic data available is the publication of the barley genome gene space by Mayer et al. (2012), a resource that provides access to the majority of barley genes in a highly structured physical and genetic framework. The consortium released a physical map, representing more than 95% of the barley genome with a size of 4.98 gigabases (Gb), and more than 3.9 Gb anchored to a high-resolution genetic map. The physical map was constructed of the barley cultivar Morex by high-information-content fingerprinting (Luo et al., 2003) and contig assembly (Soderlund et al., 2000) of 571,000 bacterial artificial chromosome (BAC) clones originated from six independent BAC libraries. Consistent with the genome sequence of maize (Schnable et al., 2009) the pericentromeric and centromeric regions of the barley chromosomes present significantly reduced recombination frequency, an attribute that hampers the utilization of genetic diversity and impedes plant breeding. Approximately 1.9 Gb or 48% of the genetically anchored physical map (3.9 Gb) was assigned to these regions (Mayer et al., 2012). The barley genome is characterized by high amount of repetitive DNA, as known from Maize (Schnable et al., 2009). Approximately 84% of the genome consists of mobile elements or other repeat structures. The majority of this repeat structure (76%) consists of retrotransposons; out of them 99.6% are long terminal repeat retrotransposons (LTR). Concerning the assembly along the chromosome, there is reduced repetitive DNA content within the terminal 10% of the physical map of each barley chromosome (Mayer et al., 2012). A total of 24,154 high-confidence genes could be associated and positioned in the physical/genetic framework, averaged gene density of five genes per Mb, proximal and distal ends of chromosomes being more gene-rich, with a mean of 13 genes per Mb (Mayer et al., 2012). Approximately 175,000 in exons located single-nucleotide variants (SNVs), out of 15 million detected non-redundant SNVs by sequencing four diverse barley cultivars (Bowman, Barke, Igri, Haruna Nijo) and one *Hordeum spontaneum* accession, were integrated into the genetic/physical framework. This provides a source material to establish true genome-wide marker technology for high-resolution genetics and genome-assisted breeding (Mayer et al., 2012).

1.3 Barley landraces

Landraces evolved directly from their wild progenitor through natural and human selection and are still used as a main source of seeds in a lot of countries. They are often highly variable in their appearance and often get local names from farmers. They can be classified by certain characteristics, for example early or late maturing or by their use, for animal food, human food or constructing material. Landraces are adapted to certain climate conditions and biotic stresses. But most important, they are genetically diverse populations – variable, in equilibrium with both

environment and pathogens and genetically dynamic (Harlan, 1975). The beginning of barley breeding in Germany accompanied with defined rules and requirements concerning the Seed Marketing Act changed the demand of a "variety". A variety has to be homogeneous and invariable to be on the market for sale. This was not in accordance with the structure of landraces. Landraces were used as primary material for the breeding process in Germany. That's why modern varieties available right now on the market have always landraces as ancestors in their pedigree, so there are landraces in Germany that can be called founder of the German barley breeding.

1.4 Phenotyping with sensor technology

To benefit from all the information from genomics for agricultural application, it has to be carefully and comprehensively linked to phenotypes (Furbank and Tester, 2011). Phenotyping populations, e.g. for QTL-studies, is a labour and time intense part of research and main work for breeders, releasing new varieties through phenotyping thousands of genotypes each year. Conventional phenotyping methods are often destructive, and involve the removal of plant biomass for analysis, especially for water status in plants or part of plants. Alternative phenotyping methods enable the researcher to obtain multiple images of the same plant during a time series and whole plant developmental stages, offering a new dimension of quantitative data, and possibilities for screening genotypes under abiotic stresses (Berger et al., 2010). One of these new phenotyping approaches, TeraHertz time-domain spectroscopy (THz-TDS), will be introduced in this research project.

1.4.1 THz-TDS system

In physics, terahertz radiation consists of electromagnetic waves at frequency ranging from 0.1 to 10 terahertz (THz). With this range it comprises the high-frequency edge of microwave band to long-wavelength edge of far infrared light as seen in Fig. 1. For a long time, THz radiation was a black hole of the spectroscopic portfolio; neither electronic nor optical sources could illuminate that shadowy region (Jansen et al., 2010). But the potential of the THz technology, the power and efficiency of cost-effective emitter and detector from microwave and near infrared technology helped to enlighten the frequency region. THz systems are now used in several fields of application, ranging from medical technique, security check at airports, characterisation and quality inspection of material (building material, polymers), and spectroscopy at the molecular level and in biological systems.

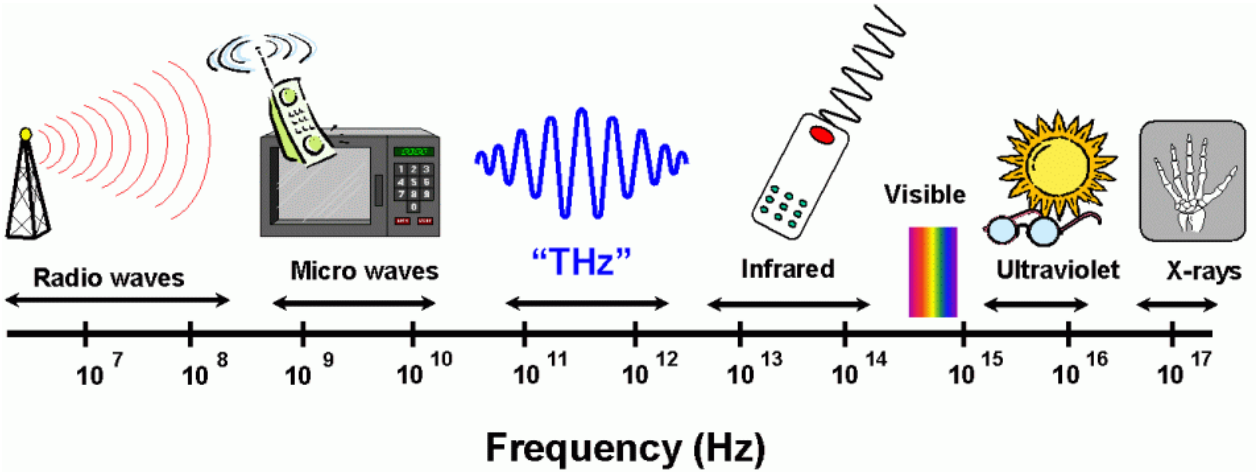

Fig. 1: Frequency range of THz and others

There are two categories of optoelectronic THz spectrometer systems suitable for different approaches: Spectrometer with continuous waves at constant frequency ("continuous wave" (CW)-systems) or with a THz-TDS system. The CW-systems offers sharp spectral features and a frequency resolution down to one Megahertz (MHz), the time domain spectroscopy offers broad spectral information from a single scan in the timescale of seconds (Karpowicz et al., 2005).

THz radiation is highly absorbed by water. Therefore measuring the moisture status of a plant leaf was one of the first applications in THz imaging a drying leaf (Hu and Nuss, 1995), providing a non destructive method for the instantaneous monitoring of the water status in living tissues. Other contactless measurements were developed, for example infrared radiation (Tucker, 1980) and microwaves (Matzler, 1994). Concerning the infrared technology there is still ongoing discussions of the suitability of the employed spectral indices (Eitel et al., 2006). The relatively large wave length of the microwave is strongly affected by the salinity of the water in the leaves, picturing one disadvantage of this technique. THz radiation provides lots of advantages compared to other techniques. Due to the smaller THz wavelength compared with microwaves it offers a better spatial resolution. Furthermore, the influence of dissolved salt on the permittivity of water is low. With a technical setup shown in Fig. 2 the average measuring time is less than ten seconds per sample, leading the way to a high-throughput phenotyping of the water status in leaves. Consequently, physiological studies of a leaf hydration status are possible and diverse approaches to estimate the water status were conducted (Hadjiloucas et al., 2002; Hadjiloucas et al., 1999; Jordens et al., 2009; Mittleman et al., 1996). Evaluation of leaf water status or leaf water content as a non-invasive measurement is of great importance for researchers and plant breeders.

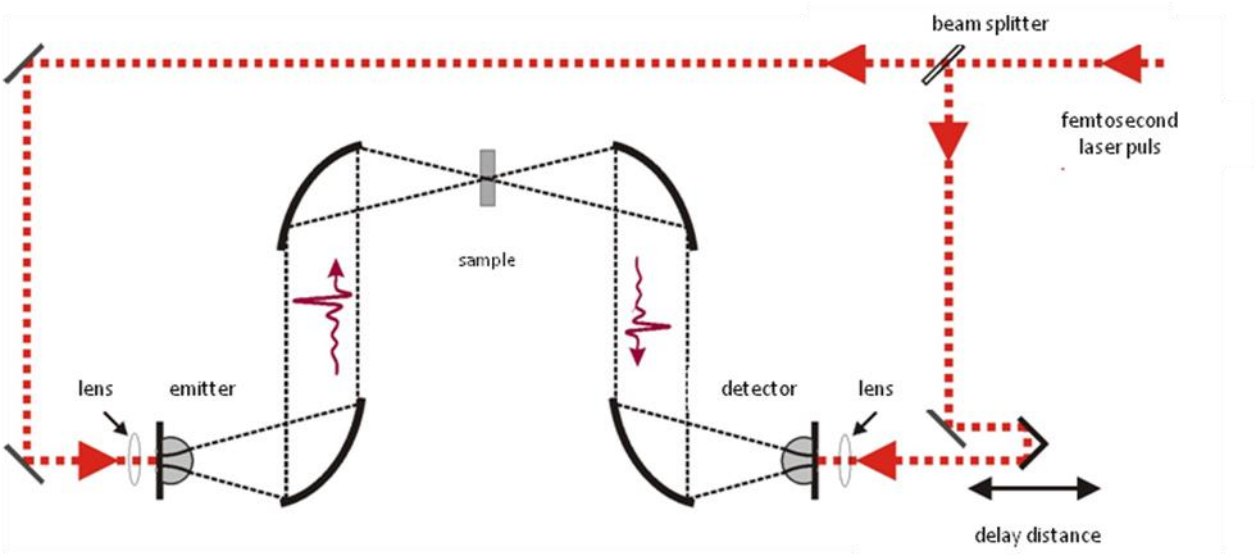

Fig. 2: Schematic installation of a pulsed THz system

1.5 Drought and drought tolerance

Among different abiotic stresses, drought is by far the most complex and devastating one on a global scale. Worldwide it is one of the major limitations to food production (Pennisi, 2008). Jian-Kang Zhu, a molecular geneticist at the University of California, Riverside, says: "Drought stress is as complicated and difficult to plant biology as cancer is to mammalian biology" (Pennisi, 2008). Blum defines "agricultural drought" as insufficient moisture for maximum or potential growth of crops. This condition can arise, even in times of average precipitation, owing to specific soil conditions, topography or biotic factors. It follows that agricultural drought can be expressed on very wide range of plant growth reductions up to complete crop failures. It does not necessarily imply that plants must wilt or die or fail in any spectacular manner. By definition, agricultural drought can cause small reductions in yield when it is mild (Blum, 2010). Passioura defines drought as circumstances in which plants suffer reduced growth or yield because of insufficient water supply, or because of too large humidity deficit despite there being seemingly adequate water in the soil (Passioura, 1996; Pennisi, 2008).

As the definition of drought itself seems to be similar between researchers, the definition of drought tolerance and drought tolerance traits in plants is more difficult. "There is not a single, magical drought-tolerance trait" says Mark Tester, plant physiologist at the Australian Centre for Plant Functional Genomics (Pennisi, 2008).

Up to the late 1970's, defining criteria for improving yield under drought stress was a haphazard affair. There was no great deal of attention given to the complex nature of drought or to separate productivity under drought, which was important for agricultural plants, from survival mechanisms, which characterize xerophytes. Yet, many adaptations favouring survival tend to reduce economic

yield (Richards, 1996). Passioura (1996) pictured the same concept in the article "Drought and drought tolerance". It is well known, that a cactus is more drought tolerant than a carnation. But regarding crops, drought tolerance cannot only concern survival during drought periods. In crops one is concerned with production. The term "drought tolerance" in an agricultural context, only gives a meaning when defined in terms of yield in relation to a limiting water supply. In the late 1970's there was a change in identifying criteria for improving yield under drought. Maximising the economic product when water is limited was and still is the main aim, pioneered by Passioura (1977). Several scientists worked on the mechanisms underlying drought tolerance and the strategies that can improve yield under such conditions (Blum, 1996; Blum, 2011a; Mir et al., 2012; Passioura, 2007; Passioura, 1996; Passioura and Angus, 2010; Reynolds and Tuberosa, 2008; Richards, 1996; Richards et al., 2010).

The years of breeding activities have led to yield increase in drought environments for many crop plants. Meanwhile, fundamental research has provided significant gains in the understanding of the physiological and molecular response of plants to water deficits, but there is still a large gap between yields in optimal and in stress conditions (Cattivelli et al., 2008). Minimizing the yield gap and maximising yield stability are the main tasks for the future. With this challenging task in mind, molecular approaches (Ashraf, 2010; Bohnert et al., 2006; Deikman et al., 2012; Forster et al., 2000; Tuberosa and Salvi, 2006; Vij and Tyagi, 2007) offer novel opportunities for the dissection and more targeted manipulation of the genetic and functional basis of yield under drought stress (Tuberosa, 2012).

1.6 Quantitative trait loci (QTL) mapping

A quantitative trait is one that has measurable phenotypic variation owing to genetic and/or environmental influences (Abiola et al., 2003). In crop plants most traits of biological or economic interest are of quantitative nature and under polygenetic control (Falconer and Mackay, 1996), and therefore display continuous variation within or between species and have complex inheritance, e.g. flowering time, yield.

The term "quantitative trait loci (QTL)" was introduced by Geldermann to describe those regions of the genome underlying a continuous trait (Geldermann, 1975). Quantitative trait loci play an important role in understanding complex traits, whether in human, animal or plant genetic. Detection of QTL by conventional phenotyping is not possible. The breakthrough of developing genetic markers in the 1980s paved the way for characterising QTL. These enabled to build a linkage map of the experimental mapping population that shows the position of genetic markers relative to each other. The process of constructing a linkage map and associate phenotypic traits

with genomic regions is known as QTL mapping (also ‘genetic’, ‘gene’ or ‘genome’ mapping) (Mccouch and Doerge, 1995). A traditional QTL mapping approach involves (1) the development of a mapping population out of parents segregating for the trait of interest, (2) genotyping the population with polymorphic markers, (3) accurate phenotyping for the traits of interest, (4) construction of a linkage map, (5) QTL mapping by combining phenotypic values and genotypic data (Mir et al., 2012).

The first whole genome QTL mapping was performed in tomato (Paterson et al., 1991; Paterson et al., 1988), followed by soy bean (Keim et al., 1990) and maize (Beavis et al., 1991). The first QTL analysis in barley was conducted by Heun (1992) and Hayes et al. (1993). Since a lot of QTL analysis in barley have been performed, focusing on different traits (yield, resistance etc.), on different populations (advanced backcross, recombinant inbred lines (RILs), near isogenic lines (NILs)) and on different environments (drought, salinity). Progresses in statistical methods play an important role in the improvement of QTL detection. The three commonly used methods are single – marker analysis, interval mapping and composite interval mapping.

(1) The statistical methods for single-marker analysis include t-test, analysis of variance (ANOVA) and regression. The major advantage of this method is that it does not require a linkage map. Furthermore it is flexible concerning different mapping populations, different experimental designs with further factors (environments, treatments) and epistatic effects. The disadvantage of underestimating QTL (Tanksley, 1993) with the single-marker methods will be minimized trough a dense genotypic marker approach (Collard et al., 2005).

(2) The interval mapping method was first proposed by Lander and Botstein (1989) and is based on maximum likelihood methods or multiple regressions. It makes use of linkage maps and analyses intervals between adjacent pairs of linked markers along the chromosome simultaneously and is considered statistically more powerful compared to the single-marker method (Lander and Botstein, 1989). With a high density map of genetic markers, as available now, the advantages are negligible.

(3) Composite interval mapping (Jansen, 1993; Rodolphe and Lefort, 1993; Zeng, 1994) includes partial regression coefficients from markers (cofactors) in other regions of the genome. The main advantage is the more precise and effective QTL mapping, especially when linked markers are involved. Unfortunately epistatic effects cannot be calculated as well as genotype*environment interactions (Collard et al., 2005).

Teulat et al. (1997) were the first one to use QTL analysis to identify genomic segments related to drought tolerance. Since then six different mapping populations with drought stress tolerant parents were under investigation by different scientist (Chen et al., 2010; Diab et al., 2004; Guo et al., 2008;

Mardi et al., 2005; Peighambari et al., 2005; Teulat et al., 2001a; Teulat et al., 2001b; Teulat et al., 1998; Teulat et al., 2003; Zhang et al., 2005). Altogether 117 QTL were detected in 12 studies for a variety of drought related traits, for example days to heading, grain yield, plant height and thousand seed weight (Li et al., 2013). These traits and the corresponding QTL that affect yield in drought environments can be categorized as constitutive (i.e., also expressed under well-watered conditions) or drought-responsive (i.e., expressed only water shortage) traits (Lafitte and Edmeades, 1995).

1.7 Multi-parent mapping populations

Most of the QTL studies in plants were conducted in individual bi-parental populations. Highly diverse parents, segregating for the trait of interest were crossed with each other and the offspring, F_2, DH-lines or RILs were analyzed for QTL. Bi-parental mapping populations are grateful with respect to population development and the high power of QTL detection (Doerge, 2002). But their soft spot is the mapping with low resolution (large genetic intervals) as a result of limited opportunity of recombination (Huang et al., 2012). Inferences from bi-parental studies suggested that plant populations segregate for a limited set of small-effect QTL plus a very few QTL that have large effects. This is due to genetic heterogeneity between the mapping populations, if a trait is controlled by many genes, different subsets can segregate in different mapping populations (Holland, 2007). Researchers started to study complex traits in larger populations because small populations biased the effects of QTL with statistical artefacts by sampling (Salvi and Tuberosa, 2005). The results detected in a very large maize population concerning seed oil content (Laurie et al., 2004) and grain yield (Schön et al., 2004), relative large numbers of QTL but low genetic effects, were consistent with QTL analysis in mouse population (Valdar et al., 2006) and Drosophila (Mackay, 2004). A concept to overcome the low explained genetic variation through the QTL in bi-parental crosses, to reduce linkage disequilibrium (LD) and to improve mapping resolution, was proposed by Darvasi and Soller (1995) with the advanced intercross (AIC). It is an extension of RILs and consists of a repeatedly random intermated F_2 population from a bi-parental cross, followed by generations of selfing, with the effect of reducing the level of LD and increasing the precision of QTL mapping (Cavanagh et al., 2008). But QTL mapping in purpose build bi-parental crosses reveals only a slice of the genetic architecture of a complex trait, because only alleles that differ between the parents will segregate within the offspring (Holland, 2007). In contrast, association panels (Core Collections etc.) enclose a high genetic variation, due to large number of recombination events in the past and therefore promise a high resolution of QTL (Myles et al., 2009). One major disadvantage from QTL mapping with association panels is the variation in pairwise relationships of genotypes, leading to a genetic structure within the panel that hampers the

differentiation of true-positive and false-positive QTL. A different way to enhance the genetic variation and to avoid limitations of genetic structure within a population was spurred by Mott et al. (2000). The AIC approach was extended by Mott et al. (2000) to produce highly recombinant outbred populations in mice from multiple parents, so called heterogeneous stocks (HS). The application of HS in research increased the power to detect and localise QTL, and to fine map QTL controlling complex traits in mice to small confidence intervals (Yalcin et al., 2005). The use of HS is cost intensive and time consuming because each individual genome is exclusive and heterozygous and requires genotyping each time it is phenotyped.

A strategy to overcome this problem is to produce RILs from several parents (Churchill et al., 2004) which has been termed multi-parent populations in crops (Cavanagh et al., 2008). These populations combine the high mapping resolution exhibited by multiple generations of recombination with the high mapping power afforded by linkage-based design (King et al., 2012). Four multi-parent population have been described in plants, the Arabidopsis multi-parent recombinant inbreed line (AMPRIL) population (Huang et al., 2011), the Arabidopsis multi-parent advanced generation intercross (MAGIC) (Kover et al., 2009), the maize nested associated mapping population (NAM) (Buckler et al., 2009; McMullen et al., 2009) and the four parent MAGIC population in wheat (Huang et al., 2012). These populations are composed of a series of homozygous, genotyped RILs, they represent stable genetic reference panels that facilitate systems-level analyses of genetic architecture (King et al., 2012).

The aspired high mapping resolution was achieved in the four parent MAGIC population of Huang et al. (2012). The mean LD dropped down to <0.8 within ~5 cM and to <0.2 within 40 cM. The average LD between markers on different chromosomes was 0.0037. In the multi-parent population in *Arabidopsis* from Huang et al. (2011) the mean correlation between SNPs decayed to 0.17 by about 0.5 Mb. Minimal LD between the chromosomes was detected, the mean R^2 value was 0.04. A population structured implied a low chance of ghost QTL (Huang et al., 2011).

1.8 Single nucleotide polymorphism (SNP)

Molecular markers have become increasingly important during the last decades to investigate and dissect the genetic fraction underlying quantitative traits. Different classes of DNA markers were develop and implemented over time. Co-dominant restriction fragment length polymorphism (RFLP), implemented in 1980 (Botstein et al., 1980), were the first molecular markers widely used. Random amplified polymorphic DNA (RAPD) markers were developed in 1990 and first described by Williams et al. (1990). In the following, amplified fragment length polymorphism (AFLP) marker (Vos et al., 1995) and single sequence repeat (SSR) marker were developed which were

used in plant studies in 1993 (Morgante and Olivieri, 1993) for the first time. With the development of diversity array technology (DArT) by Jaccoud et al. (2001) the first generic whole genome genotyping technology was implemented which allows genome profiling and diversity analysis. These marker techniques differ in costs, work, range of use and repeatability and need to be chosen in respect to the investigated population and application area.

A SNP is an individual nucleotide base difference between two DNA sequences. Every SNP within the genome could be used as a genetic marker. In the last years SNP markers gained a lot of interest in the scientific community across all species and its power is clearly represented in the human genome analysis (Sachidanandam et al., 2001). In plants, SNP in genic regions are abundant with the preliminary estimate ranging from 1 SNP per 60 bp in out breeding maize (Ching et al., 2002) to ca. 1 SNP per 300 bp for inbreeding rice and *Arabidopsis* (Schmid et al., 2003; Yu et al., 2005). SNPs offer an important source of molecular markers that can be utilized in genetic mapping, map-based position cloning, detection of marker-trait gene associations through linkage and linkage disequilibrium mapping and the estimation of genetic relationships between individuals (Oraguzie, 2007). SNPs underlie a low mutation rate, which makes them excellent, stable markers for dissecting complex traits and a tool for the understanding of the genome (Syvanen, 2001). The abundance of SNPs within the genome largely offers the greatest level of genetic resolution. This offsets the disadvantage of SNPs being biallelic and makes them the most attractive molecular system so far. Complementary approaches for the detection of SNP in barley have been explored, i.e. searching for electronic SNPs in expressed sequence tags (EST) assemblies (Kota et al., 2003) and resequencing selected sets of unigens in different barley accessions (Rostoks et al., 2005). SNPs are of potential functional relevance and they are also well suited to high throughput analytical methods (Rostoks et al., 2005). Several barley linkage maps (Close et al., 2009; Comadran et al., 2012; Sato et al., 2009; Stein et al., 2007) and a SNP based map featuring gene sequences expressed differentially in response to various abiotic stresses have been published (Rostoks et al., 2005). QTL mapping or association mapping in barley were effectively conducted with SNP recently (Burris et al., 1998; Cockram et al., 2010; Comadran et al., 2011a; Comadran et al., 2011b; Wang et al., 2012). International collaborators subsequently initiated the development of a highly multiplex unigene-based SNP assay platform for barley (Rostoks et al., 2006) and chose Illumina's oligo pool assay (OPA) as a marker platform (Waugh et al., 2009). The latest development, the 9K iSelect chip contains 7864 SNPs (Comadran et al., 2012).

1.9 Haplotypes

Genetic markers can be analysed independently of each other, SNP by SNP. The SNPs are organized in the chromosome of individuals. If SNPs that are close to each other are examined, a sequence of bequeathed SNPs, forming a typical order of SNPs (Fig. 3) can be observed. The combination or sequence of the SNPs is called a haplotype (*Haplo*id Geno*type*) (Zhao et al., 2003).

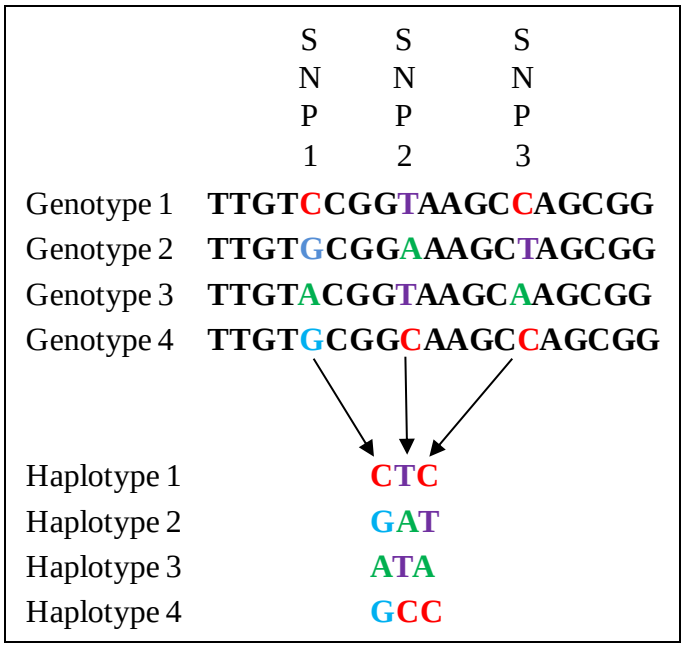

Fig. 3: Haplotype construction out of a chromosomal region of four genotypes with three SNP markers

Due to LD each chromosome can be divided into many haplotype blocks. There are several definitions for the term haplotype block: a region where a small number of common haplotypes account for the majority of chromosomes (Patil et al., 2001; Zhang et al., 2002); a chromosomal segment with reduced levels of haplotype diversity (Zhao et al., 2003); regions with both limited haplotype diversity and strong LD except for a few marker (Dawson et al., 2002); regions with absolutely no evidence for historical recombination between any pair of SNPs (Wang et al., 2002). I used the term “haplotype block” according to following definition: a contiguous set of markers in which the average LD is greater than some predetermined threshold (Reich et al., 2001). Arguments for using association between haplotype blocks and phenotypes have been proposed by different scientists in humans: haplotype blocks capture epistatic effects between SNPs (Bardel et al., 2005; Clark, 2004) and provide more power than single SNPs when an allelic series exists at a locus (Morris and Kaplan, 2002) and allow informed testing between clades of haplotype alleles by

capturing information from evolutionary history in *Drosophila* (Templeton et al., 1987). Comparison of "haplotype block" and "single-marker based" approaches were conducted in human and livestock with contrasting results. Single-marker based approaches with greater power were detected by Long and Langley (1999) in human population genetics. Results from simulation in livestock populations by Hayes et al. (2007) and others (Calus et al., 2009; Grapes et al., 2004) resulted in greater QTL detection power and mapping accuracy with "haplotype blocks" then with the "single-marker based" approach. Zhao et al. (2007) detected no differences between the two approaches in conducting simulations designed to resemble the demography and population history of livestock.

A comparison of the two approaches in plants was conducted in barley by Lorenz et al. (2010). In his research the "haplotype block" approach performed better, when QTL were simulated as polymorphisms that arose subsequent to marker variants and in the analysis of empirical heading date. The results from the study demonstrate that the information content of haplotype blocks is dependent on the recombinational history of the QTL and the nearby markers. The analysis of the empirical data confirmed that the use of haplotype information can capture association that is neglected by the "single-marker SNP" approach (Lorenz et al., 2010).

1.10 Epistasis

Epistatic effects are statistically defined as interactions on a phenotype between effects of alleles from two or more genetic loci which do not correspond to the sum of their separate effects (Fisher, 1918). The existence of epistatic interactions in barley populations was already demonstrated by Fasoulas and Allard (1962) before the age of molecular marker. The advent of molecular markers was supposed to make analysis of epistatic effects on the basis of a genome-wide scale possible. Early efforts using molecular markers were not really successful or did not provide evidence for important epistatic effects (Tanksley, 1993) for example in maize (Blanc et al., 2006; Edwards et al., 1987; Melchinger et al., 1998; Mihaljevic et al., 2005; Schön et al., 2004). But studies in self-pollinated crops have been more successful in given evidence for important epistasis, for example concerning yield in rice (Li et al., 1997; Mei et al., 2005; Yu et al., 1997), *Arabidopsis* (Malmberg et al., 2005) and in barley (Thomas et al., 1995). The contrasting results might be due partly to the differences in breeding scheme of the species discussed above (inbreeding and out-crossing) and partly to differences in the statistical model used in the determination of the epistatic effects.

Statistical methods for detecting epistasis in QTL studies are improving (Holland, 2001), searching for effects throughout the genome (Wang et al., 1999) while other methods just test the interactions

of QTL with significant main effects (Holland, 2001). Recent results have demonstrated the power and importance of epistatic interactions in the studied domestication-related traits heading date, plant height and yield (von Korff et al., 2010), where the interaction of QTL with background loci, as promoted by Wang et al. (1999) were tested. Strong epistatic effects were detected in BC_2DH lines between a QTL on chromosome 4H and the *Vrn-H1* gene where genotypes carrying the exotic allele from the wild barley accession ISR42-8 on both markers flowered eight days earlier than the lines with the elite allele from variety Scarlett at both loci. This identification of the epistatic effects is important in prospects of marker assisted selection and gene cloning (von Korff et al., 2010).
Tanksley (1993) suggested that the power to detected epistatic effects not only depends on the trait but as well on the mapping population, making NILs a powerful tool due to a stabilized genetic background compared to first approaches using F_2 populations. The MAGIC DH-lines with the high amount of recombination during the crossing procedure and the 100% homozygosity is assumed to be a favourable population to dissect complex traits and to measure epistatic effects precisely.

1.11 Objective and Hypotheses

QTL mapping for yield and yield related traits under drought conditions was conducted in different research projects with different populations as mentioned above. A MAGIC population instead is a new kind of mapping population, adapted from mouse genetic and only established so far in *Arabidopsis* (Huang et al., 2011; Kover et al., 2009) and wheat (Huang et al., 2012). QTL analyses under drought conditions have not been conducted in a MAGIC population. The application of sensor technology for precise phenotyping is an emerging research field in agriculture and especially in plant breeding. The non invasive measurement of water content in leaves has been conducted in coffee (Jordens et al., 2009) and *Catalpa* (Hadjiloucas et al., 1999). The determination of the water content in an agricultural important crop, the application of the THz-sensor in a segregating population, and the estimation of QTL for water content in barley has not been conducted so far. The use of a dense genetic map and a large amount of genotypes in a segregating population are good source for a QTL mapping approach. The combination of the integration of cross validation to estimate the performance of the model and multi-locus analysis to reduce the number of false-positive QTL and the estimation of epistatic effect will enable a precise QTL detection and localisation. The primary aim of this project is the detection of QTL in a MAGIC population in spring barley. Relevant traits are yield and yield related traits under drought conditions, using the combination of classical phenotypic traits and THz-sensor as a non-invasive approach for measuring water content in leaves. Specific objectives of the study are listed below.

- The THz-Sensor is able to measure the water content in living leaves.
- The MAGIC population is suitable for QTL mapping concerning its population structure and decay of linkage disequilibrium.
- The information content from the genotypic data enables to estimate haplotypes.
- The QTL will be calculated with two approaches, with the SNP data and the haplotype data. The approaches differ from each other concerning information content, cover ratio and estimation of the allele effect.
- QTL for yield, yield related traits and water content of leaves from THz-sensor and their interaction with a drought stress environment will be determined with both approaches.
- The MAGIC population and the QTL program are a perfect source to identify epistatic effects between genomic regions for the traits of interest due to a high number of meiosis and therefore smaller genomic fragments along the chromosomes.

2. Materials und Methods

This chapter outlines the phenotypic and genotypic studies of the MAGIC DH-lines and their parents as well as the materials and methods for the THz sensor.

2.1 Plant Material

To create the genetic material used in this research, eight spring barley genotypes (Ackermanns Bavaria, Ackermanns Danubia, Barke, Criewener 403, Heils Franken, Heines Hanna, Pflugs Intensiv, Ragusa (Table 1) (hereinafter named: parents)) were intermated in an eight-way-cross. The parental genotypes were selected due to their contribution to the German barley breeding. Seven of them are old landraces and so called founder of the German barley breeding, contributing as a crossing partner in the pedigree of most German spring barley cultivars. The eighth genotype is 'Barke', a modern German spring barley variety, released in 1996, and important model in barley genetics. The parental genotypes can be traced back to a single plant. They were crossed in G_0 in four pairs to produce F_1 seeds (Fig. 4): Ack. Bavaria x Barke (AB), Heils Franken x Heines Hanna (CD) Pflugs Intensiv x Ragusa (EF) Ack. Danubia x Criewener 403 (GH).
In G_1 the two-way-crosses were intermated with each other to a four-way-cross, (AB x CD) and (EF x GH). The crosses G_1 and further crosses can be traced back to subfamilies and sub-subfamilies (Table 2); more than one crossing per combination was conducted to reduce the loss of alleles. Starting from G_2 the double crosses segregated, replicated crosses involving more recombinant plants were required. At G_3 the progenies of G_2 are intercrossed to effect the eight-way intercrossing to produce F_1 seeds for (ABCDEFGH). Each ABCDEFG F_1 seed was harvested and 252 seeds from twelve subfamilies were sent to Saaten-Union Biotec GmbH, Leopoldshöhe, Germany. Doubled haploid lines were produced via anther and microspore culture to shorten the breeding cycle. 534 MAGIC DH-lines were selected out of approximately 5000 DH-lines to be investigated in this thesis.

Table 1: Accession number and registration date of MAGIC parents

Accession name	IPK number	Registration
Ackermanns Bavaria	HOR 100	1903
Ackermanns Danubia	BCC 1427	1912
Barke	Saatzucht Josef Breun GdbR	1996
Criewener 403	HOR 62	1910
Heils Franken	BCC 1433	1895
Heines Hanna	HOR 59	1884
Pflugs Intensiv	BCC 1441	1921
Ragusa	BCC 1359	1929

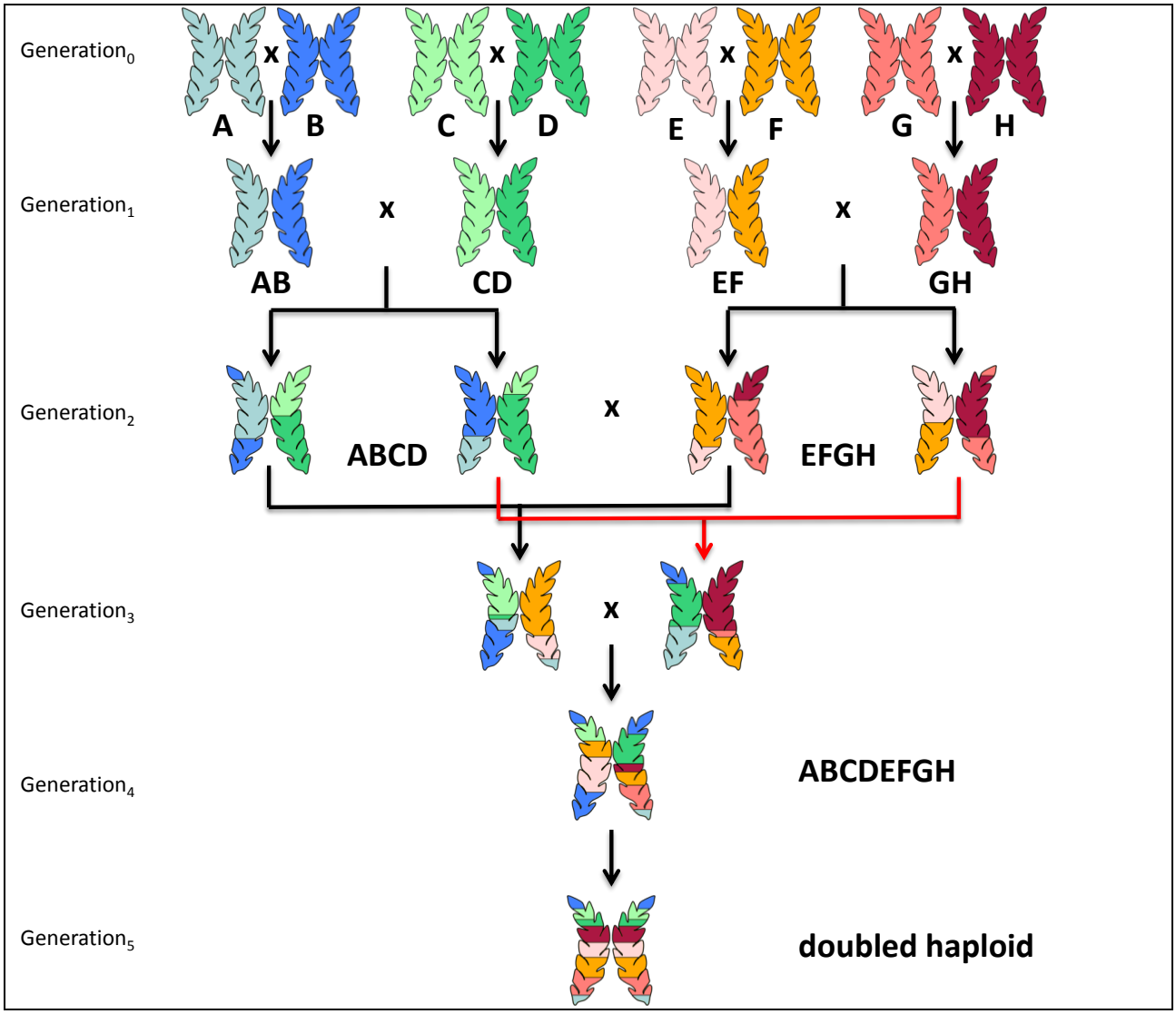

Fig. 4: Crossing scheme of the eight parent MAGIC cross.
A=Ackermanns Bavaria, B=Barke, C=Heils Franken, D=Heines Hanna, E=Pflugs Intensiv, F=Ragusa, H=Ackermanns Danubia, H=Criewener 403. Based on Cavanagh et al. (2008)

Table 2: Subfamilies and sub-subfamilies from the crossing scheme of the MAGIC population. 21 kernels from each subfamily were sent to produce DH-lines.

Subfamily	Sub-subfamilies	Crossing pattern
1	3	((Ackermanns Bavaria x Barke) x (Heils Franken x Heines Hanna) P 1-4) x (Pflugs Intensiv x Ragusa) x ((Ackermanns Danubia x Criewener 403) P 9-12)
2	4	((Ackermanns Bavaria x Barke) x (Heils Franken x Heines Hanna) P 5-8) x ((Pflugs Intensiv x Ragusa) x ((Ackermanns Danubia x Criewener 403) P 1-4)
3	3	((Ackermanns Bavaria x Barke) x (Heils Franken x Heines Hanna) P 9-12) x ((Pflugs Intensiv x Ragusa) x (Ackermanns Danubia x Criewener 403) P 5-8)
4	3	((Ackermanns Bavaria x Barke) x (Heils Franken x Heines Hanna) P 13-16) x ((Pflugs Intensiv x Ragusa) x (Ackermanns Danubia x Criewener 403) P 13-16)
5	3	((Heils Franken x Heines Hanna) x (Ackermanns Danubia x Criewener 403) P 1-4) x ((Ackermanns Bavaria x Barke) x (Pflugs Intensiv x Ragusa) P 13-16)
6	2	((Heils Franken x Heines Hanna) x (Ackermanns Danubia x Criewener 403) P 5-8) x ((Ackermanns Bavaria x Barke) x (Pflugs Intensiv x Ragusa) P 1-4)
7	3	((Heils Franken x Heines Hanna) x (Ackermanns Danubia x Criewener 403) P 9-12) x ((Ackermanns Bavaria x Barke) x (Pflugs Intensiv x Ragusa) P 9-12)
8	2	((Heils Franken x Heines Hanna) x (Ackermanns Danubia x Criewener 403) P 13-16) x ((Ackermanns Bavaria x Barke) x (Pflugs Intensiv x Ragusa) P 5-8)
9	3	((Ackermanns Bavaria x Barke) x (Ackermanns Danubia x Criewener 403) P 1-4) x ((Pflugs Intensiv x Ragusa) x (Heils Franken x Heines Hanna) P 1-4)
10	3	((Ackermanns Bavaria x Barke) x (Ackermanns Danubia x Criewener 403) P 5-8) x ((Pflugs Intensiv x Ragusa) x (Heils Franken x Heines Hanna) P 13-16)
11	3	((Ackermanns Bavaria x Barke) x (Ackermanns Danubia x Criewener 403) P 9-12) x ((Pflugs Intensiv x Ragusa) x (Heils Franken x Heines Hanna) P 9-12)
12	3	((Ackermanns Bavaria x Barke) x (Ackermanns Danubia x Criewener 403) P 13-16) x ((Pflugs Intensiv x Ragusa) x (Heils Franken x Heines Hanna) P 13-16)

P=plant, symbolizes a particular plant that was used for the crossing

2.2 Phenotyping analyses

The phenotypic experiments were carried out at the experimental research station at University of Bonn, Poppelsdorf, Institute for Plant Breeding in 2010, 2011 and 2012. A preliminary test for drought tolerance was conducted in 2010, characterising a set of spring barley genotypes including the parents of the MAGIC population under well watered and terminal drought conditions. The MAGIC DH-lines and the parents were tested under well watered and terminal drought conditions in the vegetation period of 2011 and 2012.

2.2.1 Preliminary experiment 2010

The experiment was set up in a polytunnel which enables natural growth behaviour under water controlled conditions. 30 spring barley genotypes were selected to be phenotyped at terminal drought and well watered conditions. The experiment was conducted in 22 x 22 cm plastic pots containing 11.5 l of Terrasoil® (a mixture of top soil, silica sand, milled lava and peat dust, Terrasoil®, Cordel & Sohn, Salm, Germany). The pots were arranged in a split plot design with four replications. Twelve seeds per pot were sown on the 7th of April 2010 to simulate a plant population within the pot. Water was supplied with a computer mediated drip irrigation system three times a day (6:15 am, 0:15 pm, 6:15 pm) to hold the volumetric water content (VWC) at 40%. Terminal drought stress started 30 days after sowing (DAS). It was aimed to reduce the water content in the pots during 21 days to the permanent wilting point (15% VWC) and to stabilize it at 15% for seven days. Subsequently the pots under terminal drought were re-watered after 28 days of reduced water supply to gain approximately 40% VWC within a few hours. The well watered treatment was continuously kept at 40% VWC. Weather data was collected by HOBO U30 weather station measuring the following parameters every 15 minutes:

- volumetric water content with HOBO soil moisture smart sensors S-SMB-M003
- soil temperature with HOBO soil temperature smart sensor S-TMB-M006
- air temperature and radiation with HOBO smart sensor S-THB-M002

Fertilizer, fungicides and insecticides were applied referring to agricultural practice. The recorded traits, the method and dates of measurement in days after sowing (DAS) are listed in Table 3.

Table 3: List of phenotypic traits and their abbreviations, measured unit, methods and time after sowing (DAS) investigated in preliminary experiment in 2010

Trait	Abbr.	Unit	Methods of measurement	DAS
repeated measurements				
number of tillers	**NT**	no/plant	number of tillers	33-82
number of leaves	**NL**	no/plant	number of fully developed leaves	33-82
number of green leaves	**NGL**	no/plant	number of leaves with at least 50% photosynthetic activity	33-82
number of yellow leaves	**NYL**	no/plant	number of leaves with less than 50% photosynthetic activity	33-82
plant height	**PLH**	cm	distance between soil ground level and tip of awns in cm	33-82
SPAD value	**SPAD**		value measured with SPAD-502plus (Konica Minolta)	33-61
wilting score	**WS**	0 – 9	Dedatta et al., 1988	33-61
invasive measurements				
plant fresh biomass	**PFB**	g/plant	amount of fresh biomass	61
plant dry biomass	**PDB**	g/plant	amount of dry biomass	61
water content	**WC**	%	gravimetric measured % of water in plant	61
root biomass	**RB**	g/plant	amount of dry root biomass	61
root length	**RL**	cm	root length starting from nod	61
leaf area	**LA**	cm^2	whole leaf area/plant	61
green leaf area	**GLA**	cm^2	green leaf area/plant	61
yield and yield components				
straw biomass	**SB**	g/plant	amount of dry straw biomass	harvest
number of ears	**NE**	no/plant	number of ears	harvest
number of ripe ears	**NRE**	no/plant	number of ripe ears	harvest
number of green ears	**NGE**	no/plant	number of green ears	harvest
number of kernels	**NK**	no/ear	amount of kernels per ear	harvest
grain yield	**YLD**	g/plant	weight of barley grain	harvest
thousand kernel weight	**TKW**	gram	weight of 1000 kernels	harvest
harvest index	**HI**	0 – 1	ratio of generative to vegetative biomass	harvest

DAS=days after sowing
Abbr.=abbreviation

Seven of these traits were repeatedly scored (listed in Table 3 as repeated measurements) to evaluate the most significant trait and date*trait interaction for drought tolerance phenotyping, starting from 33 DAS (before water supply was reduced), 40 DAS, 47 DAS, 54 DAS, 61 DAS and 82 DAS. SPAD value and wilting score could not be scored at 82 DAS due to reduced chlorophyll content and advanced ripening progress in the plants. Yield and yield components were scored after harvest (listed in Table 3 as yield and yield components).

2.2.2 Phenotyping experimental setup 2011 and 2012

The trial in 2011 and 2012 was located at the same experimental site like 2010. 534 MAGIC DH-lines, the parents of the MAGIC cross and a set of check varieties of spring barley were sown into 19.5 x 25.5 cm plastic pots, filled with 5.5 l of Terrasoil®. Two water treatments were evaluated, well watered and terminal drought. Four seeds per genotype for each treatment were sown at the 4th of April 2011 and 3rd of April 2012. The experiment was arranged in an augmented experimental block design in the polytunnel, using 20 varieties as checks, providing replicates every 20 pots. The experiments contained 1184 pots, 1068 pots with MAGIC DH-Lines, 116 pots with check varieties. The terminal drought conditions started 35 DAS and extended to five weeks. It was aimed to reduce the water content in the pots during 21 days to the permanent wilting point (15% VWC) and stabilize it at 15% for seven days. At 65 DAS the pots under terminal drought conditions were re-watered slowly to 30% VWC, and re-watered to 40% VWC at 73 DAS. The recorded traits, the method and dates of measurement for 2011 and 2012 are listed in Table 4. Leaf senescence was measured repeatedly and evaluated as area under drought progress curve (AUDPC), which was calculated from leaf senescence taking time between measuring dates into account.

Table 4: List of phenotypic traits and their abbreviations, measured unit, methods and time after sowing (DAS) investigated in the MAGIC population in 2011 and 2012

Trait	Abbr.	Unit	Methods of measurement
sum of area under drought progress curve	**AUDPC**		Shaner and Finney, 1977
above ground biomass	**AGB**	g/plant	amount of dry above-ground biomass
days to heading	**DHE**	D	number of days from sowing until emergence of 3 cm of awns
grain filling period	**DGF**	D	number of days from heading to hard dough ripening
floret abortion	**FA**	no/ear	amount of sterile fully developed florets
number of ears	**NE**	no/plant	number of ripe ears
number of kernels	**NK**	no/ear	amount of kernels per ear
plant height	**PLH**	cm	distance between soil ground level and tip of awns in cm
thousand kernel weight	**TKW**	gram	weight of 1000 kernels
grain yield	**YLD**	g/plant	weight of barley grain

Abbr. = abbreviation

2.2.3 Time domain spectroscopy

The THz-TDS used in this research project was built at University of Marburg, Department of Physics, Fachbereich Experimentelle Halbleiterphysik, Prof. Koch, Germany, and will be explained in details hereafter.

The measurements were conducted using a THz-TDS system based on an ER:Fiber laser providing around 65 fs pulses with a central wavelength of 1550 nanometre (nm) at a repetition rate of around 80 MHz. A fraction of this pulse was sent through a polarization maintaining fiber-piezo-driven fiber stretcher producing a delay of around 15 ps at 10 THz. The pulses were used to excite a LT-InGaAs stripline photoconductive emitter. The remaining fraction of the pulse was used to gate an LT-InGaAs dipole photoconductive detector. After emission, the THz radiation was collected and refocused by a pair of polyethylene lenses producing an around 3 mm focus where the sample was placed (Fig. 2).

Measuring a reference first, a pulse without sample in the THz beam path and second a pulse with the sample allowed for the simultaneous extraction of the refractive index, the absorption coefficient (a), the thickness of the sample (b) providing detailed information of the object (Scheller et al., 2009).

The measurements with the THz sensor were carried out on plants grown in a climate chamber, to rely on accurately defined climate terms during weeks of cultivation and measurements. Einheitserde Typ VM, Werkverband E.V., Germany, was filled into 96 QuickPot plates, HerkuPlast, Kubern GmbH, Germany. Each pot was 7.8 * 3.8 * 3.8 cm in size, with a soil volume of 75 cc. Two seeds of each genotype were sown into the soil, watered and cultivated in the climate chamber. Ten DAS the weaker seedling was removed from the soil. The 96 QuickPot plate was placed into a water bath 16 DAS to reach maximum water content. Afterwards the plate was removed after eleven hours and left in the climate chamber for two hours. Subsequently the plants were removed from the 96 QuickPot plate into 7 * 8 cm pots from Pöppelmann, Lohne, Germany to assure uniform drying. These pots were lined with a 17.5 * 10 cm Crispac, cut to 12 * 10 cm from Baumann Saatzuchtbedarf, Waldenburg, Germany preventing the soil from rapid drying. The plants were left in the climate chamber for 96 hours and were only removed from the climate chamber for the measurement with the THz sensor every 24 hours. The measurements took place at INRES, department of Crop Genetics and Biotechnology, Plant Breeding in Bonn. The leaves of the plants were marked with an ink pen and measured every 24 hours at the same position of the leaves. The two oldest leaves per plant were used for measurement. A program to process the measured data was written in MATLAB (The MathWorks Inc.) by Ralf Gente, University Marburg. The measured THz value was automatically recalculated into following values taking the leaf thickness into account: water volume (%), water content (%), plant material (%). The values for water content were used to calculate the traits listed in Table 5, that were used in QTL mapping.

Table 5: Calculated values measured with THz-TDS-System used for marker-trait-sensor association

Trait	Abbr.	Unit	Methods of measurement
water content	WCT	%	water content after 96 hours of not watering
water loss	WL	%	difference between basic and final water content value

Abbr. = abbreviation

2.3 Genotyping

The DNA isolation from the MAGIC DH lines and their parents was conducted in the lab at University of Bonn, Institute of Plant Breeding in Bonn. TraitGenetis in Gatersleben, Germany was commissioned to genotype the DNA with the Illumina 9K iSelect-SNP chip (Comadran et al., 2012).

2.3.1 Extraction of genomic DNA

For the isolation, frozen leaf material of 2-week-old seedlings grown in the greenhouse was harvested for each MAGIC DH-line. Per line, leaf material from three MAGIC DH-lines was pooled. 30 to 50 mg of fresh leaf material was transferred into a 96well Collection Microtube from Qiagen, Hilden, Germany. One tungsten bead (Qiagen) per well was added. Leaf samples were homogenized using a TissueLyser bead mill (Qiagen) at 20 Hz for one minute and centrifuged at 3000 rpm for two minutes. 300 µl of fresh buffer working solution was added, shaken gently. The samples were incubated for one hour at 65°C, gently shaken every 15 minutes. Afterwards the samples were cooled down for five minutes on ice. 300 µl of chloroform/isoamyl alcohol (24:1) was added to each sample and mixed well for 15 minutes under the hood. The samples were centrifuged for ten minutes at 6000 rpm. 150 µl of the supernatant was transferred into a new set of 96well Collection Microtubes, which was prepared with 150 µl of ice cold isopropanol and stored in the freezer. The tubes were inverted 10 times and centrifuged for 30 minutes at 6000 rpm. The supernatant was discarded and the DNA-pellets washed with 300 µl of 70% ETOH. The samples were centrifuged again for ten minutes at 6000 rpm, and the supernatant was discarded. The DNA-pellets were dried and dissolved in 100 µl of TE-Buffer (modified protocol for DArT marker analysis: www.diversityarrays.com). DNA concentration was measured with Nanodrop spectrophotometer 2000c, Thermo Fisher Scientific Inc, and rechecked on a 2% agarose gel to check the quality and to quantify the amount of DNA by staining with ethidium bromide after electrophoresis. If required, samples were diluted to achieve a final concentration of 50 ng/µl. A sample volume of 25 µl was provided for TraitGenetics for SNP genotyping.

Buffer and solutions

Buffers and solutions used in the DNA extraction will be itemised.

Extraction buffer for 96 samples

Sorbitol	350 mM
TrisHCl	100 mM
EDTA	500 mM

Lysis Buffer Stock for 96 samples

Tris	20 mM
EDTA	5 mM
NaCl	200 mM
CTAB	2%

Sarcosyl stock 5%

Lauryl sarcosine	170.42 mM
H2O (high ourity)	ad 500 ml

Fresh buffer working solution for 96 samples

Sodiumdisulfite	0.5 g
PVP-40	2.0 g
Extraction buffer	41.6 ml
Lysis buffer	41.6 ml
Sarcosyl stock	16.6 ml

Chloroform/isoamyl alcohol 24:1

24 volumes chloroform and one volume isoamyl alcohol

2.3.2 Molecular maker genotyping and data cleaning

The Illumina 9k iSelect chip from TraitGenetics was used to genotype 542 barley genotypes (534 MAGIC DH-lines, eight parents) with 7864 SNP markers. The Data was transcribed into a binary matrix, for each genotype the minor represented allele was defined as zero, the major represented allele was defined as one.

Data cleaning included the following steps: Monomorphic markers were removed from the dataset. Markers with missing data for the parents were removed. Markers with a minor allele frequency (MAF) < 5% were removed. Heterozygous scores were scored as missing data. Since the MAGIC DH-lines where doubled haploid lines and 100% inbred, the genotypic data were treated as effectively haploid.

2.4 Statistical analyses

The statistical analyses were conducted using the software SAS version 9.2 (SAS Institute 2008) and R 2.15.1, using the package R/mpMap (Huang and George, 2011).

2.4.1 Preliminary phenotyping experiments

The means of the data, their variance and covariance were modelled using a mixed linear model with the Proc mixed procedure in SAS 9.2. The unknown covariance parameters were

estimated with the maximum likelihood method. Asymptotic tests were requested for all covariance parameters.

$$Y_{ijkl} = \mu + G_i + D_j + T_k + G_i*D_j + G_i*T_k + D_j*T_k + G_i*D_j*T_k + B_l + \epsilon_{ijkl}$$

Where Y_{ijkl} is response variable; μ is general mean; G_i is the random effect of *i*-th genotype; D_j is the fixed effect of *j*-th sampling date; T_k is the fixed effect of *k*-th treatment; G_i*D_j is the random interaction effect of *i*-th genotype with *j*-th sampling date; G_i*T_k is the random interaction effect of *i*-th genotype with *k*-th treatment; D_j*T_k is the fixed interaction effect of *j*-th sampling date with *k*-th treatment; $G_i*D_j*T_k$ is the random interaction effect of *i*-th genotype with *j*-th sampling date and with *k*-th treatment; B_l is the random effect of the *l*-th block and ϵ_{ijkl} is random errors.

Significant differences between treatments, genotypes, sampling dates and their interactions were calculated using pair-wise contrasts, using the LSMEANS statement with the DIFF option in Proc mixed.

2.4.2 Phenotyping experiments of MAGIC DH-lines 2011 and 2012

Due to the augmented experimental design, the data was analyzed by restricted maximum likelihood (REML) to fit a mixed model with check varieties as fixed effects and non-replicated MAGIC DH-lines as random effect (Comadran et al., 2008). Best linear unbiased predictors were requested. The mean, variance and covariance were modelled using the following mixed linear model with Proc mixed procedure in SAS 9.2.

$$Y_{ijk} = \mu + L_i + T_j + C_k + L_i*T_j + \epsilon_{ijk}$$

Where Y_{ijk} is response variable; μ is general mean; L_i is the random effect of *i*-th DH-line; T_j is the fixed effect of *j*-th treatment; C_k is the random effect of the *k*-th calendar year; L_i*T_j is the random interaction effect of *i*-th DH-line with *j*-th treatment and ϵ_{ijk} is the random error.

2.4.3 Genetic correlation of MAGIC DH-lines

Genetic correlations between trait values were calculated with Proc corr procedure for each treatment. Lsmeans were used to calculate the Pearson's coefficient (r).

2.4.4 Population structure

The principal component analysis (PCA) was conducted as in Price et al. (2006) using Proc princomp in SAS 9.2 to clarify population structure in the MAGIC DH-lines. The PCA was calculated with 5117 SNP markers and 533 MAGIC DH-lines using the SNP markers as covariance matrix. Significant principal components were identified according to Franklin et al. (1995).

2.4.5 Linkage disequilibrium

Pair-wise measures of linkage disequilibrium (LD) were calculated (R^2) for the established SNP set and after data cleaning using SAS 9.2. Information about linkage groups and genetic position of the SNPs were used from Comadran et al. (2012). Values were plotted for each linkage group by genetic distance. R/LDheatmap was used to construct heat maps for each linkage group. The same procedure was conducted with the number of SNP marker that was used to construct the genetic map with R/mpMap.

2.4.6 Genetic map construction for the MAGIC DH-lines

The genetic map of the seven linkage groups of barley was constructed using R/mpMap (Huang and George, 2011). Altogether 1416 SNP markers and 533 MAGIC DH-lines were considered in map construction during the following steps: Recombination fraction between all pair of loci was calculated using the function 'mpestrf'. The markers were grouped into linkage groups based on the estimated recombination fraction and logarithm of the odds (LOD) score using 'mpgroup'. Within each linkage group, markers were ordered with 'mporder', minimizing the total chromosome length based on the maximum likelihood estimates of recombination fractions (Huang et al., 2012). Map positions were computed using 'computemap' as the sum of adjacent recombination fractions transformed by the Kosambi map function. The haplotypes are constructed from marker data by identifying the parental origin of the marker alleles (Huang and George, 2011). Recombination events for all MAGIC DH-lines were estimated using 'mpprob'. It calculates the multipoint probability at each locus that the observed genotype is inherited from each of the eight founders, using the information from flanking markers with the outcome of haplotype blocks (Huang et al., 2012).

2.4.7 QTL mapping

The QTL detection was carried out as a multiple QTL model in SAS 9.2 using proc mixed. Forward/backward selection or so called multi-locus analysis, according to Bauer et al. (2009) a very effective selection strategy was applied within the model to reduce the number of false-positive QTL. The multi-locus selection strategy was described by Sillanpaa and Corander (2002) and applied by Kilpikari and Sillanpaa (2003). During the first round of multi-locus analysis a single-locus analysis was conducted. According from these results, the marker with the most significant effect (in regards to the *P* value) was chosen as fixed cofactor in the model for the following estimation. With the information from the extended model the marker effects are estimated again, markers were included or excluded from the model, regarding their performance.

This procedure was repeated until no further significant markers were found (Bauer et al., 2009). Beside incorporation of the control of the QTL false-discovery rate into statistical model the multi-locus analysis should provide a better balance declaring too many false-positive QTL and sacrificing power to detect QTL that have small effects (Benjamini and Yekutieli, 2005). Cross validation was used to reduce high bias of explained variance. QTL were calculated using two different approaches, common "binary" approach (BA) and "haplotype" approach (HA). The genetic marker information from the binary matrix was used for the BA, resulting in two allele information per marker. The calculated haplotype probabilities for each parent, or haplotype blocks, were used in the HA, resulting in an allele information for each parent if present in the genome. The following model was used:

$$Y_{ijkl} = \mu + M_i + L_j(M_i) + T_k + C_l + M_i*T_k + L_j(M_i*T_k) + \epsilon_{ijkl}$$

Where Y_{ijkl} is response variable; μ is general mean; M_i is the fixed effect of *i*-th marker; $L_j(M_i)$ is the random effect of *j*-th MAGIC DH-line nested in the *i*-th marker genotype; T_k is the fixed effect of *k*-th treatment; C_l is the random effect of the *l*-th calendar year; M_i*T_k is the fixed interaction effect of *i*-th marker genotype with the *k*-th treatment, $L_j(M_i*T_k)$ is the random effect of the of *j*-th MAGIC DH-line nested in the *i*-th marker genotype interaction with the *k*-th treatment and ϵ_{ijkl} is the residual of $Y_{ijkl.}$

Significant main marker effects and marker*treatment interactions with $p \leq 0.05$ or 0.001 (depending on the trait) were accepted as putative QTL and included in the next iteration of the cross validation leading to the final hierarchical model with applied multi-locus analysis:

$$Y_{ijkl} = \mu + \sum QTL + M_i + L_j(M_i) + T_k + C_l + M_i*T_k + L_j(M_i*T_k) + \epsilon_{ijkl}$$

Where $\sum QTL$ represents the detected QTL from multi-locus analysis.

2.4.8 Epistatic interaction model

Digenic epistatic interactions were tested with SAS 9.2 using the cross validation multi-locus approach and resulted in the following hierarchical model:

$$Y_{ijklm} = \mu + \sum QTL + M1_i + M2_j + M1_i*M2_j + L_k(M1_i*M2_j) + T_l + C_m + M1_i*M2_j*T_l + L_k(M1_i*M2_j*T_l) + \epsilon_{ijklm}$$

Where Y_{ijklm} is response variable, μ is general mean, $\sum QTL$ represents the detected QTL from multi-locus analysis, $M1_i$ and $M2_j$ are fixed effects of the *i*-th marker and the *j*-th marker, respectively; $M1_i*M2_j$ is the fixed interaction effect of the *i*-th M1 marker genotype with the *j*-th M2 marker genotype; $L_k(M1_i*M2_j)$ is the random effect of the *k*-th DH-line nested in the *i*-th M1 marker genotype and *j*-th M2 marker genotype interaction; T_l is the fixed effect of *l*-th treatment; C_m is the random effect of the *m*-th calendar year; $M1_i*M2_j*T_l$ is the fixed interaction of the *i*-th M1 marker

genotype with the *j*-th M2 marker genotype and the *l*-th treatment, $L_k(M1_i*M2_j*T_{l)}$ is the random effect of the *k*-th DH-line nested in the *i*-th M1 marker genotype, *j*-th M2 marker genotype and *l*-th treatment interaction and ϵ_{ijklm} is the residual of $Y_{ijklm.}$

2.4.9 Multiple mean comparison

Multiple mean comparison were conducted with SAS 9.2 within the QTL mapping approach for a selected group of allele effects from the HA. Pairwise differences of the Lsmeans were calculated with Proc mixed using the Diff statement.

3. Results

First, the results from the preliminary phenotyping and the resultant traits for phenotyping the MAGIC population are described. Subsequently the phenotypic variations within the MAGIC population and in comparison with the parents are characterized for the traits of interest including the THz-values. The genetic constitution of the MAGIC population is characterized through analysis of population structure and linkage disequilibrium. The results for genetic linkage map and haplotype block building are presented. The detected QTL with both approaches and finally the results for digenic marker interactions for the traits are presented.

3.1 Preliminary phenotyping experiment: traits and analysis of variance

The parents of the MAGIC population were characterized with 22 agronomical traits under 2 water treatments (well watered and terminal drought) in the polytunnel in 2010. The results from analysis of variance for the repeated measurements are listed in Table 6, the ones from destructive measurements and yield and yield component related traits in Table 7. Based on the results from Table 6 significant differences between the genotype, treatment and genotype*treatment interaction were scored starting from 47 DAS to 61 DAS. The evaluation of SPAD was time consuming and less significant. The same accounted to the leaf orientated traits (NL, NGL, NYL), the cost-significant benefit analysis has no justifiable ratio. These traits will therefore not be scored in the MAGIC DH-lines. NT and PLH are the most distinctive traits concerning significant differences between genotypes, treatment as well as genotype*treatment interaction already at early stage of plant development (33 DAS). Root related traits (RB, RL) listed in Table 7 showed no significant results for the listed effects and plant biomass related traits (FB, PB, WC) showed no significant genotype*treat interaction. The destructive measurements were highly time consuming and will not be scored in the MAGIC DH-lines despite to significant results in leaf related traits (LA, GLA). All traits evaluated at harvest (Table 7), except NGE and HI, show significant results for the effects and will be scored in the MAGIC DH-Lines.

Table 6: Degrees of freedom, F and p value of fixed effects in the analysis of variance for the parents of MAGIC population for repeated traits

			33 DAS		40 DAS		47 DAS		54 DAS		61 DAS		82 DAS	
Trait	Effect	DF	F	P	F	P	F	P	F	P	F	P	F	P
NT	genotype	7	2.95	0.0255	4.54	0.0032	8.08	0.0001	3.72	0.0090	18.22	<0.0001	8.35	0.0060
	treat	1	0.29	0.6280	2.58	0.2065	2.17	0.2374	63.92	0.0041	236.29	0.0006	51.50	0.0056
	genotype*treat	7	2.44	0.0538	0.72	0.6560	1.03	0.4370	16.20	<0.0001	3.74	0.0088	5.52	0.0390
NL	genotype	7	1.99	0.1054	1.66	0.1725	2.42	0.0555	3.04	0.0226	3.55	0.0112	0.13	0.9921
	treat	1	9.51	0.0540	8.78	0.0594	10.29	0.0490	114.34	0.0017	149.83	0.0012	23.53	0.0167
	genotype*treat	7	2.33	0.0631	1.20	0.3475	2.29	0.0665	2.24	0.0720	4.79	0.0024	1.11	0.4712
NGL	genotype	7	1.99	0.1054	1.54	0.2071	1.75	0.1512	4.02	0.0061	4.96	0.0019	8.04	0.0067
	treat	1	9.51	0.0540	7.07	0.0764	15.99	0.0280	182.08	0.0009	178.29	0.0009	0.00	1.0000
	genotype*treat	7	2.33	0.0631	0.82	0.5780	2.07	0.0927	3.89	0.0072	3.87	0.0074	0.23	0.9592
NYL	genotype	7	NA	NA	6.45	0.0004	4.91	0.0021	1.53	0.2116	2.25	0.0713	1.96	0.1967
	treat	1	NA	NA	0.07	0.8105	1.95	0.2570	0.05	0.8380	29.61	0.0122	53.29	0.0053
	genotype*treat	7	NA	NA	0.94	0.4990	2.59	0.0432	0.60	0.7495	2.23	0.0737	3.06	0.1181
PLH	genotype	7	10.94	<0.0001	8.30	0.0001	6.98	0.0002	3.50	0.0120	7.03	0.0002	0.35	0.9052
	treat	1	0.80	0.4358	2.16	0.2380	3.13	0.1752	16.40	0.0271	77.17	0.0031	10.84	0.0460
	genotype*treat	7	0.56	0.7806	1.25	0.3206	5.25	0.0014	3.50	0.0120	1.96	0.1102	1.13	0.4634
SPAD	genotype	7	1.93	0.1148	1.46	0.2338	10.57	<0.0001	7.66	0.0001	6.99	0.0002	8.04	0.0067
	treat	1	1.67	0.2868	0.03	0.8777	34.76	0.0097	56.56	0.0049	122.03	0.0016	0.00	1.0000
	genotype*treat	7	0.95	0.4893	1.37	0.2685	0.31	0.9415	1.11	0.3904	3.59	0.0107	0.23	0.9592
WS	genotype	7	NA	NA	NA	NA	2.90	0.0277	6.37	0.0004	1.07	0.4162	0.35	0.9052
	treat	1	NA	NA	NA	NA	155.50	0.0011	766.97	0.0001	44.27	0.0069	10.84	0.0460
	genotype*treat	7	NA	NA	NA	NA	5.51	0.0010	0.85	0.5618	0.80	0.5983	1.13	0.4634

Where: P= P value with *: 0.01 < P < 0.05 level, ** : 0.001 < P < 0.01, *** P < 0.001, F=F value, DF=degree of freedom, NA=data not available

DAS= days after sowing

Genotype = Ackermanns Bavaria, Ackermanns Danubia, Barke, Criewener, Heils Franken, Heines Hanna, Pflugs Intensiv, Ragusa

Treat= treatment: ww (well watered), td (terminal drought)

Traits: NT (number of tillers), NL (number of leaves), NGL (number of green leaves), NYL (number of yellow leaves), PLH (plant height), SPAD (SPAD value), WS (wilting score.

Table 7: Degrees of freedom, F and p value of fixed effects in the analysis of variance for the parents of MAGIC population for non-recurrent traits

61 DAS					Harvest				
Trait	Effect	DF	F	P	Trait	Effect	DF	F	P
PFB	genotype	7	13.65	0.0014	SB	genotype	7	8.23	0.0063
	treat	1	563.02	0.0002		treat	1	545.98	0.0002
	genotype*treat	7	2.32	0.1861		genotype*treat	7	3.06	0.1185
PB	genotype	7	0.99	0.5073	NE	genotype	7	12.80	0.0017
	treat	1	61.28	0.0043		treat	1	241.36	0.0006
	genotype*treat	7	0.46	0.8298		genotype*treat	7	11.98	0.0074
WC	genotype	7	3.67	0.0540	NRE	genotype	7	12.66	0.0017
	treat	1	33.93	0.0101		treat	1	337.37	0.0004
	genotype*treat	7	0.32	0.9147		genotype*treat	7	5.04	0.0468
RB	genotype	7	3.93	0.0457	NGE	genotype	7	0.00	1.0000
	treat	1	5.79	0.0953		treat	1	0.00	1.0000
	genotype*treat	7	1.79	0.2994		genotype*treat	7	2.64	0.1513
RL	genotype	7	0.14	0.9913	NK	genotype	7	86.98	<0.0001
	treat	1	2.15	0.2385		treat	1	5.23	0.1063
	genotype*treat	7	0.23	0.9576		genotype*treat	7	1.28	0.4056
LA	genotype	7	14.39	0.0011	YLD	genotype	7	2.71	0.1055
	treat	1	99.04	0.0022		treat	1	766.16	0.0001
	genotype*treat	7	6.10	0.0319		genotype*treat	7	1.01	0.5141
GLA	genotype	7	8.97	0.0049	TKW	genotype	7	29.96	0.0001
	treat	1	272.67	0.0005		treat	1	253.05	0.0005
	genotype*treat	7	5.37	0.0413		genotype*treat	7	9.10	0.0136
					HI	genotype	7	3.86	0.0477
						treat	1	4.84	0.1151
						genotype*treat	7	0.33	0.9090

Where: P= P value with *: 0.01 < P < 0.05 level, ** : 0,001 < P < 0.01, *** P < 0.001, F=F value, DF=degree of freedom

DAS=days after sowing

Genotype=Ackermanns Bavaria, Ackermanns Danubia, Barke, Criewener, Heils Franken, Heines Hanna, Pflugs Intensiv, Ragusa

Treat=Treatment: ww=well watered, td=terminal drought

Traits: PFB (plant fresh biomass), PB (plant dry biomass), WC (water content), RB (root biomass), RL (root length), LA (leaf area), GLA (green leaf area), SB (straw biomass), NE (number of ears), NRE (number of ripe ears), NGE (number of green ears), NK (number of kernels), YLD (grain yield), TKW (thousand kernel weight), HI (harvest index)

3.2 Phenotypic variation in MAGIC DH-lines

The 534 MAGIC DH-lines and their parents were investigated in an augmented experimental design in pots for two consecutive years. Environmental and phenotypic results are listed in the following chapter.

3.2.1 Environmental factors

The soil moisture condition in the pots for both water treatments in both years in the poly tunnel is shown in Fig. 5. The water supply via the irrigation system was accurately used and allowed a similar soil moisture trend, making both experimental years comparable for environmental effects. The blue line represents the soil moisture content under well watered conditions, the red line under terminal drought conditions in years 2011 and 2012.

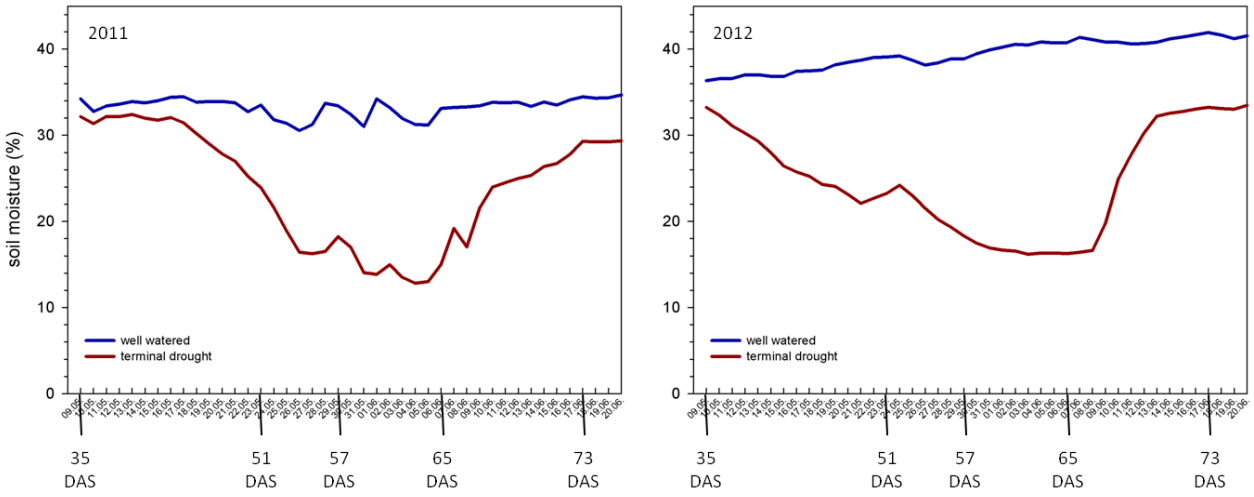

Fig. 5 Soil moisture content (%) for well watered (blue) and terminal drought (red) treatment in 2011 and 2012

3.2.2 Means and analysis of variance for phenotypic traits

Based on the results from preliminary investigation of the MAGIC parental genotypes in 2010 the 534 MAGIC DH-lines were investigated for 10 traits related to yield at two different water treatments in two consecutive years (Table 4). The phenotypic values for the traits of interest were investigated with multiple comparisons between the parents within each treatment (Table 8). The parents showed significant differences within each treatment for all traits, except AUDPC, DGF and YLD under terminal drought conditions. At most of the traits the parents clustered into two groups which were significant from each other. Multiple comparisons at the traits NK and PLH under well watered conditions revealed the clustering of the parents into four groups.

Table 8: Multiple mean comparisons of the phenotype values between the MAGIC parents

Trait	Treat	AB		AD		B		C		HF		HH		PI		R	
AUDPC	ww	33.50	b	37.88	a	38.50	a	37.63	a	42.63	a	28.38	b	41.13	a	33.63	b
	td	62.25	a	64.00	a	58.00	a	64.00	a	64.00	a	65.50	a	63.13	a	59.63	a
AGB	ww	14.17	a	12.06	a	9.09	b	11.53	a	10.53	b	11.28	a	9.94	b	13.83	a
	td	10.30	a	6.41	b	6.11	b	6.82	a	6.44	b	5.36	b	5.88	b	6.97	a
DHE	ww	55.00	b	56.25	b	56.50	a	54.25	b	54.50	b	53.25	b	54.50	b	56.75	a
	td	54.00	b	56.75	a	56.00	b	55.00	a	53.00	b	55.00	a	55.25	a	56.25	a
DGF	ww	41.50	a	39.75	a	40.00	a	37.00	b	37.25	b	38.00	b	35.75	b	38.00	b
	td	40.00	a	37.00	a	40.00	a	37.25	a	38.25	a	36.75	a	36.25	a	37.50	a
FA	ww	1.43	b	0.98	b	2.55	b	1.67	b	3.98	b	1.43	b	1.98	b	13.83	a
	td	2.03	b	0.99	b	0.47	b	2.17	b	3.78	b	2.84	b	2.58	b	11.89	a
NE	ww	5.38	b	4.44	b	4.38	b	4.06	a	4.31	b	4.44	b	4.06	a	2.81	a
	td	4.85	b	2.94	b	3.38	b	3.00	b	3.13	b	2.50	a	2.81	a	1.63	a
NK	ww	20.43	bc	23.94	b	17.26	c	23.71	bc	19.89	c	21.48	bc	22.10	bc	49.37	a
	td	17.77	b	18.98	b	16.19	b	18.25	b	18.12	b	17.27	b	19.53	b	36.17	a
PLH	ww	100.75	bc	98.00	bc	69.50	a	104.00	bc	85.75	a	93.00	c	95.50	bc	106.00	b
	td	96.75	a	84.50	a	69.00	b	88.25	a	84.50	a	77.75	b	78.50	b	94.75	a
TKW	ww	54.76	a	50.54	b	51.46	a	51.15	a	56.34	a	52.63	a	49.19	b	52.28	a
	td	48.41	b	46.24	b	55.18	a	48.34	b	55.55	a	49.11	b	45.95	b	55.18	a
YLD	ww	6.31	a	5.38	b	4.09	b	5.09	b	4.89	b	5.31	b	4.75	b	7.33	a
	td	4.29	a	2.71	a	3.20	a	2.91	a	3.06	a	2.30	a	2.66	a	3.17	a

Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), DHE (days to heading), DFG (grain filling period), FA (floret abortion), NE (number of ears), NK (number of kernels), PLH (plant height), TKW (thousand kernel weight), YLD (grain yield)
Treat: ww=well watered, td=terminal drought
AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, C=Criewener 403, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa
Different letter indicate significant differences ($p<0.05$)

The mean values for scored traits under well watered and terminal drought conditions were calculated for the parents and the MAGIC DH-lines to investigate significant differences within the parents and the MAGIC DH-lines between the watering conditions (Table 9). The parents differed significantly between the watering conditions for the traits AUDPC, AGB, NE, NK, PLH and YLD. The MAGIC DH-lines were significantly different between the watering conditions for traits listed above and additional for DGF and TKW.

The mean between the parents and the MAGIC DH-lines was significantly different within each watering condition for DHE, NE, NK, TKW for terminal drought and well watered and additionally for PLH under terminal drought (Table 10).

Table 9: Mean values and comparison for scored traits under both watering conditions for the mean of the eight parents and for the MAGIC DH-lines

	Parents			MAGIC DH-lines		
Trait	ww	td		ww	td	
AUDPC	36.70	63.00	***	36.50	65.60	***
AGB	11.60	6.70	***	12.40	6.70	***
DHE	54.90	55.10		56.90	56.80	
DGF	38.20	38.00		38.50	38.00	***
FA	3.60	3.60		4.40	4.50	
NE	4.20	2.90	***	5.30	3.40	***
NK	25.50	20.80	***	21.00	17.00	***
PLH	95.90	85.00	***	92.10	79.50	***
TKW	52.20	50.30		49.70	46.80	*
YLD	5.40	3.00	***	5.60	2.80	***

With: *: 0.01 < P < 0.05, ** : 0.001 < P < 0.01, ***: P < 0.001,

Treat: ww=well watered, td=terminal drought

Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), DHE (days to heading), DFG (grain filling period), FA (floret abortion), NE (number of ears), NK (number of kernels), PLH (plant height), TKW (thousand kernel weight), YLD (grain yield)

Parents: mean of AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, C=Criewener 403, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

Table 10: Mean comparison for scored traits within each treatment (well watered and terminal drought) between the mean of the MAGIC DH-lines and the mean of the parents

	MAGIC DH-lines	Parents		MAGIC DH-lines	Parents	
Trait	ww	ww		td	td	
AUDPC	36.0	36.7		65.6	63.0	
AGB	12.4	11.6		6.7	6.7	
DHE	56.0	54.9	***	56.8	55.1	***
DGF	38.5	38.2		38.0	38.0	
FA	4.4	3.6		4.5	3.6	
NE	5.3	4.2	***	3.4	2.9	***
NK	21.0	25.5	***	17.0	20.8	***
PLH	92.1	95.9		79.5	85.0	***
TKW	49.7	52.2	***	46.8	50.3	***
YLD	5.6	5.4		2.8	3.0	

With: *: 0.01 < P < 0.05, ** : 0.001 < P < 0.01, ***: P < 0.001,

Treat: ww=well watered, td=terminal drought

Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), DHE (days to heading), DFG (grain filling period), FA (floret abortion), NE (number of ears), NK (number of kernels), PLH (plant height), TKW (thousand kernel weight), YLD (grain yield)

Parents: mean of AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, C=Criewener 403, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

Analysis of variance was calculated for all traits and treatment within the MAGIC DH-lines (Table 11) to investigate the differences within the MAGIC DH-lines. Genotypes, treatment and their interaction are in most traits highly significantly different. No significantly different effects are

found in FA and DHE which are only significant for genotypes and in DGF which are not significant for the genotype*treatment interaction (Table 11).

Table 11: Degrees of freedom, F and p value of fixed effects in the analysis of variance 534 MAGIC DH-lines over two years for non-recurrent traits

Trait	effect	DF	F	P	Trait	Effect	DF	F	P
AUDPC	genotype	533	3.79	<0.0001	NE	genotype	533	4.16	<0.0001
	treat	1	18176.14	<0.0001		treat	1	2352.16	<0.0001
	genotype*treat	533	1.38	<0.0001		genotype*treat	533	1.49	<0.0001
AGB	genotype	533	3.22	<0.0001	NK	genotype	533	8.74	<0.0001
	treat	1	8072.32	<0.0001		treat	1	822.93	<0.0001
	genotype*treat	533	1.97	<0.0001		genotype*treat	533	2.59	<0.0001
DHE	genotype	533	14.92	<0.0001	PLH	genotype	533	7.15	<0.0001
	treat	1	0.96	0.3265		treat	1	2123.14	<0.0001
	genotype*treat	533	0.5	1		genotype*treat	533	1.63	<0.0001
DGF	genotype	533	4.44	<0.0001	TKW	genotype	533	11.18	<0.0001
	treat	1	63.98	<0.0001		treat	1	561.77	<0.0001
	genotype*treat	533	0.9	0.9089		genotype*treat	533	1.68	<0.0001
FA	genotype	533	14.07	<0.0001	YLD	genotype	533	2.95	<0.0001
	treat	1	0.31	0.5791		treat	1	5921.31	<0.0001
	genotype*treat	533	1.1	0.0923		genotype*treat	533	1.95	<0.0001

Where: P= P value with *: 0.01 < P < 0.05, **: 0.001 < P < 0.01, *** P < 0.001, F=F value, DF=degree of freedom
Genotype = 533 MAGIC DH-lines
Treat= treatment: ww=well watered, td=terminal drought
Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), DHE (days to heading), DFG (grain filling period), FA (floret abortion), NE (number of ears), NK (number of kernels), PLH (plant height), TKW (thousand kernel weight), YLD (grain yield)

3.2.3 Time Domain Spectroscopy

The 534 MAGIC DH-lines and the parents were measured with the THz-TDS-Sensor to testify the water content and dehydration in leaves over time. Multiple comparisons of the MAGIC parents revealed Ackermanns Danubia as significantly different to Heines Hanna at trait WCT. Pflugs Intensiv was significantly different to Ackermanns Bavaria, Barke, Heils Franken and Heines Hanna for the trait WL. Ragusa was as well significantly different to Barke (Table 12).

Table 12: Multiple comparisons of MAGIC parents for two traits evaluated with the THz-sensor

Trait	AB		AD		B		C		HF		HH		PI		R	
WCT	80.39	ab	85.54	a	83.12	ab	82.44	ab	80.52	ab	77.83	b	81.65	ab	78.91	ab
WL	6.14	bc	3.72	abc	9.58	b	4.43	abc	7.80	bc	6.90	bc	0.00	ac	0.35	ac

Traits: WCT=water content in leaves after 96 hours without irrigation, WL= water loss, difference in water content within the leaves between 0 and 96 hours of no irrigation
AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, C=Criewener 403, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa
Different letter indicate significant differences ($p<0.05$)

The mean, minimum and maximum values for the traits were calculated to compare the performance of the MAGIC DH-lines with their parents (Table 13). The minimum – maximum range for WCT increased in the MAGIC DH-lines compared to their parents. A water content of 100% was measured after 96 hours without irrigation within the MAGIC population. Differences between the population and the parents were also evaluated with the WL. Interestingly Pflugs Intensiv is the only parent that showed no water loss in the leaves during 96 hours without irrigation. Ragusa as a second parent showed low water loss (Table 13).

Table 13: Mean, minimum (min) and maximum (max) values for THz traits for mean of MAGIC DH-lines and their parents

	WCT			WL		
	mean	min	max	mean	min	max
MAGIC DH-lines	75.5	19.8	100.0	5.1	0.0	51.2
Ackermanns Bavaria	80.4	75.8	85.0	6.1	4.7	7.6
Ackermanns Danubia	85.5	84.0	87.1	3.7	2.3	5.1
Barke	83.1	82.2	84.1	9.6	3.2	15.9
Criewener	82.4	78.9	86.0	4.4	3.3	5.5
Heils Franken	80.5	77.7	83.3	7.8	5.5	10.1
Heines Hanna	77.8	73.0	82.7	6.9	0.5	13.3
Pflugs Intensiv	81.6	80.0	83.3	0.0	0.0	0.0
Ragusa	78.9	77.1	80.7	0.4	0.0	5.9
mean parents	81.3	73.0	87.1	4.6	0.0	15.9

Traits: WCT=water content in leaves after 96 hours without irrigation, WL= water loss, difference in water content within the leaves between 0 and 96 hours of no irrigation

3.2.4 Phenotypic correlations

The genetic correlations between the traits were calculated with Lsmeans for each treatment. A total of 74 significant correlations (37 for ww and 37 for td) were calculated. The strongest positive correlation under well watered conditions was found between AGB and YLD with r=0.89, and with AGB and PLH, and AGB and NE r=0.72 and r=0.68, respectively, all highly significant. Except from correlations between YLD and NE and PLH with r=0.74 and r=0.58, respectively, other correlations between traits were rather low but still mostly highly significant.

The strongest positive correlation under terminal drought conditions was found as well between AGB and YLD with r=0.90 and highly significant. The correlation pattern did not change much under terminal drought conditions, detecting the highest values between AGB and NE and AGB and PLH with r=0.70 and r=0.59, respectively (Table 14).

Table 14: Pearson correlation coefficient (r) for traits measured in MAGIC DH-lines. Values in *italic* show correlations between traits under ww, others under td conditions; high correlations are bold.

	AUDPC	AGB	DHE	DGF	FA	NE	NK	PLH	TKW	YLD
AUDPC		*-0.15* ***	*-0.09* **	*-0.13* ***	*0.06* *	*-0.08* **	*0.01*	*-0.04*	*-0.09* **	*-0.12* ***
AGB	0.28 ***		*-0.23* ***	*0.10* ***	*-0.11* ***	***0.68*** ***	*0.28* ***	***0.72*** ***	*0.42* ***	***0.89*** ***
DHE	-0.44 ***	-0.39 ***		*0.01*	*0.03*	*-0.13* ***	*-0.11* ***	*-0.37* ***	*-0.23* ***	*-0.23* ***
DGF	-0.39 ***	-0.11 ***	0.12 ***		*-0.05*	*0.05*	*0.02*	*-0.01*	*0.12* ***	*0.14* ***
FA	0.14 ***	0.06	-0.04	-0.11 ***		*-0.14* ***	*0.28* ***	*-0.07* *	*-0.49* ***	*-0.11* ***
NE	0.15 ***	**0.70** ***	-0.21 ***	-0.05	-0.03		*-0.12* ***	*0.35* ***	*0.21* ***	***0.74*** ***
NK	0.34 ***	0.27 ***	-0.31 ***	-0.17 ***	0.32 ***	-0.02		*0.27* ***	*-0.19* ***	*0.41* ***
PLH	0.26 ***	**0.59** ***	-0.25 ***	-0.09 ***	0.05	0.27 ***	0.27 ***		*0.39* ***	***0.58*** ***
TKW	0.03	0.10	-0.17 ***	0.07 *	-0.37 ***	-0.15 ***	-0.24 ***	0.22 ***		*0.39* ***
YLD	0.33 ***	**0.90** ***	-0.42 ***	-0.12 ***	0.06 *	**0.78** ***	0.42 ***	0.49 ***	0.03	

Where: *: 0.01 < P < 0.05, **: 0.001 < P < 0.01, *** P < 0.001

Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), DHE (days to heading), DFG (grain filling period), FA (floret abortion), NE (number of ears), NK (number of kernels), PLH (plant height), TKW (thousand kernel weight), YLD (grain yield)

The values from THz-sensor were correlated with AUDPC, AGB and YLD, to search for correlations between the water content in leaves and the phenotypic traits mostly affected by the drought treatment. The result in Table 15 pointed out that there is no correlation between the water status of leaves and the traits AUDPC, AGB and yield under both water treatments.

Table 15: Pearson correlation coefficient (r) for traits measured with the THz-sensor and AUDPC, AGB and YLD. Values in *italic* are correlations between traits under ww, others under td conditions; high correlations are bold.

	AUDPC	AGB	YLD	WCT	WL
AUDPC		*-0.15* ***	*-0.12* ***	*0.02*	*0.00*
AGB	0.28 ***		***0.89*** ***	*-0.06*	*-0.04*
YLD	0.33 ***	**0.90** ***		*-0.01*	*-0.07* *
WCT	0.02	-0.06	-0.01		*-0.28* ***
WL	0.01	0.00	-0.03	-0.27 ***	

Where: *: 0.01 < P < 0.05, **: 0.001 < P < 0.01, *** P < 0.001

Traits: AUDPC (area under drought progress curve), AGB (above ground biomass), YLD (grain yield), WCT=water content in leaves after 96 hours without irrigation, WL= water loss, difference in water content within the leaves between 0 and 96 hours of no irrigation

3.3 Genetic characterisation of the MAGIC population

The Illumina 9k iSelect SNP chip was chosen for genotyping the MAGIC population and the parents. It is the most informative and highly reproducible genotyping method with the most data points available to date. The following chapters include the results from genotyping and the classification of the MAGIC population as a mapping population.

3.3.1 Data cleaning

Genotyping with the Illumina 9k iSelect chip resulted in 7864 SNP information for 534 MAGIC DH-lines and eight parents. 866 SNP markers were removed due to missing value for all eight parents. 1666 SNP markers were monomorphic for the same allele for all eight parents. Another 215 markers were dismissed from the dataset due to minor allele frequency (MAF). One genotype from the MAGIC DH-lines was removed from the data set due to poor genotyping results. After removing all undesirable SNPs and genotypes, the final data set consisted of 5117 SNPs in 541 genotypes (8 parents, 533 MAGIC DH-lines). With the information about the location of the SNP markers (Comadran et al., 2012), downloadable from http://bioinf.hutton.ac.uk/waugh/iselect,

the remaining markers could be grouped to linkage groups and ordered within the linkage groups. With this information 1906 SNP marker were not assigned to any linkage group. 5117 SNPs were used to calculate population structure and linkage disequilibrium. The 5117 SNPs were partly mapped to the same position. Only one marker was used from positions with doubled mapped SNP markers to reduce the programming complexity and to maximize the correlation between the marker order and position of the iSelect marker assay and the map results from the R program 'mpMap' (Huang and George, 2011).

3.3.2 Population structure

Population structure was calculated with 5117 SNP marker using principal component analysis (PCA) with SAS 9.2. The first principal component explained 6.8%; the second explained 4.1% of the variation within the population (Fig. 6). No significant principal components according to Franklin et al. (1995) could be identified. The MAGIC population is unstructured.

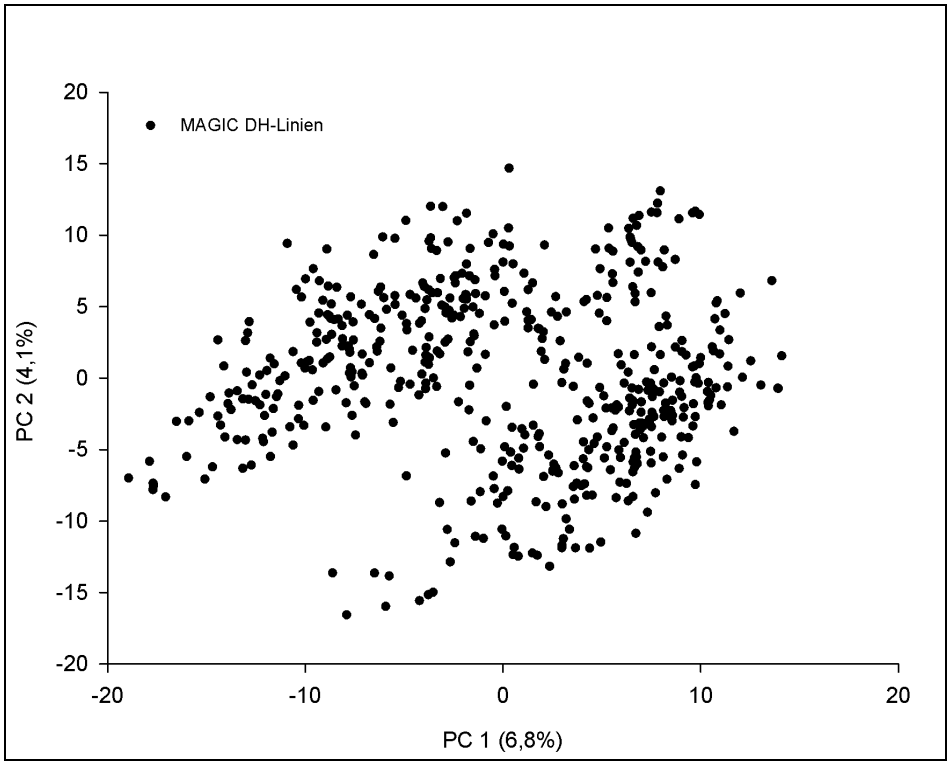

Fig. 6: Principal component analysis with 5117 SNP markers and 533 MAGIC DH-lines
The first principal component (PC 1) represents 6.8% of the variation, the second principal component (PC 2) only 4.1%, this refers to no structure within the MAGIC DH-lines.

3.3.3 Linkage disequilibrium

The analysis of LD decay in Fig. 7 showed the genome-wide LD with R^2 values plotted against the genetic distance in cM. The figure showed that the strongest and significant LD is

observed at very short distance, around 5 cM. Beyond 5 cM, LD became constant at a value of R^2=0.1 which allowed a precise genetic analysis. Low intra-chromosomal linkage along the barley chromosomes is shown in Fig. 7 for the mean of all chromosomes. The LD for each chromosome in comparison of the two datasets is shown in the Appendix 1 as heat maps.

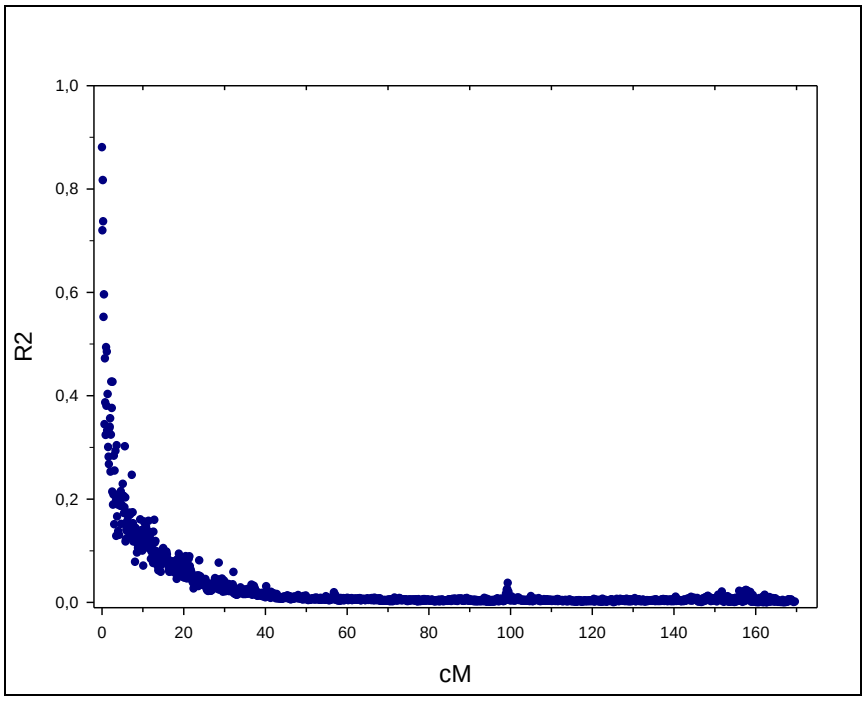

Fig. 7: LD as a function of genetic distance.
Mean of all chromosomes (1H to 7H) with 5117 SNP markers.

3.3.4 Genetic map with R/mpMap

In total 1416 SNP markers were used to construct the genetic map with 541 genotypes (8 parents, 533 MAGIC DH-lines) across 7 chromosomes. The total genome size measured 1714 cM in length (Table 16). The highest density of genetic markers was located on chromosome 6H with a SNP marker each 0.9 cM, the lowest density with a marker every 1.52 cM was investigated on chromosome 4H. On average, one marker was mapped each 1.2 cM on the chromosome. The biggest gap between two markers was determined on chromosome 1H with 23.91 cM distance between two SNP markers, located at the end of the long arm of chromosome 1H. The full list of SNP markers and genetic positions is attached as Appendix 2.

Table 16: Summary of MAGIC genetic linkage map

Chromosome	nr SNP	Length (cM)
1H	184	225
2H	238	283
3H	225	281
4H	137	206
5H	272	292
6H	179	160
7H	181	267
total	1416	1714

SNP=single nucleotide polymorphism, 1H to 7H are the linkage groups of barley

3.3.5 Haplotype probability

On the basis of the map results the multipoint probability at each locus to be inherited from each of the eight parents could be calculated with 'mpprob' from the program R/mpMap. The calculated percentages are listed in Table 17 for every parent for each chromosome and the mean of each parent for all chromosomes. The parents Ackermanns Bavaria, Barke, Heils Franken, Heines Hanna and Ragusa were equally distributed within each chromosome and on average over all chromosomes. The probability of the parents Pflugs Intensiv and Criewener 403 were compared to the theoretical approach underrepresented on chromosome 2H, 3H, 4H, 5H, 6H, 7H and 1H, 2H, 3H, 4H, 5H, 6H, 7H, respectively (Table 17). Ackermanns Danubia was underrepresented for 1H, 2H, 4H, 5H, 6H and 7H, too. The unexplained probability for each chromosome was quite high with a mean of 37.8%.

Table 17: Percentage of each chromosome with each founder ancestry

Parent	Chromosome							
	1H	2H	3H	4H	5H	6H	7H	mean
Ackermanns Bavaria	10.1	11.4	9.9	10.5	9.9	13.2	14.2	11.3
Barke	14.9	9.7	11.7	8.7	14.3	14.7	10.7	12.1
Heils Franken	9.4	12.7	13.6	5.5	8.3	11.1	7.9	9.8
Heines Hanna	12.1	3.7	15.4	20.5	9.3	10.5	7.4	11.3
Pflugs Intensiv	10.0	0.0	2.6	0.0	0.1	0.0	0.0	1.8
Ragusa	9.2	8.6	8.9	10.3	12.1	10.4	9.8	9.9
Ackermanns Danubia	3.9	6.3	9.9	6.2	5.0	2.5	8.2	6.0
Criewener 403	0.2	0.0	0.2	0.0	0.0	0.0	0.0	0.6
unexplained	30.4	47.5	27.9	38.4	41.1	37.6	41.8	37.8
total	100	100	100	100	100	100	100	100

3.4 QTL determination in the MAGIC population

The QTL mapping with multi-locus analysis and cross validation was conducted with two QTL mapping approaches (BA, HA) for 12 traits with $p<0.001$ or $p<0.05$. If the analysis of variance for the phenotypic trait showed significant results for treatment or genotype*treatment interaction the QTL mapping was conducted for genotype*treatment interaction, too. 143 QTL for twelve traits were detected with both approaches.

A total of 78 QTL were detected for twelve traits with the binary approach. The main marker effect was significant at 61 QTL, the marker*treatment interaction was significant at twelve QTL and the main marker and the marker*treatment interaction was significant at five QTL. The results for the putative QTL are presented separately for each trait and are listed in Table 18.

A total of 65 QTL were detected for twelve traits with the haplotype approach. The main marker effect was significant at 57 QTL, the marker*treatment interaction was significant at eight QTL and the main marker and the marker*treatment interaction was significant at three QTL. The results for the putative QTL are presented separately for each trait and are listed in Table 19.

3.4.1 Above ground biomass (AGB)

Altogether 16 QTL for the trait AGB were detected with BA. Eight putative QTL for main marker effects were located on chromosome 2H, 3H, 4H, 5H and 7H with $p<0.05$. Six putative QTL with marker*treatment interaction were assigned to chromosome 1H, 2H, 3H, 5H and 6H with $p<0.05$. Two QTL were significant for main marker and marker*treatment interaction, located on chromosome 4H and 5H. The strongest probability for a main marker QTL was investigated on chromosome 7H (SNP marker: i_12_10979) genotypes carrying the less frequent allele had a reduced above ground biomass by 6.4% (-0.6 g). The QTL with the strongest effect for marker*treatment interaction was located on chromosome 1H (SNP marker: i_SCRI_RS_120053). Genotypes with the less frequent allele produced a higher above ground biomass by 5.2% under well watered, but had no effect under terminal drought conditions.

Altogether eleven QTL for ABG were detected with HA. Eight putative QTL with main marker effects were detected on all chromosomes except 6H with $p<0.05$. Three additional QTL were detected for marker*treatment interaction on chromosome 1H, 2H and 6H. The QTL with the strongest probability for a main marker effect was located on chromosome 2H (SNP marker: i_11_21242), the allele from Barke increased the AGB to 10.3 g/plant, the allele from Ragusa decreased the AGB to 9.5 g/plant. The strongest probability for marker*treatment interaction was located on chromosome 6H (SNP marker: i_SCRI_RS_151280), the allele from Ragusa increased the AGB to 13.1 g/ plant and the allele from Heils Franken decreased the AGB to 11.7 g/ plant

under well watered conditions. Under terminal drought conditions the lowest AGB with 6.5 g/ plant was detected at genotypes carrying the allele from Heines Hanna, the highest AGB with 6.9 g/ plant from Ragusa.

3.4.2 Leaf senescence (AUDPC)

Altogether seven QTL for the trait leaf senescence (AUDPC) were detected with the BA. Five putative QTL for main marker effects were detected on chromosome 1H, 2H, 3H, 4H, and 6H with $p<0.05$. Two different QTL were detected for marker*treatment interaction on chromosome 5H and 7H. The strongest probability for the main marker QTL was detected on chromosome 4H (SNP marker: i_12_30718), genotypes carrying the less frequent allele showed intensified leaf senescence by 13.4%. The strongest probability for a marker*treatment interaction effect was detected on chromosome 5H (SNP marker: i_SCRI_RS_173583), genotypes carrying the less frequent allele showed less leaf senescence (3.6%) under well watered conditions, but intensified leaf senescence (1.5%) under terminal drought conditions.

Altogether six QTL for AUDPC were detected with HA. Five putative QTL with main marker effects were detected on chromosome 1H, 2H, two on 4H and one on 5H with $p<0.05$. One QTL on chromosome 5H was detected for marker*treatment interaction. The strongest probability for main marker effects was located on chromosome 4H (SNP marker: i_11_11470), genotypes carrying the allele from Heines Hanna showed the lowest leaf senescence; the one carrying the allele from Barke showed the highest leaf senescence. The marker*treatment interaction effect on chromosome 5H (SNP marker: i_SCRI_RS_173583) resulted in lowest leaf senescence in genotypes carrying the allele from Barke, the highest leaf senescence was detected at genotypes carrying the allele from Pflugs Intensiv under well watered conditions. Under terminal drought conditions the lowest leaf senescence was detected with the allele from Heils Franken, the highest with the allele from Pflugs Intensiv.

3.4.3 Days to heading (DHE)

The genotype*treatment interaction was not significant in the analysis of variance and therefore not considered in the QTL mapping approaches. The BA QTL model detected eight putative QTL for days to heading on chromosomes 3H, 4H, 5H and 7H for $p<0.001$. The strongest F value was detected on chromosome 7H (SNP marker: i_11_20126), the less represented allele resulted in a reduction till heading by up to 6.5% (-3.7 days).

Seven putative QTL were detected on chromosome 3H, 4H, 5H and 7H for p<0.001 with the HA. The strongest F value was detected on 7H (SNP marker: i_11_11348), the allele from Ackermanns Bavaria reduced DHE to 53.7 days, and the allele from Ragusa extended DHE to 59.7 days.

3.4.4 Grain filling period (DGF)

Four QTL with main marker effects were detected with BA for days to grain filling on chromosome 3H, two on 5H and 6H for p<0.001. No significant marker*treatment interaction was detected. The strongest probability was measured on chromosome 5H (SNP marker: i_11_20713), the less represented allele resulted in an elongation of grain filling by 3.2% (1.2 days).

Three putative QTL with main marker effects were detected with HA, one on chromosome 2H, one on 5H and one on 6H with p<0.001. No significant marker*treatment interaction was detected. The marker with the strongest F value was located on chromosome 2H (SNP marker: i_SCRI_RS_153693), the allele from Ragusa shortened the grain filling period to 34.5 days, the allele from Barke extended the grain filling period to 39.3 days.

3.4.5 Flower abortion (FA)

The genotype*treatment interaction was not significant in the analysis of variance and therefore not considered in the QTL mapping approaches. Two putative QTL with BA for main marker effects were detected on chromosome 2H and 3H with p<0.001. The strongest probability was located on chromosome 2H (SNP marker: i_11_10287), genotypes carrying the less represented allele had an enhanced flower abortion by over 100% (25.2 flowers).

One putative QTL with HA was detected for main marker effect on chromosome 2H at the same region like the one detected with BA with p<0.05. The strongest probability was detected at SNP marker i_SCRI_RS_196270; the allele from Heils Franken resulted in 1.5 sterile flowers/ear, the allele from Ragusa in 29.9 sterile flowers/ear.

3.4.6 Number of ears per plant (NE)

Four putative QTL with BA for main marker effects were detected on chromosome 2H, 3H and 5H with p<0.001. No significant marker*treatment interaction was detected. The strongest probability was located on chromosome 5H (SNP marker: i_11_10146), genotypes carrying the less represented allele enhanced the number of ears per plant by 14.5% compared to the more frequent allele. No significant QTL for marker*treatment interaction were detected.

Two putative QTL with the HA for main marker effects were detected on chromosome 5H with p<0.05. No significant marker*treatment interaction was detected. The strongest F value was

located the short arm of chromosome 5H (SNP marker: i_12_30975), the allele from Ragusa resulted in 3.7 ears per plant and the allele from Heils Franken in 4.7 ears per plant.

3.4.7 Number of kernels per ear (NK)

Altogether two QTL for the trait NK were detected with BA. One putative QTL for main marker effect was detected on chromosome 4H for $p<0.001$. One QTL was significant for main marker and marker*treatment interaction, located on chromosome 2H. At the position of SNP marker i_12_30897 the strongest F value was detected, genotypes carrying the less represented allele produced 59.4% (10.4) more kernels per ear. The marker*treatment interaction allele effects at 2H increased the number of kernels by 70.1% under well watered and by 41.9% by terminal drought conditions compared to the more represented allele.

Altogether two QTL for the trait NK were detected with the HA at the same position as with the BA. The marker with the strongest F value for main marker and marker*treatment interaction was located on chromosome 2H (SNP marker: i_SCRI_RS_160958), the allele from Ackermanns Bavaria reduced the number of NK to 17.6; the allele from Ragusa increased the NK to 28.4 as main marker effect. The allele from Ackermanns Bavaria reduced the number of kernels to 19.2; the allele from Ragusa increased the NK to 33.7 under well watered conditions. The same pattern was detected under terminal drought conditions with 16 kernels per ear and 22.4 kernels per ear, respectively.

3.4.8 Plant height (PLH)

Altogether six QTL for the trait PLH were detected with BA. Five putative QTL for main marker effects were detected on chromosome 3H, 4H, 5H and 7H and one with marker *treatment interaction on chromosome 3H with $p<0.001$. The QTL with the strongest F value for a main marker QTL was located on 3H (SNP marker: i_SCRI_RS_121052), genotypes carrying the less frequent allele reduced plant height by 15.3% (-13.3 cm). The less frequent allele for the QTL for marker*treatment interaction on 3H (SNP marker: i_11_11086) increased plant height by 8.6% (7.7 cm) under well watered and 4.5% (3.6 cm) under terminal drought conditions.

Altogether eight QTL for the trait PLH were detected with HA on all chromosomes except 4H with $p<0.05$. The QTL with the strongest F value for a main marker QTL was detected on 3H (SNP marker: i_11_10312), position 161.6 cM. The effect was based on the allele from Pflugs Intensiv, which increased the plant height to 90.2 cm, and the allele from Barke which reduced it to 73.9 cm. Compared to the BA no marker*treatment interaction effects were detected with the HA.

3.4.9 Thousand kernel weight (TKW)

Altogether three QTL for the trait TKW were detected with the BA. Two putative QTL for main marker effects were detected on chromosome 5H and 6H for $p<0.001$. One significant main marker and marker*treatment interaction was detected on chromosome 2H. This was the region (SNP marker: i_11_10287) with the strongest probability for the main marker and marker*treatment interaction and reduced the thousand kernel weight by 22.8% (-11.2 g), decreasing the thousand kernel weight under well watered conditions by 25.9% (-13.2 g) and under terminal drought conditions by 19.6% (-9.3 g).

Altogether five QTL for TKW were detected with the HA. Five putative main QTL effects on chromosome 2H, 4H, 5H and 6H were detected with $p<0.05$. One marker*treatment QTL effect was detected on 2H, which was at the same position as the main marker effect on 2H. This position (SNP marker: i_11_10214) also inhibited the strongest statistical probability; the highest TKW was assigned to the parent Barke (50.3g), the lowest to the parent Ragusa (37.8 g). The same parental pattern was detected under well watered and terminal drought conditions for the marker*treatment interaction effect.

3.4.10 Grain yield (YLD)

Altogether eleven QTL for the trait YLD were detected with the BA. Eight putative QTL for main marker effects for grain yield were detected on chromosome 2H, 5H, 6H and 7H with $p<0.05$. Three QTL were detected for a significant marker*treatment interaction on chromosome 1H and 2H. One QTL was detected for significant main marker and significant marker*treatment interaction effect on chromosome 4H. The strongest probability for the main effects was located on chromosome 2H (SNP marker: i_SCRI_RS_15537), genotypes carrying the minor frequent allele yielded higher by 9.2% (0.4 g). The strongest effect for the marker*treatment interaction was located on chromosome 2H (SNP marker: i_11_10429) and increases the kernel yield under well watered conditions by 8.7% (0.5 g), and under terminal drought conditions by 2.4% (0.1 g).

Altogether six QTL for the trait YLD were detected with the HA. Five putative QTL for main marker effects were detected on chromosome 1H, 4H and two on 5H with $p<0.05$. One significant QTL for marker*treatment interaction was detected on chromosome 6H. One QTL on 2H was significant for main marker and marker*treatment interaction effects. This was the strongest QTL main marker effect (SNP marker: i_SCRI_RS_179555), the highest yield with 4.8 g/plant was detected in genotypes carrying the allele from Ragusa, the lowest with 4.1 g/plant in genotypes carrying the allele from Barke. The strongest probability for a marker*treatment interaction was detected on chromosome 6H (SNP marker: i_11_10175), under well watered conditions the highest

yield with 6.0g/plant resulted from the allele from Barke, the lowest yield with 5.2 g/plant from allele from Heines Hanna. Under terminal drought conditions the highest yield with 2.9 g/ plant the derived from the allele from Ackermanns Bavaria, the lowest with 2.7 g/plant derived from the allele from Heines Hanna.

3.4.11 THz: water content after 96 hours of not watering (WCT)

Eight putative QTL with the BA for main marker effects were detected on chromosome 1H, 2H, 4H, 5H and 6H with $p<0.05$. The QTL with the strongest F value was detected on 5H (SNP marker: i_SCRI_RS_145275), genotypes carrying the less frequent allele had a reduced water content by 12.1%.

Seven putative QTL with HA for main marker effects were detected on chromosome 2H, 5H and 6H with $p<0.05$. The QTL with the highest probability was detected on 5H (SNP marker: i_SCRI_RS_174091), the allele from Ackermanns Bavaria resulted in a water content of 80.6% in the leaves, the allele from Barke in 67.5%.

3.4.12 THz: Difference between day1 and day5 (WL)

Seven putative QTL with BA for main marker effects were detected on chromosome 3H, 4H and 5H with $p<0.05$. The QTL with the strongest probability was detected on 5H (SNP marker: i_SCRI_RS_184564); genotypes carrying the allele 1 had a 98.1% lower difference between water content at day 1 and day 5.

Seven putative QTL with main marker effects were mapped with the HA with $p<0.05$, located on chromosome 1H, 3H, 4H, 5H and 6H. The strongest probability was detected on 4H (i_SCRI_RS_229116), the allele from Heils Franken had the lowest, the allele from Ragusa the highest differences between the water contents at day 1 and day 5. For both approaches no marker*treatment interaction was calculated and no epistatic effects were detected.

Table 18: List of QTL mapped with the BA for twelve traits in the MAGIC DH-lines

							Diff	
QTL-name BA[a]	**Chr[b]**	**Pos[c]**	**Genetic interval[d]**	**Effect[e]**	**-log10(p)**	**BA[f]**	**ww[g]**	**td[h]**
Above ground biomass (AGB)								
QAgb.MAGIC.BA-1H.a	1H	36.4	36.4-37.1	I	2.7		0.6	0.0
QAgb.MAGIC.BA-2H.a	2H	154.6	145.2-154.6	M	2.3	0.3		
QAgb.MAGIC.BA-2H.b	2H	208.0	204.8-208.0	I	1.7		0.6	-0.1
QAgb.MAGIC.BA-3H.a	3H	57.2	57.2-72	M	2.3	0.5		
QAgb.MAGIC.BA-3H.b	3H	93.6	93.6-96.6	M	1.5	0.3		
QAgb.MAGIC.BA-3H.c	3H	246.3	246.3	I	1.4		0.4	-0.1
QAgb.MAGIC.BA-3H.d	3H	261.0	261.0	I	1.4		0.5	-0.2
QAgb.MAGIC.BA-4H.a	4H	10.6	10.6	M	1.8	-0.3		
QAgb.MAGIC.BA-4H.b	4H	105.2	105.2	M	2.9	-0.5		
QAgb.MAGIC.BA-4H.c	4H	158.4	158.4-163.6	M/I	1.6	0.5	1.0	0.2
QAgb.MAGIC.BA-5H.a	5H	0.0	0.0	I	1.4		-0.4	0.0
QAgb.MAGIC.BA-5H.b	5H	80.5	53.4-80.5	M	2.1	0.4		
QAgb.MAGIC.BA-5H.c	5H	198.0	191.3-198.0	M/I	1.3	0.4	0.7	0.1
QAgb.MAGIC.BA-5H.d	5H	233.6	233.6-245.8	M	1.6	-0.3		
QAgb.MAGIC.BA-6H.a	6H	31.6	31.6	I	2.8		-0.8	0.0
QAgb.MAGIC.BA-7H.a	7H	36.9	33.8-36.9	M	3.4	-0.6		
Leaf senescence (AUDPC)								
QAuc.MAGIC.BA-1H.a	1H	109.1	106.8-126.4	M	2.3	-1.4		
QAuc.MAGIC.BA-2H.a	2H	125.2	124.8-125.2	M	7.0	3.0		
QAuc.MAGIC.BA-3H.a	3H	261.0	261.0	M	2.5	1.8		
QAuc.MAGIC.BA-4H.a	4H	152.6	152.6	M	11.9	4.7		
QAuc.MAGIC.BA-5H.a	5H	217.6	217.6	I	2.4	-1.1	-2.7	0.4
QAuc.MAGIC.BA-6H.a	6H	160.0	147.3-160.0	M	2.5	1.4		
QAuc.MAGIC.BA-7H.a	7H	236.6	236.6	I	1.4	0.0	-1.4	1.5
Grain filling period (DGF)								
QDgf.MAGIC.BA-3H.a	3H	27.7	27.7	M	4.1	0.9		
QDgf.MAGIC.BA-5H.a	5H	53.4	53.4	M	6.0	1.2		
QDgf.MAGIC.BA-5H.b	5H	263.1	263.1-271.6	M	3.4	-1.4		
QDgf.MAGIC.BA-6H.a	6H	106.1	106.1	M	5.5	1.0		
Das to heading (DHE)								
QDhe.MAGIC.BA-3H.a	3H	65.2	58.6-65.2	M	5.3	-1.4		
QDhe.MAGIC.BA-3H.b	3H	168.9	161.6-168.9	M	6.9	-1.2		
QDhe.MAGIC.BA-4H.a	4H	2.1	0-2.1	M	5.8	1.6		
QDhe.MAGIC.BA-4H.b	4H	69.7	68.2-69.7	M	8.7	-1.3		
QDhe.MAGIC.BA-5H.a	5H	143.6	136.4-143.6	M	3.3	1.3		
QDhe.MAGIC.BA-5H.b	5H	206.4	205.0-206.4	M	27.4	2.4		
QDhe.MAGIC.BA-7H.a	7H	30.7	30.5-32.7	M	15.2	4.1		
QDhe.MAGIC.BA-7H.b	7H	36.9	33.5-36.9	M	34.0	-3.7		
Flower abortion (FA)								
QFla.MAGIC.BA-2H.a	2H	144.2	142.8-144.2	M	169.0	25.2		
QFla.MAGIC.BA-3H.b	3H	129.2	129.2	M	4.4	3.4		
Number of ears (NE)								
QNep.MAGIC.BA-2H.a	2H	126.2	126.2-144.2	M	4.0	-0.6		
QNep.MAGIC.BA-3H.a	3H	82.3	72-82.3	M	7.4	-0.5		
QNep.MAGIC.BA-5H.a	5H	0.0	0-15.1	M	5.7	-0.7		
QNep.MAGIC.BA-5H.b	5H	206.4	198.0-206.4	M	9.2	0.7		
Number of kernels (NK)								
QNke.MAGIC.BA-2H.a	2H	144.2	144.2	M/I	17.2	10.4	13.9	6.9
QNke.MAGIC.BA-4H.a	4H	33.0	33.0-34.1	M	4.1	-1.9		

QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	-log10(p)	BA[f]	Diff ww[g]	Diff td[h]
Plant height (PLH)								
QPlh.MAGIC.BA-3H.a	3H	72.0	65.2-73.7	I	19.0		7.7	3.6
QPlh.MAGIC.BA-3H.b	3H	134.6	134.6-145.6	M	5.3	5.1		
QPlh.MAGIC.BA-3H.c	3H	161.6	161.6	M	33.5	-13.3		
QPlh.MAGIC.BA-4H.a	4H	163.6	158.4-163.6	M	5.2	3.6		
QPlh.MAGIC.BA-5H.a	5H	0.0	0-15.1	M	9.9	5.7		
QPlh.MAGIC.BA-7H.a	7H	36.9	30.7-36.9	M	4.8	-3.6		
Thousand kernel weight (TKW)								
QTkw.MAGIC.BA-2H.a	2H	144.2	144.2	M/I	7.1	-11.2	-13.2	-9.3
QTkw.MAGIC.BA-5H.a	5H	211.7	211.7-213.8	M	6.9	2.0		
QTkw.MAGIC.BA-6H.a	6H	64.6	64.6	M	6.9	1.6		
Water loss (WL)								
QWhc.MAGIC.BA-3H.a	3H	27.7	23.4-54.2	M	4.2	-3.2		
QWhc.MAGIC.BA-3H.b	3H	82.3	82.3-96.6	M	2.9	-5.6		
QWhc.MAGIC.BA-3H.c	3H	191.2	191.2	M	2.3	2.7		
QWhc.MAGIC.BA-4H.a	4H	204.6	179-206.4	M	2.1	-4.6		
QWhc.MAGIC.BA-5H.a	5H	0.0	0.0	M	2.0	1.8		
QWhc.MAGIC.BA-5H.b	5H	26.6	23.9-28.2	M	4.3	4.5		
QWhc.MAGIC.BA-5H.c	5H	111.7	111.7-113.8	M	1.7	-1.7		
Water content (WCT)								
QWct.MAGIC.BA-1H.a	1H	103.5	103.5-134.4	M	1.7	2.3		
QWct.MAGIC.BA-2H.a	2H	55.4	49.2-55.4	M	1.4	3.0		
QWct.MAGIC.BA-4H.a	4H	25.1	25.2-30.8	M	1.5	3.6		
QWct.MAGIC.BA-4H.b	4H	85.6	85.6-98.7	M	2.1	5.7		
QWct.MAGIC.BA-5H.a	5H	62.2	53.4-67.0	M	8.3	-9.3		
QWct.MAGIC.BA-5H.c	5H	271.6	271.6	M	4.6	4.3		
QWct.MAGIC.BA-6H.a	6H	17.3	17.3	M	5.6	-7.1		
QWct.MAGIC.BA-6H.b	6H	110.4	110.4	M	4.7	-8.5		
Grain yield (YLD)								
QYld.MAGIC.BA-1H.a	1H	36.4	36.4	I	1.5		0.3	0.0
QYld.MAGIC.BA-2H.a	2H	128.0	127.7-128.7	M	2.1	0.3		
QYld.MAGIC.BA-2H.b	2H	154.6	154.6	I	2.8		0.5	0.1
QYld.MAGIC.BA-2H.c	2H	187.4	187.4	M	4.0	0.4		
QYld.MAGIC.BA-2H.d	2H	241.3	241.3	I	1.7		0.5	0.1
QYld.MAGIC.BA-4H.a	4H	10.6	10.6	M/I	1.5	-0.3	-0.4	-0.1
QYld.MAGIC.BA-5H.a	5H	0.0	0.0	M	1.7	0.2		
QYld.MAGIC.BA-5H.b	5H	205.0	205.0-206.4	M	2.3	0.3		
QYld.MAGIC.BA-6H.a	6H	139.2	139.2	M	2.3	-0.2		
QYld.MAGIC.BA-7H.a	7H	149.6	138.3-149.6	M	3.0	0.2		
QYld.MAGIC.BA-7H.b	7H	217.6	216.4-236.8	M	1.8	-0.2		

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] CentiMorgan range from the first to the last significant marker in a QTL

[e] A putative QTL was assumed in a vicinity of a marker locus, if the marker main effect (M) or /and marker*treatment interaction (I) was significant with P<0,05 or P<0,001, depending on the trait of interest

[f] Difference between the mean effect of allele 0 and allele 1

[g] Difference between the mean effect of allele 0 and allele 1 under well watered conditions

[h] Difference between the mean effect of allele 0 and allele 1 under terminal drought conditions

Table 19: QTL mapped with the HA for twelve traits in the MAGIC DH-lines

QTL-name HA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	-log10(p)	Treat	AB	AD	B	HF	HH	PI	R
Above ground biomass (AGB)													
QAgb.MAGIC.HA-1H.a	1H	37.1	36.4-50.3	I	1.5	ww	12.9		12.5	11.7	12.6		13.1
						td	6.8		6.8	6.6	6.7		6.6
QAgb.MAGIC.HA-1H.b	1H	130.1	129.3-130.6	M	2.3		9.8	9.7	9.6	9.5	9.5	9.7	9.9
QAgb.MAGIC.HA-2H.a	2H	127.1	119.4-141.7	M	2.8		9.8		10.3	9.7			9.5
QAgb.MAGIC.HA-2H.b	2H	249.0	241.3-251.2	I	2.0	ww	12.6		13.3	12.1	12.1		12.9
						td	6.6		6.8	6.9	6.8		6.7
QAgb.MAGIC.HA-3H.a	3H	168.9	168.9	M	2.7		9.6	9.5	9.3	9.2	9.6	9.5	10.0
QAgb.MAGIC.HA-4H.a	4H	10.6	0-10.6	M	2.3		9.7	9.8	9.8	10.0	9.6		9.1
QAgb.MAGIC.HA-4H.b	4H	163.6	155.5-163.6	M	2.5		9.8		9.1	9.9	9.7		10.1
QAgb.MAGIC.HA-5H.a	5H	53.4	49.6-53.4	M	2.7		9.6		10.1	10.2	9.2		10.0
QAgb.MAGIC.HA-5H.b	5H	245.8	243.8-254.3	M	3.6		10.3	9.5	9.7	9.4	9.9	9.0	9.1
QAgb.MAGIC.HA-6H.a	6H	147.9	139.2-160.0	I	2.1	ww	12.2	12.8	12.5	11.7	11.8		13.1
						td	6.8	6.7	6.6	6.8	6.5		6.9
QAgb.MAGIC.HA-7H.a	7H	36.9	30.7-48.4	M	2.1		9.1	9.5	9.8	9.6	9.9		10.0
Leaf senescence (AUDPC)													
QAuc.MAGIC.HA-1H.a	1H	126.4	126.4-127.14	M	2.1		49.7	51.1	51.4	52.3	51.5	50.5	50.3
QAuc.MAGIC.HA-2H.a	2H	125.2	124.8-125.2	M	6.3		51.6	50.3	48.8	54.1			49.4
QAuc.MAGIC.HA-4H.a	4H	61.3	61.3	M	3.5		51.2	51.5	50.9	51.6	50.3		49.7
QAuc.MAGIC.HA-4H.b	4H	151.2	151.2-158.4	M	9.5		50.4		55.7	51.3	49.7		49.9
QAuc.MAGIC.HA-5H.a	5H	67.3	67.0-67.3	M	1.8		51.2		49.8	51.0	51.2		49.2
QAuc.MAGIC.HA-5H.b	5H	217.6	217.6	I	2.0	ww	35.7	36.8	34.1	36.3	38.4	38.8	37.5
						td	65.5	65.8	65.9	65.2	66.2	69.3	64.2
Grain filling periode (DGF)													
QDgf.MAGIC.HA-2H.a	2H	29.9	27.5-42.6	M	6.4		38.3	38.5	38.8	37.7	38.5		33.9
QDgf.MAGIC.HA-5H.a	5H	49.6	49.6-53.4	M	6.2		37.8		38.9	39.6	38.7		39.3
QDgf.MAGIC.HA-6H.a	6H	101.9	101.9-112.6	M	3.7		39.1		38.3	37.9	38.9		38.2
Days to heading (DHE)													
QDhe.MAGIC.HA-3H.a	3H	56.8	54.2-56.8	M	10.3		58.0	56.4	55.7	56.6	56.2		57.2
QDhe.MAGIC.HA-3H.b	3H	168.9	156.2-168.9	M	10.3		55.5	56.9	58.4	56.4	56.2	56.3	57.8
QDhe.MAGIC.HA-4H.a	4H	190.3	190.3	M	3.8					57.2			58.4
QDhe.MAGIC.HA-5H.a	5H	198.0	191.5-198.0	M	3.1		55.7	55.4	57.1	57.6	57.2		58.5

QTL-name HA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	-log10(p)	Treat	AB	AD	B	HF	HH	PI	R
QDhe.MAGIC.HA-5H.b	5H	206.4	206.4	M	19.7		55.6	56.2	56.9	56.8	57.0		58.8
QDhe.MAGIC.HA-7H.a	7H	32.7	30.7-32.7	M	7.2		54.9		55.6	56.9	57.3		60.6
QDhe.MAGIC.HA-7H.b	7H	48.0	48.0-48.4	M	34.3		53.8	57.6	55.9	56.7	57.1		59.7
Flower abortion (FA)													
QFla.MAGIC.HA-2H.a	2H	144.2	142.8-144.2	M	128.5		2.1		2.2	1.5			29.9
Number of ears (NE)													
QNep.MAGIC.HA-5H.a	5H	0.0	0.0	M	6.0		4.4		4.4	4.7			3.7
QNep.MAGIC.HA-5H.b	5H	206.4	206.4	M	9.2		4.4	4.3	4.3	4.3	4.2		5.0
Number of kernels (NK)													
QNke.MAGIC.HA-2H.a	2H	144.2	144.2	M/I	10.1		17.6		17.8	18.9			28.4
						ww	19.2		19.7	20.2			33.7
						td	16.0		16.0	16.6			22.4
QNke.MAGIC.HA-4H.a	4H	33.7	33.7-34.1	M	4.6		17.4	19.2	19.5	19.9	19.0		17.4
Plant height (PLH)													
QPlh.MAGIC.HA-1H.a	1H	76.0	70.5-76.0	M	2.0		87.8		84.1	84.4	88.1	92.8	82.4
QPlh.MAGIC.HA-2H.a	2H	26.2	25.6-26.2	M	1.4		84.9	91.3	84.6	85.8	86.8		78.1
QPlh.MAGIC.HA-2H.b	2H	154.6	154.6	M	2.5		87.9		87.2	87.2			81.1
QPlh.MAGIC.HA-3H.a	3H	73.7	73.7-74.6	M	13.1		86.0	90.9	83.5	86.0	81.9		92.8
QPlh.MAGIC.HA-3H.b	3H	161.6	161.6-168.9	M	36.2		88.1	87.0	73.9	89.1	85.4	90.2	88.1
QPlh.MAGIC.HA-5H.a	5H	0.0	0.0	M	12.0		85.5		85.1	85.7			91.5
QPlh.MAGIC.HA-6H.a	6H	108.4	101.9-110.7	M	4.2		86.7		83.4	86.6	80.2		91.2
QPlh.MAGIC.HA-7H.a	7H	36.9	33.5-36.9	M	5.8		81.2	86.7	84.7	84.7	87.2		88.2
Thousand kernel weight (TKW)													
QTkw.MAGIC.HA-2H.a	2H	42.6	29.9-42.6	M/I	4.9		47.7	49.0	48.7	48.6	48.1		54.4
						ww	51.4		52.3	51.2			37.5
						td	47.7		48.3	48.0			38.1
QTkw.MAGIC.HA-2H.b	2H	141.7	126.2-147.7	M	79.1		49.6		50.3	49.6			37.8
QTkw.MAGIC.HA-4H.a	4H	102.4	98.7-102.4	M	3.2		48.1		50.9	47.4	49.0		49.2
QTkw.MAGIC.HA-5H.a	5H	206.3	206.3	M	11.6		48.5	48.0	46.9	49.2	49.9		46.2
QTkw.MAGIC.HA-6H.a	6H	82.2	82.2-91.3	M	10.5		49.0		48.2	46.4	50.1		47.8
Water loss (WL)													
QWhc.MAGIC.HA-1H.a	1H	97.6	95.0-97.6	M	2.6		4.0	2.7	6.1	1.9	6.4	4.7	3.8
QWhc.MAGIC.HA-3H.a	3H	15.7	8.0-15.7	M	2.2		4.6	4.7	3.4	3.4	7.5	9.5	3.5
QWhc.MAGIC.HA-3H.b	3H	82.3	82.3	M	5.3		8.1	6.6	5.6	4.9	3.6		-0.4
QWhc.MAGIC.HA-3H.c	3H	189.4	187.3-191.2	M	1.8		2.2	6.0	3.3	6.7	3.8	4.0	7.1

QTL-name HA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	-log10(p)	Treat	AB	AD	B	HF	HH	PI	R
QWhc.MAGIC.HA-4H.a	4H	190.3	190.3-206.4	M	3.2					0.7			3.4
QWhc.MAGIC.HA-5H.a	5H	67.0	65.4-67.0	M	3.7		3.3		8.9	3.7	7.1		4.8
QWhc.MAGIC.HA-6H.a	6H	81.7	77.7-82.2	M	1.3		5.5		2.2	7.0	6.3		7.8
Water content (WCT)													
QWct.MAGIC.HA-2H.a	2H	42.6	42.6-55.4	M	1.3		76.0	76.4	79.2	75.9	74.4		79.6
QWct.MAGIC.HA-2H.b	2H	254.1	254.1	M	1.9		75.6		79.0	74.2	76.7		72.3
QWct.MAGIC.HA-5H.a	5H	62.2	62.2-67.3	M	14.1		80.6		67.5	79.4	72.5		75.4
QWct.MAGIC.HA-6H.a	6H	20.2	14.1-20.2	M	8.2		69.5		79.2	71.0	80.3		75.6
QWct.MAGIC.HA-6H.b	6H	110.4	110.4-110.7	M	3.5		73.2		80.0	79.2	77.0		66.9
QWct.MAGIC.HA-6H.c	6H	132.7	127.0-132.7	M	2.9		77.4	73.6	78.2	76.6	81.6		72.4
QWct.MAGIC.HA-6H.d	6H	160.0	160.0	M	1.9			72.0		76.6	84.6		75.3
Grain yield (YLD)													
QYld.MAGIC.HA-1H.a	1H	95.0	95.0	M	2.6		4.5	4.3	4.2	4.5	4.2	4.3	4.3
QYld.MAGIC.HA-2H.a	2H	158.0	154.6-170.5	M/I	2.6		4.3		4.1	4.6			4.8
						ww	5.7		5.2	5.7	5.4		6.8
						td	2.9		2.7	2.9	3.0		2.9
QYld.MAGIC.HA-4H.a	4H	2.1	0.0-10.6	M	2.8		4.3		4.2	4.6	4.2		4.0
QYld.MAGIC.HA-5H.a	5H	0.0	0.0	M	2.7		4.3		4.2	4.6			4.1
QYld.MAGIC.HA-5H.b	5H	80.5	80.5	M	1.6		4.2		4.3	4.4	4.0		4.5
QYld.MAGIC.HA-6H.a	6H	147.3	146.1-147.9	I	2.8	ww	5.6	5.6	6.0	5.3	5.2		5.9
						td	2.9	2.8	2.9	2.8	2.8		2.9

QTL mapped with both approaches are written in italic

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] CentiMorgan range from the first to the last significant marker in a QTL

[e] A putative QTL was assumed in a vicinity of a marker locus, if the marker main effect (M) or /and marker*treatment interaction (I) was significant with P<0,05 or P<0,001, depending on the trait of interest

Treat=water treatment: ww=well watered; td=terminal drought.

AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

3.5 Epistatic effects

The mapping of epistatic effects with multi-locus analysis and cross validation was conducted with the binary approaches (BA) for each trait and identified epistatic interaction in the following traits: AUDPC, DHE, DGF, FA, NK, PLH, TKW and WCT. If the analysis of variance for the phenotypic trait showed significant results for treatment or genotype*treatment interaction the mapping of epistatic effects was conducted for the treatment, too. A total of 23 epistatic effects were detected for eight traits.

3.5.1 AUDPC

One significant epistatic effect was detected for leaf senescence with $p<0.05$ between SNP marker i_12_30718 (4H, 152.5 cM) and SNP marker i_11_11330 (3H, 145.5 cM). The combination of the most frequent alleles at both loci reduced the leaf senescence by 27.6% compared to the combination of the less frequent alleles at both loci.

3.5.2 DHE

Seven significant epistatic effects were detected for days to heading with $p<0.001$. The strongest epistatic interaction was detected between SNP marker i_11_10721 (7H, 130.9 cM) and SNP marker i_SCRI_RS_121052 (3H, 161.6 cM), reducing days to heading by 4.1 days. The highest reduction in 7.2 days was achieved by substitution of the less frequent alleles with the more frequent allele at both loci at SNP marker i_11_21528 (7H, 30.7 cM) and SNP marker i_11_10783 (5H, 206.4 cM).

3.5.3 DGF

One significant epistatic effect was detected for grain filling period with $p<0.001$, between the SNP marker i_SCRI_RS_169639 (7H, 130.9 cM) and SNP marker i_11_20002 (3H, 56.7 cM). The favourable combination of the less frequent alleles reduced the days to grain filling by 3% (-1.1 days) compared to the allele combination of the most frequent alleles.

3.5.4 FA

Four significant epistatic effects were detected for floret abortion with $p<0.001$. The strongest epistatic effect was detected between SNP marker i_SCRI_RS_223224 (6H, 87.3 cM) and SNP marker i_SCRI_RS_142188 (2H, 147 cM). The combination of the less frequent alleles enhanced the floret abortion by 1276% (32.6 florets) compared to the allele combination of higher frequent alleles.

3.5.5 NK

Two significant epistatic interactions were detected for number of kernels with p<0.001. The strongest effect was detected between SNP marker i_SCRI_RS_197190 (7H, 217.3 cM) and SNP marker i_SCRI_RS_156323 (2H, 125.1 cM). The combination of the less frequent alleles enhanced the number of kernels by 36.6% (6.7 kernels) compared to the combination of the most frequent alleles.

3.5.6 PLH

Two significant epistatic interactions were detected for plant height with p<0.001. The strongest effect was detected between SNP marker i_SCRI_RS_98225 (6H, 113.3 cM) and SNP marker i_11_10005 (3H, 70.7 cM). The combination of the most frequent alleles reduced the plant height by 6.7% (5.5 cm) compared to the combination of less frequent alleles.

3.5.7 TKW

Two significant epistatic effects for thousand kernel weight were detected with p<0.001. The strongest effect was detected between SNP marker i_11_11250 (2H, 144.2 cM) and SNP marker i_SCRI_RS_159503 (2H, 8.1 cM). The reduction in thousand kernel weight by 10.3% (4.6 g) was exhibited by lines carrying the more frequent allele at marker i_11_11250 and the less frequent allele at marker i_SCRI_RS_159503.

3.5.8 WCT

Four significant effects were detected with p<0.05. The strongest effect was detected between SNP marker i_12_30329 (7H, 217.3 cM) and SNP marker i_SCRI_RS_8671 (2H, 259.4 cM). The reduction of water content by 14.9% was exhibited by lines carrying the more frequent allele at SNP marker i_12_30329 and the less frequent allele at SNP marker i_SCRI_RS_8671.

3.6 Multiple comparison of parental means from haplotype approach

Main marker effects

Not only the allele effect between the contrasting parents can be calculated as significant, the further parental means can be evaluated regarding to their significant differences as well. Therefore a selected group of eighteen allele effects were tested for multiple comparisons from traits except FA and NK (Table 20).

The multiple comparison of QAgb.MAGIC.HA-5H.b determined three groups of allelic means: the alleles from Ackermanns Bavaria and Heines Hanna were significantly different to Ragusa and

Heines Hanna. The means of Ackermanns Danubia, Barke and Pflugs Intensiv were not significant different to both groups.

Two allele effects for AUDPC were evaluated (QAuc.MAGIC.HA-4H.a and QAuc.MAGIC.HA-4H.b). QAuc.MAGIC.HA-4H.a revealed three groups of significant allelic means; the mean of Heils Franken was significantly different to Ragusa, the remaining allelic means were not significantly different from any mean. The further analysis of QAuc.MAGIC.HA-4H.b showed that the allelic mean of Barke was significantly higher compared to all other allelic means from the parents.

Three allele effects for DHE were investigated (QDhe.MAGIC.HA-5H.b, QDhe.MAGIC.HA-7H.a and QDhe.MAGIC.HA-7H.b). QDhe.MAGIC.HA-5H.b resulted in three groups of allelic means that were significantly different from each other; the allelic mean of Ragusa was significantly different from all other parental means at that position. The mean of Ackermanns Bavaria was significantly different to the mean of Barke and the mean of Heines Hanna. The further analysis of the multiple comparisons of the allelic means of QDhe.MAGIC.HA-7H.a resulted in three groups as well. The allelic mean of Ragusa was significantly different to all other parents, and the mean of Ackermanns Bavaria and Barke were significant from the means of Ragusa, Heils Franken and Heines Hanna. The third QTL for DHE which was investigated (QDhe.MAGIC.HA-7H.b) showed significant differences for the mean of Ragusa to all other parents and the allelic mean of Ackermanns Bavaria and Barke was significantly different from Ackermanns Danubia, Heils Franken and Heines Hanna.

QNep.MAGIC.HA-5H.b was investigated for multiple comparisons for number of ears (NE). The parental mean of Ragusa was significantly different to all means of the other parental means at this position.

Five QTL for plant height were investigated for multiple comparisons of the parental alleles. The allelic effects at QPlh.MAGIC.HA-1H.a resulted in two clusters. The means of Pflugs Intensiv was significantly different to Ragusa, Barke and Heils Franken, but not to Ackermanns Bavaria and Heines Hanna. The mean of Heines Hanna and Ackermanns Bavaria were significant different to the parental mean of Barke, Heils Franken and Ragusa. Two allele effects on chromosome 3H for plant height were investigated for their parental mean, QPlh.MAGIC.HA-3H.a and QPlh.MAGIC.HA-3H.b. At QTL QPlh.MAGIC.HA-3H.a the allelic mean of Ragusa and Ackermanns Danubia were significantly different to all allelic parental means but not to each other. The low allelic mean of Heines Hanna was significantly different to the mean of Ackermanns Bavaria and Heils Franken and Heils Franken to Barke. Multiple comparisons of the allelic means resulted in three clusters. At QPlh.MAGIC.HA-3H.b the mean of Barke was significantly different

to all other parental means at that position. The mean of Heines Hanna was significant to all others as well except to the mean of Ackermanns Bavaria. At QPlh.MAGIC.HA-6H.a the allelic effect of Ragusa was significantly different to all other parents at that position. The parental mean of Heines Hanna was significant to the mean of Ackermanns Bavaria, Heils Franken and Ragusa. The mean of Barke was significant to the mean of Ackermanns Bavaria. Multiple comparisons of the allelic means resulted in three clusters. The last multiple comparison for a QTL for plant height was investigated at QPlh.MAGIC.HA-7H.a. The allelic mean of Ackermanns Bavaria was significantly different to all parental means at that position. The mean of Ragusa was significantly different to Barke as well. Multiple comparisons of the allelic means resulted in four clusters.

The multiple comparisons for one QTL for TKW were investigated. At QTKW.MAGIC.HA-2H.a all parental means were significantly different to Ragusa, but not among each other.

One QTL for water loss was investigated for multiple comparisons of the parental means. The mean of Barke at QWhc.MAGIC.HA-5H.a was significant to the mean of Ackermanns Bavaria, Heils Franken and Ragusa. The mean of Heines Hanna was only significant to the mean of Ackermanns Bavaria. Distinct differences between the means are shown exemplary in Fig. 8.

Two QTL for water content (WCT) were investigated concerning their parental means. The parental means of QWct.MAGIC.HA-5H.a clustered in three groups. The mean of Barke was significantly different to all other parental means. The mean of Ackermanns Bavaria was significantly different to Heines Hanna and Ragusa. And additionally the mean of Heines Hanna was significant to the mean of Heils Franken. The allelic means of the second QTL, QWct.MAGIC.HA-6H.c, clustered into two groups. The means of Heines Hanna, Barke and Ackermanns Bavaria were significant to the mean of Ackermanns Danubia, Heils Franken and Ragusa.

The two QTL for grain yield which were investigated for multiple comparisons of the parental alleles showed clear clustering for the significance. At QYld.MAGIC.HA-4H.a the allelic mean of Heils Franken was significant to all other parental means. At QYld.MAGIC.HA-5H.b the allelic means of Heils Franken and Barke were significantly different from the other parental means.

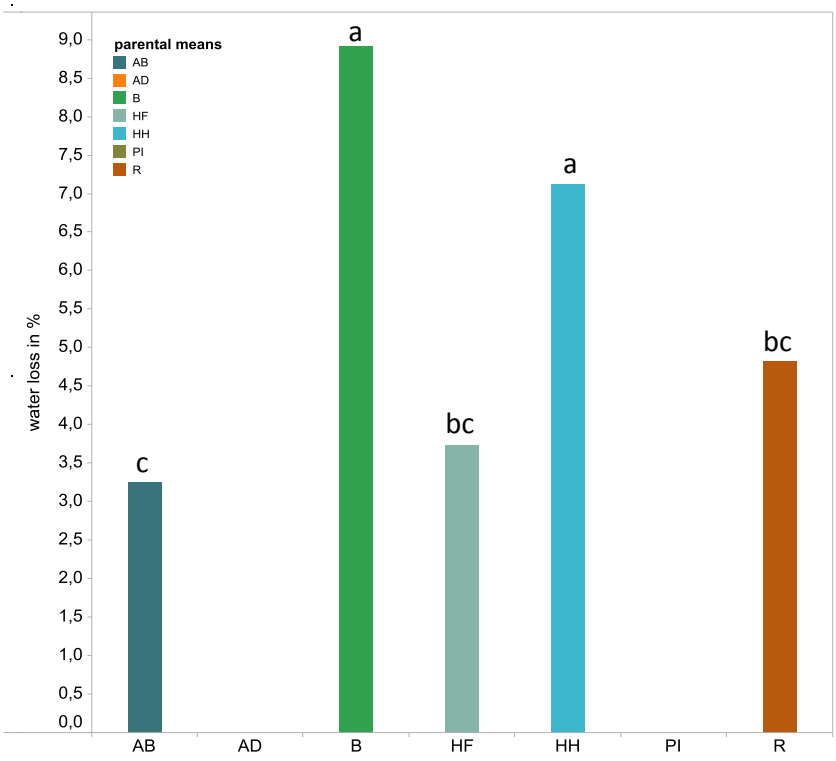

Fig. 8: Parental means for water loss (WL) at QWhc.MAGIC.HA-5H.a
Different letters indicate significant differences ($p<0.05$)

*Marker*treatment interaction effects*

The eight QTL that had significant marker*treatment interaction effects were investigated for multiple comparisons of the parental means, three for the trait AGB, one for AUDPC, one for NK, one for TKW and two for YLD (Table 21).

The multiple comparisons at QAgb.MAGIC.HA-1H.a detected two groups of parental means under well watered conditions. The mean of Heils Franken was significantly different from all other parental means. No multiple comparisons under terminal drought were significant.

The parental mean of Ackermanns Bavaria and Barke at QAgb.MAGIC.HA-2H.b were significantly different from the other parental means under well watered conditions. No multiple comparisons under terminal drought were significant. The allelic mean of Ragusa and Ackermanns Danubia at QAgb.MAGIC.HA-6H.a were not significantly different to each other but to the mean of Ackermanns Bavaria, Heils Franken and Heines Hanna under well watered conditions. No multiple comparisons under terminal drought were significant. An example for multiple comparison of marker*treatment interaction is shown in Fig. 9.

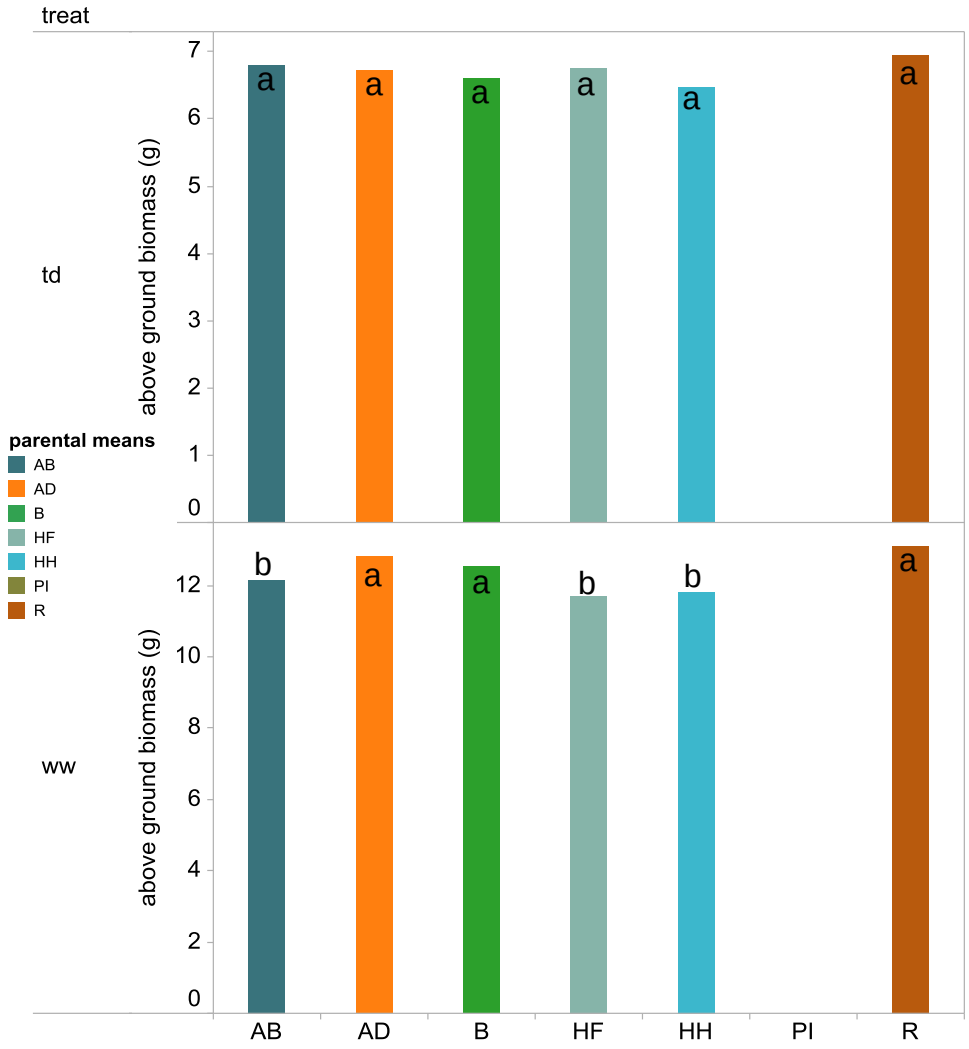

Fig. 9: Multiple comparisons between the parental means at QAgb.MAGIC.HA-6H.a for each treatment. No significant differences were detected for terminal drought, but under well watered conditions. Different letters indicate significant differences ($p<0.05$)

At QAuc.MAGIC.HA-5H.b, the multiple comparisons of the allelic means resulted in three parental clusters under well watered conditions. The mean of Barke was significant to the mean of Heines Hanna, Pflugs Intensiv and Ragusa. The remaining parental means were not significant from each other. No multiple comparisons under terminal drought were significant.

Multi comparisons at QNke.MAGIC.HA-2H.a under well watered conditions resulted in two clusters of the parental means. The mean of Ragusa was significantly different to all other parental means. The same was investigated under terminal drought conditions.

The analysis of multiple comparisons at QTKW.MAGIC.HA-2H.a showed the same pattern as QNke.MAGIC.HA-2H.a.

The mean comparison at QYld.MAGIC.HA-2H.a resulted in three clusters under well watered conditions. The mean of Ragusa was significantly different to all parental means. And the mean of

Barke was significant to the mean of Heils Franken. No multiple comparisons under terminal drought were significant.

The last investigated QTL was located on chromosome 6H, QYld.MAGIC.HA-6H.a. The allelic mean of Barke was significant to all other parental means except to Ragusa under well watered conditions. The parental means of Ragusa and Ackermanns Danubia were not significant to each other, but to the means of Heils Franken and Heines Hanna. No multiple comparisons under terminal drought were significant.

Table 20: List of selected main marker QTL from HA with multiple comparisons between the parental mean

QTL-name[a]	Trait	Chr[b]	Pos[c]	iselect-name[d]	AB		AD		B		HF		HH		PI		R	
QAgb.MAGIC.HA-5H.b	AGB	5H	245.8	i_11_10236	10.30	a	9.51	ab	9.74	ab	9.36	b	9.87	a	9.02	ab	9.08	b
QAuc.MAGIC.HA-4H.a	AUDPC	4H	61.3	i_11_11224	51.18	ab	51.52	ab	50.87	ab	51.55	a	50.34	ab		ab	49.73	b
QAuc.MAGIC.HA-4H.b	AUDPC	4H	151.2	i_11_11470	50.41	b			55.68	a	51.31	b	49.73	b			49.88	b
QDhe.MAGIC.HA-5H.b	DHE	5H	206.4	i_11_10146	55.57	c	56.19	bc	56.92	bc	56.80	bc	56.97	b			58.83	a
QDhe.MAGIC.HA-7H.a	DHE	7H	32.7	i_12_30752	54.95	c			55.63	c	56.92	b	57.32	b			60.55	a
QDhe.MAGIC.HA-7H.b	DHE	7H	48.0	i_11_11348	53.75	c	57.61	b	55.89	c	56.72	b	57.12	b			59.70	a
QNep.MAGIC.HA-5H.b	NE	5H	206.4	i_SCRI_RS_154144	4.36	b	4.29	b	4.32	b	4.33	b	4.18	b			4.96	a
QPlh.MAGIC.HA-1H.a	PLH	1H	76.0	i_SCRI_RS_152464	87.80	b			84.08	a	84.36	a	88.11	b	92.81	b	82.38	a
QPlh.MAGIC.HA-3H.a	PLH	3H	73.7	i_SCRI_RS_229693	85.99	c	90.90	a	83.47	b	85.98	c	81.88	b			92.79	a
QPlh.MAGIC.HA-3H.b	PLH	3H	161.6	i_11_10312	88.10	b	86.95	bc	73.86	a	89.06	b	85.36	c	90.17	b	88.07	b
QPlh.MAGIC.HA-6H.a	PLH	6H	108.4	i_SCRI_RS_162589	86.73	b			83.40	c	86.62	b	80.17	c			91.16	a
QPlh.MAGIC.HA-7H.a	PLH	7H	36.9	i_SCRI_RS_129779	81.17	ac	86.74	bc	84.67	c	84.75	bc	87.22	bc			88.20	b
QTKW.MAGIC.HA-2H.a	TKW	2H	42.6	i_SCRI_RS_155612	47.73	b	48.96	b	48.75	b	48.62	b	48.07	b			54.44	a
QWhc.MAGIC.HA-5H.a	WL	5H	67.0	i_SCRI_RS_133674	3.25	c			8.91	a	3.74	bc	7.12	a			4.83	bc
QWct.MAGIC.HA-5H.a	WCT	5H	62.2	i_SCRI_RS_174091	80.62	a			67.45	c	79.43	a	72.53	b			75.44	b
QWct.MAGIC.HA-6H.c	WCT	6H	132.7	i_SCRI_RS_131119	77.44	a	73.64	b	78.22	a	76.63	b	81.59	a			72.44	b
QYld.MAGIC.HA-4H.a	YLD	4H	2.1	i_12_31324	4.30	b			4.22	b	4.56	a	4.20	b			3.96	b
QYld.MAGIC.HA-5H.b	YLD	5H	80.5	i_SCRI_RS_221999	4.23	b			4.34	a	4.36	a	4.01	b			4.51	a

Trait: AGB (above ground biomass), AUDPC (area under drought progress curve), DHE (days to heading), NE (number of ears), PLH (plant height), TKW (thousand kernel weight), WCT (water content in leaves), WL (water loss), YLD (grain yield)

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] Name of SNP marker listed in http://bioinf.hutton.ac.uk/iselect/app/

AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

Different letter indicate significant differences ($p<0.05$)

Table 21: Multiple comparisons from HA for selected marker*treatment interaction

QTL-name[a]	Trait	Chr[b]	Pos[c]	iselect-name[d]	Treat	AB		AD		B		HF		HH		PI		R	
QAgb.MAGIC.HA-1H.a	AGB	1H	37.1	i_12_30969	ww	12.90	b			12.48	b	11.71	a	12.61	b			13.08	b
					td	6.78	a			6.82	a	6.56	a	6.65	a			6.62	a
QAgb.MAGIC.HA-2H.b	AGB	2H	249.0	i_11_21274	ww	12.60	a			13.31	a	12.09	b	12.07	b			12.94	a
					td	6.61	a			6.79	a	6.89	a	6.77	a			6.72	a
QAgb.MAGIC.HA-6H.a	AGB	6H	147.9	i_SCRI_RS_151280	ww	12.16	b	12.82	a	12.54	a	11.71	b	11.81	b			13.12	a
					td	6.80	a	6.74	a	6.60	a	6.75	a	6.48	a			6.95	a
QAuc.MAGIC.HA-5H.b	AUDPC	5H	217.6	i_SCRI_RS_173583	ww	35.71	ab	36.82	ab	34.13	a	36.33	ab	38.37	b	38.8	b	37.52	b
					td	65.50	a	65.81	a	65.89	a	65.20	a	66.16	a	69.25	a	64.20	a
QNke.MAGIC.HA-2H.a	NK	2H	144.2	i_SCRI_RS_160958	ww	19.16	b			19.65	b	20.15	b					33.67	a
					td	15.96	b			16.04	b	16.59	b					22.35	a
QTKW.MAGIC.HA-2H.a	TKW	2H	42.6	i_SCRI_RS_155612	ww	51.44	b			52.34	b	51.18	b					37.53	a
					td	47.74	b			48.25		47.96	b					38.08	a
QYld.MAGIC.HA-2H.a	YLD	2H	158.0	i_SCRI_RS_179555	ww	5.65	bc			5.15	c	5.75	b	5.37	bc			6.78	a
					td	2.86	a			2.66	a	2.87	a	2.96	a			2.85	a
QYld.MAGIC.HA-6H.a	YLD	6H	147.3	i_11_10175	ww	5.57	bc	5.65	c	6.05	a	5.33	b	5.24	b			5.87	ac
					td	2.91	a	2.83	a	2.89	a	2.83	a	2.76	a			2.90	a

Trait: AGB (above ground biomass), AUDPC (area under drought progress curve), NK (number of kernels), TKW (thousand kernel weight), YLD (grain yield)

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] Name of SNP marker listed in http://bioinf.hutton.ac.uk/iselect/app/

AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

Treat: ww=well watered, td=terminal drought

Different letter indicate significant differences ($p<0.05$)

3.7 Pyramidisation of QTL

The MAGIC DH-lines were analysed for the accumulation of favourable QTL within each trait in single DH-lines and in combination of favourable QTL of different traits in single DH-lines for each mapping approach.

Within each trait: BA

Seven traits were investigated for the binary approach, the remaining four traits only showed one favourable QTL.

Six QTL mapped for main marker effects for AGB were investigated for pyramidisation within the MAGIC DH-lines. No combination of all six favourable QTL (high AGB was defined as favourable) in a DH-line was detected. Two DH-lines (211 and 459) carried five favourable alleles; but only the mean of line 211 was greater than the population mean. Lines that carried four favourable alleles and had a greater mean than the population were: 232, 280, 328, 390, 468, from which line 390 had the greatest mean.

Four QTL for DHE were mapped with favourable effect (reduced DHE). Four DH-lines (153, 171, 431 and 552) were detected to carry the combination of the favourable QTL, three of those had a mean lower than the population mean. DH-line 171 had the lowest mean with 49 DHE.

Two positive effects for PLH were detected. 41 DH-lines combined the positive effects. However, the mean of 20 DH-lines was smaller than the population mean.

Two QTL for TKW had positive effects on the trait (higher TKW). 26 DH-lines carried the combination of these favourable QTL. The mean for TKW of half of the 26 DH-lines was higher than the mean of the population. DH-line 549 was outranging with a mean of 53.8 g for TKW.

Four QTL with favourable effects (reduced water loss) were mapped for the trait WL. No DH-line combined all four favourable alleles, three favourable QTL were mapped in DH-lines 76, 92 and 397. Out of these, only DH-lines 76 and 92 had a smaller value for WL than the population mean.

Five QTL with favourable effects (high amount of water content) were detected for the trait WCT. No DH-line combined all five favourable alleles. Fifteen DH-lines combined four out of five favourable alleles and thirteen of them had a greater mean for WCT than the population mean.

Five QTL with favourable effects were mapped for YLD. No DH-line was detected that combined all five favourable alleles. Only two DH-lines (145, 468) combined four favourable alleles and their mean was greater than the population mean.

Within the traits: HA

All traits except FA and NK were investigated for the haplotype approach.

Four QTL were detected which had significant positive effects for AGB. No DH-line combined all of the positive effects. DH-line 70 combined the three strongest allelic effects and its mean for AGB was greater than the mean of the population.

Five positive effects were mapped for AUDPC. No DH-line combined all of the positive effects. The two strongest effects were combined in three DH-lines (31, 100 and 554). The mean of all three lines for AUDPC was smaller than the population mean.

Four positive effects were detected for DHE. No DH-line combined all four positive effects. Three of the strongest positive effects were combined in four DH-lines (194, 195, 196 and 458). Each single mean for DHE was smaller than the population mean.

Three positive effects for DGF were detected. No DH-line combined all of the positive effects. The two strongest effects were combined in DH-line 3 and 392, both had a smaller mean for DGF than the population mean.

Two positive effects were detected for NE. Seventeen DH-lines combined the positive effects. Five out of them had a mean smaller for NE than the population mean.

Eight positive effects were detected for PLH. No DH-line combined all of the positive effects. The two strongest effects were combined in four DH-lines (41, 44, 161 and 527). Their mean for PLH was smaller than the population mean.

Four positive effects were detected for TKW. No DH-line combined all of the positive effects. The combinations of the two strongest effects were mapped in two DH-lines (70 and 161), from which only DH-line 70 had a higher TKW than the mean.

Six positive effects were mapped for the trait WL. No DH-line combined all of the positive effects. Only the two greatest effects were mapped in four DH-lines, (443, 437, 460 and 456). The means of the DH-lines 460, 443 and 437 were different to the population mean.

Seven positive effects were mapped for WCT. No DH-line combined all of the positive effects. The three strongest effects were mapped in two DH-lines (550 and 563); only the mean of DH-line 550 was greater than population mean.

Four positive effects were detected for YLD. No DH-line combined all of the positive effects. The two strongest effects were mapped as a combination in one DH-line (408). Its mean was greater than the population mean.

Across all traits: BA

The MAGIC population was as well analysed for the accumulation of favourable QTL of different traits in one DH-line. Therefore, the strongest effect of each trait was chosen and searched for the DH-line with the most combination of the positive effects. No DH-line combined all positive effects. Fourteen DH-lines combined six or more positive effects. From these fourteen only one DH-line, 429, had better phenotypic mean values than the population mean.

Across all traits: HA

The strongest positive effect of all twelve traits was chosen and a combination of the most positive effects in one DH-line was aspired. No DH-line combined all positive effects. Two DH-lines combined six positive allelic effects. From these two, DH-line 145 had better phenotypic values than the population mean at nine of twelve traits.

4. Discussion

The aim of the present MAGIC DH-line analysis was to use the advantage of the crossing scheme for a multi-parent cross to identify QTL for yield and yield components under two water scenarios. In addition, epistatic effects within the barley genome were identified. The discussion will be structured as following: First, the genetic characterization of the MAGIC population is discussed. Second, the advantages and drawbacks of the THz-sensor as a measurement for water content in leaves are analysed. Third, the mapped QTL with the two approaches are compared with each. Fourth, the clustering of QTL in the genome will be elucidated. Fifth, the mapped QTL are compared with QTL and genes known from literature. Sixth, the appropriateness of the chosen traits to investigate drought tolerance and the detected QTL are discussed in comparison with literature. Seventh, the investigated epistatic effects and their role in the expression of quantitative traits are outlined. Eight, the pyramidisation of positive allelic effects in DH-lines is elucidated. Finally, the MAGIC population as mapping population will be discussed.

4.1 Characterization of the MAGIC population

Population structure

The population structure was measured with a PCA to determine if the variability within the population was biased. It was expected that no correction would be needed if the crossing scheme was well conducted and balanced. With the low first and second principal component, which explained 6.8% and 4.1%, respectively, the variability within the population was low and needed no further correction.

Linkage disequilibrium

A detailed knowledge of LD has been considered a prerequisite for effective population-based, high-resolution gene mapping (Caldwell et al., 2006). Population history, breeding systems and the species of interest have an influence on the decay of LD. The analysis of LD in the MAGIC population showed a rapid decay of LD within the first 5 cM. This decay had been known from barley and reported by different researchers. It was more rapid then the decay of LD reported by Stracke et al. (2003) measured in an association panel of spring and winter barley. And it was close to the LD extent that had recently been reported (2.5-3.5 cM) by Comadran et al. (2009) in an association panel of 192 barley accessions from the Mediterranean basin. These reference populations are association panel, with a different population history and structure than the MAGIC population. In comparison with the four parent MAGIC population in wheat, where the

mean LD dropped down to <0.8 within the ~5 cM (Huang et al., 2012), the decay of LD in the barley MAGIC population formed an excellent base for QTL mapping.

Haplotype construction

The chance of each parent to be inherited to the offspring was theoretically equal. Therefore each parent was supposed to be represented by 12.5% on each chromosome of the offspring. The real distribution of each parent of the MAGIC population is listed in Table 17 and showed unequal distribution of the parents. First of all, the value of not explained regions of the chromosomes with an average of 37.81% was quite high. More than one third of the chromosomes of the offspring cannot be explained by any parent and therefore was handled as missing values. Genetic positions with a missing haplotype value were neglected in respect to allelic effect. Therefore, more than one third of the genome and at 2H nearly 50%, of the genetic positions did not present any results for the haplotype mapping approach. Time, effort and enhanced statistical methods are needed to improve the haplotype mapping approach.

The distribution of each parent within each chromosome was as well not consistent with the theory (Table 17). The mean distribution ranged from 0.05% (Criewener 403) to 12.1% (Barke). The parents Ackermanns Bavaria (11.3%), Barke (12.1%), Heils Franken (9.8%), Heines Hanna (11.3%) and Ragusa (9.9%) were inherited to the offspring like expected. The parents Pflugs Intensiv (1.8%), Ackermanns Danubia (6.0%) and Criewener 403 (0.1%) were underrepresented. Especially the parent Criewener 403 can be appointed as not represented within the MAGIC population. The analysis of the genetic data with the program Flapjack (Copyright © 2007-2012, Information & Computational Sciences, JHI.) (Milne et al., 2010) revealed that the parents Criewener 403 and Pflugs Intensiv genetically did not differ from each other (Fig. 10) and parent Ackermanns Danubia was 88.6% similar to them. Further genetic and phenotypic analysis about the similarity of these two barley landraces need to be conducted to reassure the contribution of the parents to the MAGIC population.

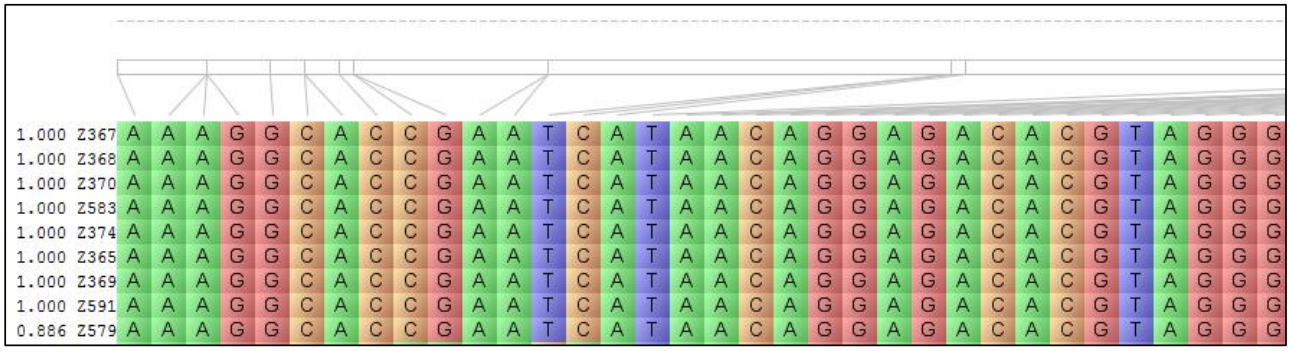

Fig. 10: Similarity of Pflugs Intensiv and Ackermanns Bavaria to parent Criewener 403 based on 5117 SNP markers used in the analysis.
Z583=Criewener 403, Z591=Pflugs Intensiv and Z579=Ackermanns Danubia. Criewener 403 and Pflugs Intensiv are to 100% similar and both to 88.6% similar to Ackermanns Danubia.

Genetic map

Recombination and crossing over happened during the crossing of the eight parents and within the following generations of crossing. Therefore, a genetic map for the offspring needed to be constructed. R/mpMap is the only program that allows a genetic map construction of a multi-parental population and was written by Huang and George (2011) and used by Huang et al. (2012) within the four parents MAGIC population in wheat. Unfortunately, in the barley MAGIC population no equal distribution of the SNP markers over the genome was achieved. On average one SNP marker was located every 1.2 cM, but big gaps between SNP markers and doubling of SNPs at one position were detected. Compared to the equal distribution of the SNP marker on the genetic map build by Comadran et al. (2012), the genetic map established with R/mpMap lacks power and precision. But compared with the genetic map of the wheat MAGIC population with a marker density of 3.3, 2.4 and 8.7 cM (Huang et al., 2012) respectively to the three genomes, the genetic map for this MAGIC population had a dense distribution of genetic markers.

4.2 THz-measurement

The multiple comparisons between the parents for the two traits measured with the THz-sensor revealed low significant differences between the parents for trait WCT. There, only two of the eight parents differed from each other. For trait WL Pflugs Intensiv was the parent with the lowest water loss value. Consequently, Ackermanns Bavaria, Barke, Heils Franken and Heines Hanna differed significantly to Pflugs Intensiv. Therefore, a high variability within the parents was detected. This high variability could not be confirmed through the mean comparisons of the inherited alleles at the detected QTL positions between the parental allelic means. No correlation has been detected between traits evaluated with the THz-Sensor and yield and yield components.

It is known from literature that the water status of leaves can be measured with a THz-sensor (Federici, 2012). One of the first applications of a THz-sensor was to measure the moisture content of tobacco products (Chan et al., 2007). Monitoring of hydration state in leaves was successfully conducted (Jordens et al., 2009; Mittleman et al., 1996). The THz-sensor was able to measure time dynamics of water transport in a leaf (Mittleman et al., 1996) and to distinguish between fully watered leaves and drying leaves. The experiments were conducted on houseplants (Mittleman et al., 1996) or on single coffee plants (Jordens et al., 2009). The following research was mostly conducted from the engineering site and focused on optimising the permittivity model. No water status measurement was ever conducted on barley before. Neither the time of plant development during drought stress nor the compensating strategies of a growing plant were taken into account, nor focused any research project on the determination of differences in water content between genotypes of the same species by the THz-sensor. Therefore, no comparison with results from literature can be undertaken. This clarifies the novelty of this study.

4.3 Comparison of the two mapping approaches

A total of 78 QTL for twelve traits were detected with the BA, a total of 65 QTL with the HA. The following chapter will discuss the simultaneously mapped QTL with both approaches and the advantages and drawbacks of each mapping approach.

4.3.1 Above ground biomass, leaf senescence and plant height

Above ground biomass

The two mapping approaches revealed 16 QTL for BA and eleven QTL for HA for above ground biomass (AGB) with $p<0.05$, of which five were mapped with both approaches. The QTL on 4H (QAgb.MAGIC.BA-4H.a and QAgb.MAGIC.HA-4H.a), mapped with both approaches, had the same most significant SNP marker position in common (10.6 cM), but the HA mapped the QTL in a wider genetic interval of 10 cM. The strength of the allelic effect was double with the HA, the strongest effect was measured between the alleles from Ragusa (9.1 g AGB) and Heils Franken (10 g AGB). The BA is not able to address the effect to a certain parent, this approach is lacking power. The same accounted for the second QTL mapped with both approaches on 4H (QAgb.MAGIC.BA-4H.c and QAgb.MAGIC.HA-4H.b), where the allele effect with BA is calculated to 0.4 g and to ±1 g with the HA. The information from the raw binary data identified Ragusa as the parent carrying the less frequent allele and the increase in AGB can be assigned to Ragusa. The results from the HA disclosed the contrasting parents Ackermanns Bavaria (9.1 g AGB) and Ragusa (10.1 g AGB) as the main allele effect.

The two QTL QAgb.MAGIC.BA-5H.d and QAgb.MAGIC.HA-5H.b were mapped into the same genetic interval but to different most significant SNP marker position, which were 12.2 cM apart. Due to the overlapping genetic intervals they were considered as same QTL. As mentioned above, the BA had less power to dissect the QTL effect compared to the HA, in this particular case the effect was four times smaller. This lack of power in the BA was particular strong if more than one parent carried the less frequent allele. This can be identified with the raw data. In case of QAgb.MAGIC.BA-5H.d, Ragusa, Pflugs Intensiv and Criewener 403 were assigned to the less frequent allele, the other parents to the more frequent allele. The allelic mean of the genotypes from different parents which carried the same alleles, due to the binary code, can interfere with each other and neutralise the effect between allele 0 and 1.

The position of the most significant marker for the QTL mapped to 7H (QAgb.MAGIC.BA-7H.a and QAgb.MAGIC.HA-7H.a) with both approaches were the same (36.9 cM), but the HA mapped the QTL into a wider genetic interval. The QTL effect was slightly higher with the HA, reason for that are mentioned above.

The only marker*treatment interaction, mapped parallel with both approaches was located with a distance of 0.7 cM between the most significant markers to chromosome 1H. The genetic interval of the QTL mapped with HA (QAgb.MAGIC.HA-1H.a) was greater (13.9 cM) than the one mapped with BA (QAgb.MAGIC.BA-1H.a) (0.7 cM). The observed differences in the QTL effect (BA= 0.6; HA= ±1.4 under well watered and BA=0; HA= ±0.2 under terminal drought) resulted from the lack of power mentioned above in the BA.

Ten QTL detected with the BA were not detected with the HA, six QTL detected with the HA but not with the BA. Two of them were overlapping with the genetic interval in which they were mapped, but the most significant SNP markers were 27.5 cM (chromosome 2H) and 27.1 cM (chromosome 5H) apart and will therefore not be counted as the same QTL.

Therefore 22 different QTL for AGB were mapped with the two mapping approaches.

Leaf senescence

The two mapping approaches revealed seven QTL for BA and six QTL for HA for leaf senescence (AUDPC), of which four could be mapped with both approaches. The QTL on 1H, QAuc.MAGIC.HA-1H.a and QAuc.MAGIC.BA-1H.a, were mapped with the most significant SNP marker 17.3 cM apart, but mapped into overlapping genetic intervals and therefore considered as the same QTL. The other parallel mapped QTL on 2H, 125.2 cM, QAuc.MAGIC.HA-2H.a and QAuc.MAGIC.BA-2H.a, and 5H, 217.6 cM, QAuc.MAGIC.HA-5H.b and QAuc.MAGIC.BA-5H.a, were mapped to the same marker position and at the QTL mapped with both approaches on 4H with

a distance of 1.4 cM. The allele effect of the HA was stronger for all parallel mapped QTL. The allelic effects came from different parents, at 1H, the biggest difference in AUDPC is measured between the allele from Ackermanns Bavaria (49.7) and Heils Franken (52.3), whereas at chromosome 2H between Barke (48.8) and Heils Franken (54.1). The only QTL with marker*treatment interaction which was mapped with both approaches was located on 5H, 217.6 cM. The HA identified the allele from Barke as the one with lowest leaf senescence under well watered conditions. The same was detected using the raw binary data. Under terminal drought conditions genotypes with the allele from Ragusa had the lowest leaf senescence. This effect could not be detected with the BA.

All the QTL that was not mapped simultaneously with both approaches have small effects and can maybe therefore not be mapped with the other approach.

Therefore, nine different QTL for AUDPC were mapped with the two mapping approaches.

Plant height

The two mapping approaches revealed six QTL for BA and eight QTL for HA for plant height (PLH), of which four could be mapped with both approaches. Three of them were main marker QTL effects, mapped to the same most significant SNP marker position with both approaches, respectively. In all cases the HA detected a stronger QTL effect than the BA and could address, in case of the QTL on 3H, QPlh.MAGIC.HA-3H.b and QPlh.MAGIC.BA-3H.c Pflugs Intensiv (90.2 cm) and Barke (73.9 cm) as the parents with most contrasting alleles. At chromosome 5H, QPlh.MAGIC.HA-5H.a and QPlh.MAGIC.BA-5H.a, Ragusa (91.5 cm) and Barke (85.1 cm) carried the most contrasting alleles. Ragusa (88.2 cm) and Ackermanns Bavaria (81.2 cm) at the QTL on 7H, QPlh.MAGIC.HA-7H.a and QPlh.MAGIC.BA-7H.a were defined as most contrasting parents. No marker*treatment interaction effects were detected with the HA, but a main marker effect at the same position like a marker*treatment interaction effect mapped with the BA on chromosome 3H, around 72 cM, QPlh.MAGIC.HA-3H.a and QPlh.MAGIC.BA-3H.a. The main marker effect from the HA can be explained by the differences from contrasting alleles from Ragusa (92.8 cm) and Heines Hanna (81.9 cm). The QTL effect from the marker*treatment interaction is 7.7 cm under well watered conditions and 3.6 cm under terminal drought between genotypes carrying the less frequent and the more frequent allele.

Ten different QTL for plant height (PLH) were mapped with the two mapping approaches.

4.3.2 Days to heading and grain filling period

Days to heading

The two mapping approaches revealed eight QTL for BA and seven QTL for HA for days to heading (DHE), of which only three could be mapped with both approaches. The three QTL that were mapped with both approaches are located on chromosome 3H with the most significant SNP marker mapped to 168.9 cM, on 5H at 206.4 cM and on 7H in a genetic interval of 30.5-32.7 cM. The comparison of the allele effects between the approaches, BA= -1.2 days and HA= -2.9, on chromosome 3H (QDhe.MAGIC.HA-3H.b and QDhe.MAGIC.BA-3H.b) pointed out the power of the HA. Not only the QTL effect was higher with the HA, but also the contribution of each parent to the effect can be assigned. The differences between the alleles from Ackermanns Bavaria and Barke were responsible for the strong QTL effect.

The same accounted for the QTL mapped to 5H, 206.4 cM (QDhe.MAGIC.HA-5H.b and QDhe.MAGIC.BA-5H.b). Information from the binary raw data assigned Ragusa as the only parent carrying the less frequent allele, which enhanced DHE by 2.4 days. The allele effect is stronger with the HA (3.2 days) and revealed the biggest differences between the allele from Ragusa (58.8 DHE) and the allele from Ackermanns Bavaria (55.6 DHE). Fig. 11 pictured the differences in the mean allelic effects as an example for the haplotype approach. Due to the raw data the mean value for allele 0 (grey) from the BA coincided with the parental allelic mean from Ragusa (blue) as seen on Fig. 11. The loss of power in the BA derived from the biased mean for allele 0 (black) which low information content compared to the parental allelic mean of Ackermanns Bavaria (red) was explicit visible in Fig. 11. This figure demonstrated as well, that the parental allelic mean, for example from Barke (orange) changed along the chromosome (here on chromosome 5H). This allowed a precise allocation of the best contributing parent. The same parental allele pattern like at QDhe.MAGIC.HA-5H.b and QDhe.MAGIC.BA-5H.b was found for the QTL on 7H, 30.5-32.7 cM. The QTL QDhe.MAGIC.HA-3H.a mapped on 3H by HA could be identical with QDhe.MAGIC.BA-3H.a, but the most significant SNPs were 8.4 cM apart and the genetic intervals were not overlapping. The rather small QTL effects on 4H and 5H detected by BA were not detected with HA and vice versa. The strong effect of QDhe.MAGIC.BA-7H.b at 36.9 cM could not be validated with the HA, a QTL at 48.0 cM, QDhe.MAGIC.HA-7H.b, was detected instead. But this QTL showed the same tendency with greater effect in DHE between Ackermanns Bavaria (53.8 DHE) and Ragusa (59.7 DHE). If these are two different QTL or the same, needs to be clarified.

Therefore, twelve different QTL for DHE were mapped with the two mapping approaches.

Grain filling period

For the trait grain filling period (DGF) four QTL were mapped with the BA and three with the HA, of which two were mapped with both programs. Whereas the two QTL were mapped with only one significant SNP marker by the BA to chromosome 5H, 53.4 cM and 6H, 106.1 cM, the HA mapped the QTL into genetic intervals of 3.8 cM and 10.7 cM, respectively. The allele effect calculated with the HA was stronger in both cases than the one from BA.

Interestingly at chromosome 5H, QDgf.MAGIC.HA-5H.a and QDgf.MAGIC.BA-5H.a, the two contrasting alleles came from Ackermanns Bavaria (37.8 DGF) and Heils Franken (39.6 DGF). At chromosome 6H, QDgf.MAGIC.HA-6H.a and QDgf.MAGIC.BA-6H.a, the pattern was vice versa, the allele from Ackermanns Bavaria led to 39.1 DGF and the one from Heils Franken to 37.9 DGF. QDgf.MAGIC.HA-2H.a, the QTL with the strongest effect, 4.9 days difference between Ragusa (33.9 DGF) and Barke (38.8 DGF), was not detected by BA. The rather small effects detected with the BA on 3H and 5H were not detected with the HA. Interaction with water treatment was calculated, but no genotype*treatment interaction was detected.

Therefore, five different QTL for DGF were mapped with the two mapping approaches.

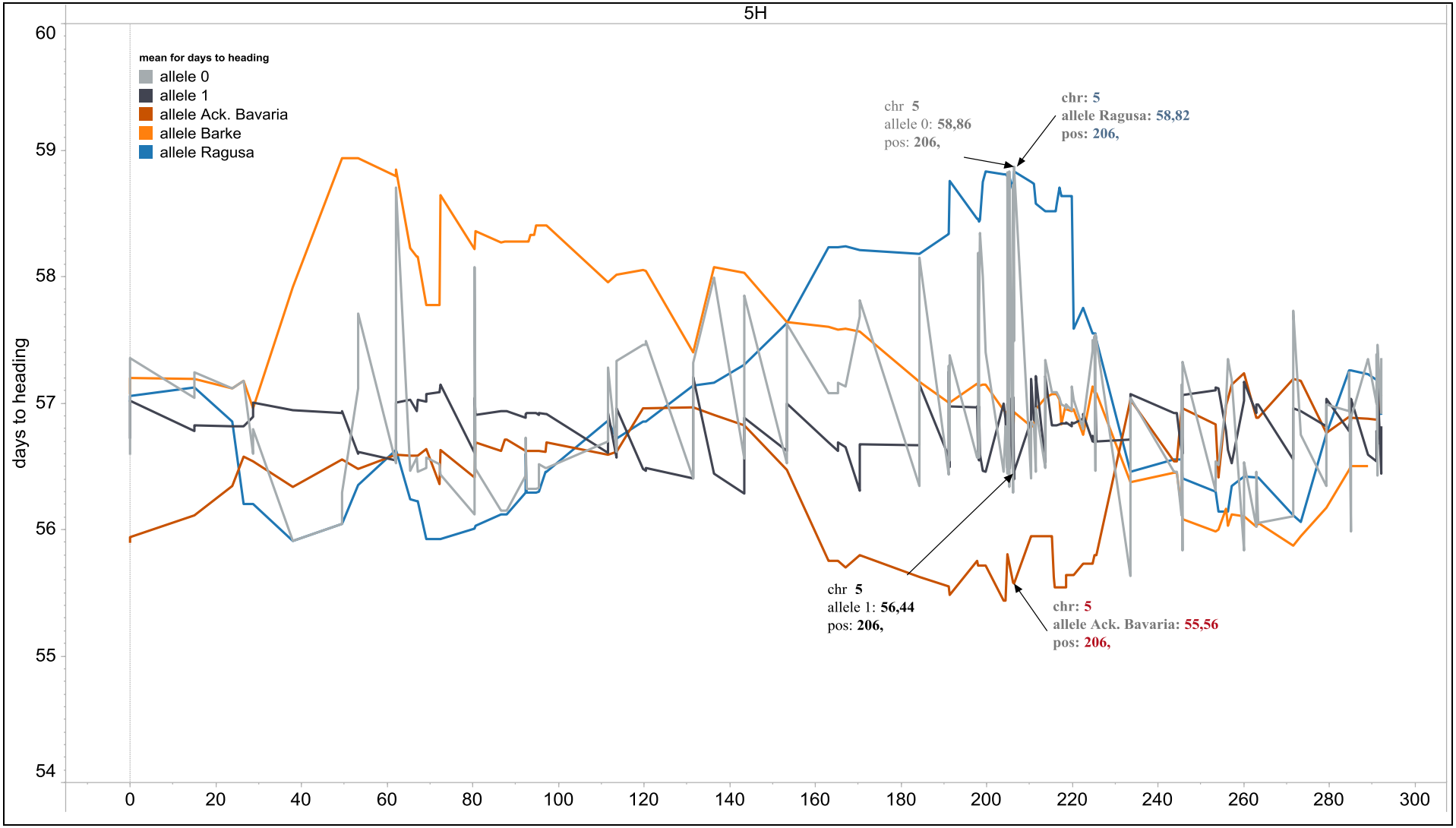

Fig. 11: Differences between the mapping power of the allelic parental means.
Ragusa (blue), Ackermanns Bavaria (red) and Barke (orange) from HA and allelic means for 0 (grey) and 1 (black) from BA for QDhe.MAGIC.HA-5H.b (QDhe.MAGIC.BA-5H.b).

4.3.3 Number of ears/ plant, number of kernels/ear and flower abortion

Number of ears/plant

Four QTL were detected with the BA on chromosome 2H, 3H and two on 5H for the trait number of ears, both on 5H were mapped with the HA as well. The HA mapped the QTL to a single significant marker at 0 cM, QNep.MAGIC.HA-5H.a and QNep.MAGIC.HA-5H.b at 206.4 cM, whereas the BA located the QTL QNep.MAGIC.BA-5H.a and QNep.MAGIC.BA-5H.b into a genetic interval of 15 cM and 8 cM, respectively. The effects of the alleles were similar with both approaches, HA enabled to address the allele from Ragusa as the one being responsible for a reduction in number of ears for QNep.MAGIC.HA-5H.a and increased number of ears for QNep.MAGIC.HA-5H.b. Therefore, four different QTL for NE were mapped with the two mapping approaches.

Number of kernels/ear

The two mapping approaches detected the same QTL at the same position or the same genetic interval for number of kernels. The most significant SNP markers were different, due to the fact that more than one marker was mapped to the same position.

Both approaches resulted in similar QTL effects for the QTL mapped to 2H, 144.2 cM, QNke.MAGIC.HA-2H.a and QNke.MAGIC.BA-2H.a. The HA addressed at the main effect the biggest differences between the alleles to the parents Ragusa and Ackermanns Bavaria. The same parental and effect pattern appeared for the marker*treatment interaction.

The allele effect mapped to 4H, QNke.MAGIC.HA-4H.a and QNke.MAGIC.BA-4H.a, differed nearly twice in its strength between the approaches but was not as strong as the one detected on 2H. The HA discovered the alleles from Ackermanns Bavaria and Ragusa as responsible for the smaller number of kernels (17.4), and from the remaining parents for a higher number of kernels (19.0 to 19.9). Due to the lower information content of the BA it underestimated the QTL effect at chromosome 4H.

Therefore, two different QTL for NK were mapped with the two mapping approaches.

Flower abortion

The number of detected QTL for flower abortion was low, two with the BA and one identical one with the HA on chromosome 2H, mapped in a genetic interval of 1.4 cM with the most significant marker at 144.2 cM, the same genetic region that was significant for a QTL for number of kernels. The effects of the QTL QFla.MAGIC.HA-2H.a and QFla.MAGIC.BA-2H.a from both

approaches were similar in their strength; the effect can be addressed with the information content from the HA to the allele from parent Ragusa.
Therefore, two different QTL for FA were mapped with the two mapping approaches.

4.3.4 Thousand kernel weight and grain yield

Thousand kernel weight

Three QTL were detected with the BA for the trait thousand kernel weight (TKW). Five QTL were detected with the HA, of which two were mapped parallel with both approaches. The parallel mapped QTL were both main marker QTL effects mapped on 2H, 141.7 cM and 5H, 206.3 cM. The QTL mapped with both approaches on 2H, QTkw.MAGIC.HA-2H.b and QTkw.MAGIC.BA-2H.a, were mapped as a main marker and marker*treatment interaction effect with the BA and only for as a main marker effect with HA. The effect for the main marker was stronger with the HA, assigning the allele from Ragusa with the lowest TKW (37.8 g) and the allele from Barke with the highest TKW (50.3 g). For the first time the information rate for the identification of a marker*treatment effect was lower in the HA compared to the BA, which detected a marker*treatment interaction with significant different allelic effects between the two water treatments. The second parallel mapped QTL, QTkw.MAGIC.HA-5H.a and QTkw.MAGIC.BA-5H.a, was a main marker effect in both approaches, the information rate with the HA was greater than with the BA.
Therefore, 6 different QTL for TKW were mapped with the two mapping approaches.

Grain yield

Eleven QTL were detected with the BA for grain yield (YLD). Six QTL were detected with the HA, of which three were mapped parallel with both approaches. The only QTL with main marker effect mapped at the same position with both approaches was on 5H at 0 cM, QYld.MAGIC.HA-5H.a and QYld.MAGIC.BA-5H.a. The HA had a greater QTL effect, addressing the alleles from Heils Franken and Ragusa for the differences in grain yield by 0.6 g.
The most significant SNP markers for the parallel mapped QTL on 2H were 4.6 cM apart, the genetic intervals of both approaches were overlapping and the QTL therefore considered as the same QTL. QYld.MAGIC.BA-2H.b was significant for a marker*treatment interaction, whereas the parallel mapped QTL with HA, QYld.MAGIC.HA-2H.a, was significant for main marker and marker*treatment interaction. The HA was able to assign the allele from Barke as the responsible one for the reduction of yield for the main QTL effect and the marker*treatment interaction under both watering treatments. The allele for the highest yield under well watered conditions came from

Ragusa, but the allele from Heines Hanna had a greater effect on increasing yield under terminal drought conditions.

Similar characteristics were detected on chromosome 4H, QYld.MAGIC.HA-4H.a and QYld.MAGIC.BA-4H.a the most significant markers are 8.5 cM apart, the HA mapped the QTL in a larger genetic interval of 10.6 cM, whereas the most significant marker of the BA represented the upper interval border. A main marker effect with HA and a main marker and marker*interaction effect with BA was detected. The alleles from Ragusa and Heils Franken were responsible for the reduced and increased yield, respectively. Further eight QTL with BA, two of them with marker*treatment interaction were detected, as well as three more with the HA, one with marker*treatment interaction.

Therefore, 14 different QTL for YLD were mapped with the two mapping approaches.

4.3.5 Water content and water loss

Water content

Eight QTL were detected with the BA for water content (WCT). Seven QTL were detected with the HA, of which four were mapped parallel with both approaches. The parallel mapped QTL on chromosome 2H, QWct.MAGIC.HA-2H.a and QWct.MAGIC.BA-2H.a, had the most significant SNP markers located 12.8 cM apart, but the location of the QTL overlapped in large genetic intervals and was therefore considered as the same QTL. The other parallel mapped QTL were located with the most significant SNP marker at the same position or 2.9 cM apart like on chromosome 6H, QWct.MAGIC.HA-6H.a and QWct.MAGIC.BA-6H.a, QWct.MAGIC.HA-6H.b and QWct.MAGIC.BA-6H.b. The allele effect explained with the HA was higher in all parallel mapped QTL, due to the greater power of detecting the contrasting alleles. But the allelic effect was not consistent to one parent, at 2H the allele from Ragusa caused the highest and in QWct.MAGIC.HA-6H.b and QWct.MAGIC.BA-6H.b, the lowest water content of all parental alleles. The same could be observed with the allele from Ackermanns Bavaria at the QTL on 5H, QWct.MAGIC.HA-5H.a and QWct.MAGIC.BA-5H.a, and QWct.MAGIC.HA-6H.a and QWct.MAGIC.BA-6H.a. Four QTL mapped with the BA and three with the HA were mapped additionally but they all had smaller effects on the trait.

Therefore, eleven different QTL for WCT were mapped with the two mapping approaches.

Water loss

Seven QTL were detected with the BA for water loss (WL). Seven QTL were detected with the HA, of which three were mapped parallel with both approaches. The position of the most

significant SNP marker for the parallel mapped QTL on 3H, QWhc.MAGIC.HA-3H.b and QWhc.MAGIC.BA-3H.b, was identical, whereas the BA mapped the QTL in a genetic interval of 14.4 cM. The other two parallel mapped QTL, one on chromosome 3H, QWhc.MAGIC.HA-3H.c and QWhc.MAGIC.BA-3H.c, and on 4H, QWhc.MAGIC.HA-4H.a and QWhc.MAGIC.BA-4H.a, had different positions for the most significant SNP marker but mapped into overlapping genetic intervals and were therefore considered as identical QTL. For the first time the calculated QTL effect at QWhc.MAGIC.BA-4H.a with the BA was greater than the one calculated for QWhc.MAGIC.HA-4H.a. The information content of the HA is quite low at this position. The probability of only two parents was assigned to haplotype blocks. Either this was due to lack of recombination within the population or to the limitation of the R/mpMap program, where a high percentage of the genome was not related to any parent (Table 17) and considered as missing data. Three QTL detected with the BA and four detected with HA were not mapped parallel with the alternative program.

Therefore, eleven different QTL for WL were mapped with the two mapping approaches.

Table 22: List of QTL mapped within the MAGIC population for twelve traits and two mapping approaches

QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	F-value	-log10(p)
Above ground biomass (AGB)							
QAgb.MAGIC.HA-1H.a	*QAgb.MAGIC.BA-1H.a*	1H	37.1	36.4-50.3	I	2.50	1.49
QAgb.MAGIC.HA-1H.b		1H	130.1	129.3-130.6	M	3.14	2.32
QAgb.MAGIC.HA-2H.a		2H	127.1	119.4-141.7	M	5.37	2.79
	QAgb.MAGIC.BA-2H.a	2H	154.6	145.2-154.6	M	12.66	2.26
	QAgb.MAGIC.BA-2H.b	2H	208.0	204.8-208.0	I	4.84	1.69
QAgb.MAGIC.HA-2H.b		2H	249.0	241.3-251.2	I	3.29	1.96
	QAgb.MAGIC.BA-3H.a	3H	57.2	57.2-72.0	M	11.26	2.35
	QAgb.MAGIC.BA-3H.b	3H	93.6	93.6-96.6	M	6.42	1.50
QAgb.MAGIC.HA-3H.a		3H	168.9	168.9	M	3.60	2.69
	QAgb.MAGIC.BA-3H.c	3H	246.3	246.3	I	7.21	1.40
	QAgb.MAGIC.BA-3H.d	3H	261.0	261.0	I	6.58	1.44
QAgb.MAGIC.HA-4H.a	*QAgb.MAGIC.BA-4H.a*	4H	10.6	0-10.6	M	3.66	2.34
	QAgb.MAGIC.BA-4H.b	4H	105.2	105.2	M	15.46	2.90
QAgb.MAGIC.HA-4H.b	*QAgb.MAGIC.BA-4H.c*	4H	163.6	155.5-163.6	M	5.32	2.52
	QAgb.MAGIC.BA-5H.a	5H	0.0	0.0	I	7.07	1.42
QAgb.MAGIC.HA-5H.a		5H	53.4	49.6-53.4	M	4.78	2.72
	QAgb.MAGIC.BA-5H.b	5H	80.5	53.4-80.5	M	10.48	2.14
	QAgb.MAGIC.BA-5H.c	5H	198.0	191.3-198.0	M/I	6.22	1.30
QAgb.MAGIC.HA-5H.b	*QAgb.MAGIC.BA-5H.d*	5H	245.8	243.8-254.3	M	4.10	3.59
	QAgb.MAGIC.BA-6H.a	6H	31.6	31.6	I	10.47	2.85
QAgb.MAGIC.HA-6H.a		6H	147.9	139.2-160.0	I	3.46	2.10
QAgb.MAGIC.HA-7H.a	*QAgb.MAGIC.BA-7H.a*	7H	36.9	30.7-48.4	M	3.07	2.14
Leaf senescence (AUDPC)							
QAuc.MAGIC.HA-1H.a	*QAuc.MAGIC.BA-1H.a*	1H	126.4	126.4-127.1	M	2.65	2.08

QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	F-value	-log10(p)
QAuc.MAGIC.HA-2H.a	*QAuc.MAGIC.BA-2H.a*	2H	125.2	124.8-125.2	M	10.83	6.30
	QAuc.MAGIC.BA-3H.a	3H	261.0	261.0	M	12.62	2.52
QAuc.MAGIC.HA-4H.a		4H	61.3	61.3	M	5.31	3.47
QAuc.MAGIC.HA-4H.b	*QAuc.MAGIC.BA-4H.a*	4H	151.2	151.2-158.4	M	16.61	9.53
QAuc.MAGIC.HA-5H.a		5H	67.3	67.0-67.3	M	3.50	1.77
QAuc.MAGIC.HA-5H.b	*QAuc.MAGIC.BA-5H.a*	5H	217.6	217.6	I	2.31	2.02
	QAuc.MAGIC.BA-6H.a	6H	160.0	147.3-160.0	M	11.34	2.51
	QAuc.MAGIC.BA-7H.a	7H	236.6	236.6	I	4.74	1.39
Grain filling period (DGF)							
QDgf.MAGIC.HA-2H.a		2H	29.9	27.5-42.6	M	10.42	6.35
	QDgf.MAGIC.BA-3H.a	3H	27.7	27.7	M	20.68	4.12
QDgf.MAGIC.HA-5H.a	*QDgf.MAGIC.BA-5H.a*	5H	49.6	49.6-53.4	M	9.39	6.24
	QDgf.MAGIC.BA-5H.b	5H	263.1	263.1-271.6	M	20.67	3.45
QDgf.MAGIC.HA-6H.a	*QDgf.MAGIC.BA-6H.a*	6H	101.9	101.9-112.6	M	6.02	3.65
Days to heading (DHE)							
QDhe.MAGIC.HA-3H.a		3H	56.8	54.2-56.8	M	12.54	10.26
	QDhe.MAGIC.BA-3H.a	3H	65.2	58.6-65.2	M	30.44	5.33
QDhe.MAGIC.HA-3H.b	*QDhe.MAGIC.BA-3H.b*	3H	168.9	156.2-168.9	M	9.80	10.34
	QDhe.MAGIC.BA-4H.a	4H	2.1	0-2.1	M	28.55	5.76
	QDhe.MAGIC.BA-4H.b	4H	69.7	68.2-69.7	M	43.50	8.74
QDhe.MAGIC.HA-4H.a		4H	190.3	190.3	M	9.78	3.78
	QDhe.MAGIC.BA-5H.a	5H	143.6	136.4-143.6	M	13.72	3.30
QDhe.MAGIC.HA-5H.a		5H	198.0	191.5-198.0	M	4.91	3.14
QDhe.MAGIC.HA-5H.b	*QDhe.MAGIC.BA-5H.b*	5H	206.4	206.4	M	23.30	19.72
QDhe.MAGIC.HA-7H.a	*QDhe.MAGIC.BA-7H.a*	7H	32.7	30.7-32.7	M	10.55	7.24
	QDhe.MAGIC.BA-7H.b	7H	36.9	33.5-36.9	M	208.29	34.05
QDhe.MAGIC.HA-7H.b		7H	48.0	48.0-48.4	M	41.87	34.28
Flower abortion (FA)							
QFla.MAGIC.HA-2H.a	*QFla.MAGIC.BA-2H.a*	2H	144.2	142.8-144.2	M	413.59	128.52
	QFla.MAGIC.BA-3H.b	3H	129.2	129.2	M	28.34	4.42
Number of ears (NE)							
	QNep.MAGIC.BA-2H.a	2H	126.2	126.2-144.2	M	18.99	3.99
	QNep.MAGIC.BA-3H.a	3H	82.3	72.0-82.3	M	37.42	7.36
QNep.MAGIC.HA-5H.a	*QNep.MAGIC.BA-5H.a*	5H	0.0	0.0	M	12.72	5.97
QNep.MAGIC.HA-5H.b	*QNep.MAGIC.BA-5H.b*	5H	206.4	206.4	M	12.08	9.18
Number of kernels (NK)							
QNke.MAGIC.HA-2H.a	*QNke.MAGIC.BA-2H.a*	2H	144.2	144.2	M/I	20.45	10.07
QNke.MAGIC.HA-4H.a	*QNke.MAGIC.BA-4H.a*	4H	33.7	33.7-34.1	M	5.81	4.58
Plant height (PLH)							
QPlh.MAGIC.HA-1H.a		1H	76.0	70.5-76.0	M	3.19	2.04
QPlh.MAGIC.HA-2H.a		2H	26.2	25.6-26.2	M	2.93	1.42
QPlh.MAGIC.HA-2H.b		2H	154.6	154.6	M	4.96	2.47
QPlh.MAGIC.HA-3H.a	*QPlh.MAGIC.BA-3H.a*	3H	73.7	73.7-74.6	M (I)	22.50	13.07
	QPlh.MAGIC.BA-3H.b	3H	134.6	134.6-145.6	M	30.12	5.33
QPlh.MAGIC.HA-3H.b	*QPlh.MAGIC.BA-3H.c*	3H	161.6	161.6-168.9	M	43.01	36.21
	QPlh.MAGIC.BA-4H.a	4H	163.6	158.4-163.6	M	25.37	5.23
QPlh.MAGIC.HA-5H.a	*QPlh.MAGIC.BA-5H.a*	5H	0.0	0.0	M	21.59	12.04
QPlh.MAGIC.HA-6H.a		6H	108.4	101.9-110.7	M	6.67	4.24
QPlh.MAGIC.HA-7H.a	*QPlh.MAGIC.BA-7H.a*	7H	36.9	33.5-36.9	M	8.25	5.76
Thousand kernel weight (TKW)							
QTkw.MAGIC.HA-2H.a		2H	42.6	29.9-42.6	M/I	6.55	4.90
QTkw.MAGIC.HA-2H.b	*QTkw.MAGIC.BA-2H.a*	2H	141.7	126.2-147.7	M (I)	186.82	79.09
QTkw.MAGIC.HA-4H.a		4H	102.4	98.7-102.4	M	6.69	3.22

QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	F-value	-log10(p)
QTkw.MAGIC.HA-5H.a	*QTkw.MAGIC.BA-5H.a*	5H	206.3	206.3	M	15.49	11.55
	QTkw.MAGIC.BA-6H.a	6H	64.6	64.6	M	37.83	6.87
QTkw.MAGIC.HA-6H.a		6H	82.2	82.2-91.3	M	14.44	10.50
Water loss (WL)							
QWhc.MAGIC.HA-1H.a		1H	97.6	95.0-97.6	M	3.41	2.60
QWhc.MAGIC.HA-3H.a		3H	15.7	8.0-15.7	M	3.05	2.20
	QWhc.MAGIC.BA-3H.a	3H	27.7	23.4-54.2	M	22.31	4.23
QWhc.MAGIC.HA-3H.b	*QWhc.MAGIC.BA-3H.b*	3H	82.3	82.3	M	7.53	5.30
QWhc.MAGIC.HA-3H.c	*QWhc.MAGIC.BA-3H.c*	3H	189.4	187.3-191.2	M	2.46	1.76
QWhc.MAGIC.HA-4H.a	*QWhc.MAGIC.BA-4H.a*	4H	190.3	190.3-206.4	M	11.30	3.17
	QWhc.MAGIC.BA-5H.a	5H	0.0	0.0	M	10.68	2.00
	QWhc.MAGIC.BA-5H.b	5H	26.6	23.9-28.2	M	27.21	4.25
QWhc.MAGIC.HA-5H.a		5H	67.0	65.4-67.0	M	7.24	3.69
	QWhc.MAGIC.BA-5H.c	5H	111.7	111.7-113.8	M	7.02	1.66
QWhc.MAGIC.HA-6H.a		6H	81.7	77.7-82.2	M	2.24	1.31
Water content (WCT)							
	QWct.MAGIC.BA-1H.a	1H	103.5	103.5-134.4	M	7.64	1.66
QWct.MAGIC.HA-2H.a	*QWct.MAGIC.BA-2H.a*	2H	42.6	42.6-55.4	M	2.69	1.34
QWct.MAGIC.HA-2H.b		2H	254.1	254.1	M	2.93	1.90
	QWct.MAGIC.BA-4H.a	4H	25.1	25.2-30.8	M	6.50	1.53
	QWct.MAGIC.BA-4H.b	4H	85.6	85.6-98.7	M	10.21	2.09
QWct.MAGIC.HA-5H.a	*QWct.MAGIC.BA-5H.a*	5H	62.2	62.2-67.3	M	21.95	14.08
	QWct.MAGIC.BA-5H.c	5H	271.6	271.6	M	27.04	4.59
QWct.MAGIC.HA-6H.a	*QWct.MAGIC.BA-6H.a*	6H	20.2	14.1-20.2	M	13.07	8.20
QWct.MAGIC.HA-6H.b	*QWct.MAGIC.BA-6H.b*	6H	110.4	110.4-110.7	M	6.69	3.51
QWct.MAGIC.HA-6H.c		6H	132.7	127.0-132.7	M	4.40	2.93
QWct.MAGIC.HA-6H.d		6H	160.0	160.0	M	4.06	1.92
Grain yield (YLD)							
	QYld.MAGIC.BA-1H.a	1H	36.4	36.4	I	5.59	1.45
QYld.MAGIC.HA-1H.a		1H	95.0	95.0	M	3.13	2.57
	QYld.MAGIC.BA-2H.a	2H	128.0	127.7-128.7	M	10.08	2.10
QYld.MAGIC.HA-2H.a	*QYld.MAGIC.BA-2H.b*	2H	158.0	154.6-170.5	M/I	3.38	2.56
	QYld.MAGIC.BA-2H.c	2H	187.4	187.4	M	21.16	3.99
	QYld.MAGIC.BA-2H.d	2H	241.3	241.3	I	5.26	1.70
QYld.MAGIC.HA-4H.a	*QYld.MAGIC.BA-4H.a*	4H	2.1	0-10.64	M (M/I)	4.98	2.77
QYld.MAGIC.HA-5H.a	*QYld.MAGIC.BA-5H.a*	5H	0.0	0.0	M	5.55	2.65
QYld.MAGIC.HA-5H.b		5H	80.5	80.5	M	3.30	1.60
	QYld.MAGIC.BA-5H.b	5H	205.0	205.0-206.4	M	13.40	2.26
	QYld.MAGIC.BA-6H.a	6H	139.2	139.2	M	10.54	2.30
QYld.MAGIC.HA-6H.a		6H	147.3	146.1-147.9	I	3.43	2.82
	QYld.MAGIC.BA-7H.a	7H	149.6	138.3-149.6	M	16.38	3.04
	QYld.MAGIC.BA-7H.b	7H	217.6	216.4-236.8	M	8.83	1.81

QTL mapped with both approaches are written in italic

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] CentiMorgan range from the first to the last significant marker in a QTL

[e] A putative QTL was assumed in a vicinity of a marker locus, if the marker main effect (M) or /and marker*treatment interaction (I) was significant with $P<0.05$ or $P<0.001$, depending on the trait of interest

The contribution of each parent at the genetic position of interest was examined through the calculated allelic mean at the QTL position. This provides an additional information content gained through the haplotype approach as mentioned in 4.3. The comparisons between the allelic means of the parents were conducted as multiple comparisons to investigate the significant differences of all parental means to each other. From the eighteen investigated QTL only one, QAuc.MAGIC.HA-4H.a, was discovered were only two of the parents, Heils Franken and Ragusa, the most contrasting ones, were significant to each other. All the remaining parents were not significant different to Heils Franken with the highest AUDPC value or Ragusa, with the lowest AUDPC value.

The multiple comparisons at four QTL discovered that one parental mean was significant to all other parental mean. This was detected at QNep.MAGIC.HA-5H.b and QTKW.MAGIC.HA-2H.a, were the parental mean of Ragusa was identified as the extreme value. The inclusion of Ragusa as a parent into the MAGIC population enhanced the allelic diversity within the population due to a different origin of Ragusa compared to the other seven parents. The extreme values identified at the other two QTL, QAuc.MAGIC.HA-4H.b and QYld.MAGIC.HA-4H.a can be assigned to Barke and Heils Franken, respectively. The mean of Barke had a high allelic effect at that position on the trait AUDPC. Barke was the only modern variety that contributed to the crossing scheme of the MAGIC population. Barke was genetically separated from the remaining parents, which are all landraces, by approximately 90 years of active barley breeding. This is illustrated in the breeding success as in the shorter phenotype of Barke with higher biomass at shorter tillers. This could lead to a tendency of higher AUDPC scores. At QYld.MAGIC.HA-4H.a, the allelic mean of Heils Franken outranged all other parental means. The parental mean for yield at this position was higher than the one from Barke, which was expected to have a higher effect on yield, due to the status as a modern variety.

The QTL for DHE under investigation for multi comparisons showed nearly the same parental pattern. The allelic effect from Ragusa was always the highest, with the longest time until heading. The allelic effect from Ackermanns Bavaria was always the lowest. Therefore, the allelic effect for the QTL was significant between these two parental means. The multiple comparisons of DHE unravelled further significant differences. The parental mean of Heines Hanna was always significant different to the mean of Ragusa and the mean of Ackermanns Bavaria. The distinct groups were investigated in all three QTL, which indicates a stable contribution of the parents to this trait DHE.

In summary, 35 QTL were detected with both approaches. Additionally, 43 QTL were detected with the binary approach and 30 with the haplotype approach (Table 22). Both approaches showed advantages and drawbacks. Rating the approaches by their strength of the -log10 (p) and

mean allelic effects the haplotype approach performed better in all except one of the 35 QTL (Fig. 12). This allows the conclusion that the haplotype approach is more precise in calculating the actual effect of a QTL. Rating the approaches by the size of the genetic interval in which the QTL was mapped, the binary approach shows advantages due to the specification of a smaller genetic interval. This is clearly demonstrated in Fig. 11.

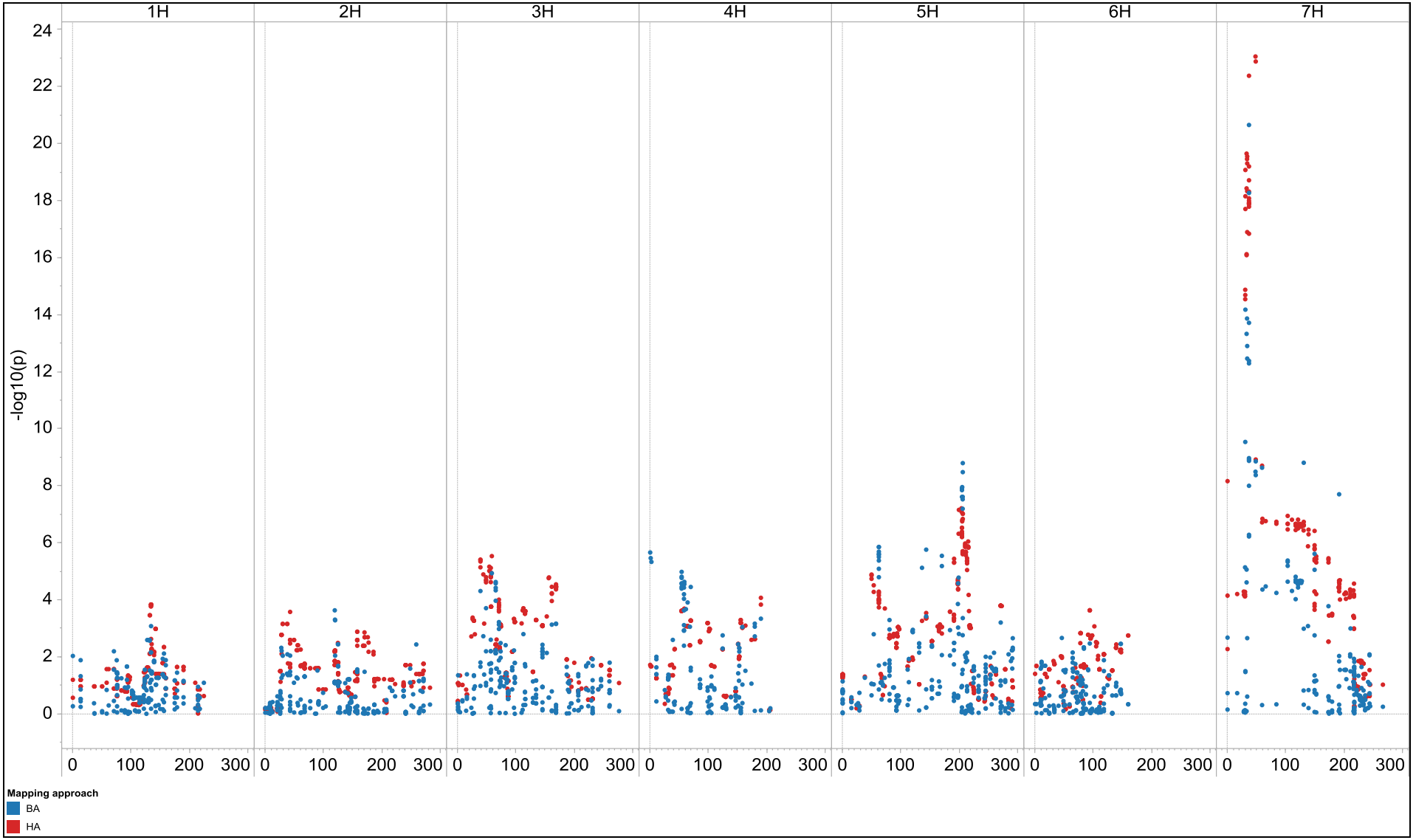

Fig. 12: Mapping power of the BA (blue) and HA (red).
Exemplified at the trait DHE represented by –log10 (p) of the first multi-locus analysis with the SAS QTL mapping program.

4.4 Distribution of QTL within the genome

The distribution of the QTL was not random within the genome for agronomic traits. The majority of the QTL was detected on chromosome 2H, 3H and 5H (Fig. 13). Several QTL for different traits were found in genetic proximity to each other and were considered as QTL cluster. The QTL were mapped at the same position or within genetic intervals. Cluster for the traits YLD and AGB were found on 1H, three on 2H, 4H, 5H and 6H, of which the cluster on 1H, 2H (around 141 cM) and 6H showed traits with marker*treatment interaction effects. A strong and highly significant correlation between these traits was detected under both watering conditions which support the idea that these traits are controlled by the same locus (McKay et al., 2003).

A second interesting group of traits clustered including QTL related to water status of leaves (WCT or WL). Two clusters were detected on 1H, the first one included QTL for YLD and WL. Due to the results from the haplotype approach, the allele from Heils Franken at this locus can be assigned as the allele for an increase in grain yield and the lowest water loss during the drying period measured with the THz sensor. A second cluster, including QTL for WCT, AUDPC and AGB was detected close by (around 103-130 cM). Unfortunately, the QTL for WCT was only detected by the BA; the alleles leading to high water content in leaves are common in Ackermanns Bavaria, Heines Hanna and Ragusa. The remaining two QTL of the cluster were mapped with the HA and assigned the positive effects, low AUDPC despite high AGB to the allele from Ackermanns Bavaria, too. Summarizing, the allele from Ackermanns Bavaria had a positive effect on the QTL in a cluster on chromosome 1H.

A group of QTL clustered on chromosome 5H, 0.0 cM for different traits, among these was a QTL for WL and YLD. Again, the QTL for WL was only mapped by the BA; the more frequent allele had a significant lower water loss over time in the leaves and was inherited by Ackermanns Bavaria, Barke, Heils Franken and Ragusa. The allele from Heils Franken was responsible for the highest allelic effect for the trait yield, mapped at the same position on the chromosome. Summarizing, the allele from Heils Franken had a positive QTL effect on water loss and grain yield. Another cluster of QTL was detected on 5H, around 62-80 cM, including QTL for WCT, WL, AUDPC and AGB. Except for the effect for AGB all were mapped with the HA. But the raw data from the BA assigned Barke as the sole parent inheriting the less frequent allele and increasing the AGB by 0.5 g. Interestingly, the allele from Barke was responsible for the second lowest leaf senescence (AUDPC) but for the lowest water content after 96 hours of drying (WCT). A comparison between the parents for the mean of AUDPC over two years showed that Barke had a quite low leaf senescence under well watered, and the lowest under terminal drought conditions. This could be due to the breeding process of the last 90 years, Barke as the only modern variety in

this set of parents could also be characterized by the QTL effect for AUDPC as a "stay green" genotype, representing the improvement in plant breeding. But that does not legitimate the high effect of the allele from Barke for the high water loss (WL) or the low water content (WCT), the other way round: a low effect on leaf senescence would expect a low water loss. This requires further analysis.

A similar pattern was detected on chromosome 6H, 160 cM with a cluster of two QTL of AUDPC and WCT. Unfortunately, the allelic effect for AUDPC was only mapped with BA, but the raw data results showed the parent Ackermanns Danubia and Heines Hanna carried the less frequent allele which was responsible for a higher AUDPC compared to the more frequent allele. The QTL effect from WCT assigned the most contrasting effects coming from the allele from Heines Hanna, which increased the water content after 96 hours of drying to 84.6%, and to the allele from Ackermanns Danubia (72%). This implied that AUDPC and water content or water loss are contrasting traits. Genotypes with low water loss during their juvenile stage cannot be selected for low AUDPC. The determination of water loss cannot be used a selection criteria for leaf senescence in the later growing stage of the plant.

Several QTL studies have reported clustering of QTL (Li et al., 2007; McCartney et al., 2006; Pillen et al., 2003). Results from the QTL analysis of the MAGIC population from *Arabidopsis* showed clustering of a QTL for days to germination within a nitrilase gene cluster on chromosome 3H (Kover et al., 2009). This cluster phenomenon could be considered as "multifactorial linkages" followed by natural selection favouring co-adapted traits. Further it is possible, that the clustering is based on pleiotropy of unknown key factors controlling various traits through diverse metabolic pathways (Cai and Morishima, 2002). In barley as an inbreeding species, natural hybridisation may have played an important role during the domestication process, preserving chromosome blocks carrying co-adapted genes.

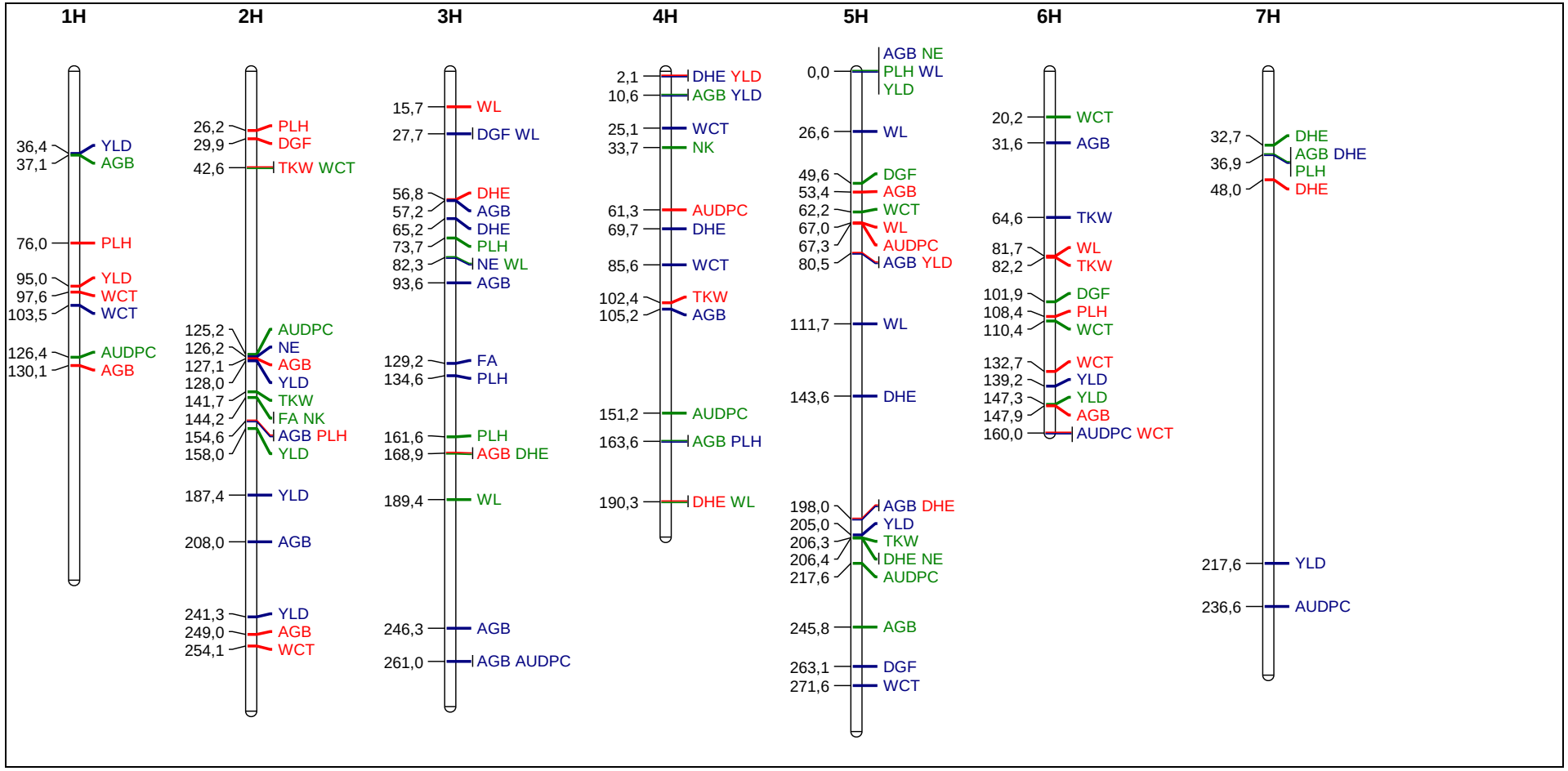

Fig. 13: Map of seven linkage groups of barley and the genetic position of the QTL in cM.
QTL in blue originated from BA, QTL in red from HA. QTL mapped with both approaches were marked in green.

4.5 Confirmed and novel QTL: comparison with known QTL and candidate genes

The results from QTL mapping for yield and yield related traits in the MAGIC population were compared with studies of candidate genes and other QTL and association mapping approaches in barley, in particular to Pasam et al. (2012), Comadran et al. (2011b), Wang et al. (2010), Schmalenbach et al. (2009) von Korff et al. (2008) and von Korff et al. (2006). The results were compared to Varshney et al. (2012), Comadran et al. (2008), Talame et al. (2004), Forster et al. (2004), Baum et al. (2003) and Teulat et al. (2001b) under the aspect of drought environments and the identification of QTL and genes responsible for drought tolerance. The mapping populations used in the compared studies had different genetic approaches for the detection of drought tolerant QTL or genes. Baum et al. (2003), von Korff et al. (2006), Schmalenbach et al. (2009), Talame et al. (2004) and Wang et al. (2010) used populations or advanced backcrosses of a genotype with a wild barley accession (*Hordeum vulgare* ssp. *spontaneum*), Forster et al. (2004) used a doubled haploid population from a cross of two genotypes, Derkado and B83-12/21/5, von Korff et al. (2008) and Teulat et al. (2001b) used progenies from the cross of Tadmor and ER/Apm to test their performance in QTL mapping and under drought stress conditions. Comadran et al. (2008), Pasam et al. (2012) and Varshney et al. (2012) tested association panels under abiotic stress conditions to investigate QTL under drought stress and to study the performance of association mapping. Table 23 and Fig. 14 displays the QTL detected in the MAGIC DH-lines as main marker and marker*treatment interaction and coinciding gene candidates from BLASTn and candidate genes and QTL from studied literature. Comparing the exact genetic position between the coinciding QTL is not feasible, different genetic maps were used for the QTL studies. The QTL from the MAGIC population listed in Table 23 as coinciding were mapped in the same genetic region. Altogether, 26 of the QTL detected in the MAGIC population corresponded to QTL and genes found in literature or in a database. Comparing the QTL effects is not feasible as well; different crossing schemes, different parents and different statistical programs were used within the studies. With the exception of the association studies, bi-parental crossings were used for QTL mapping. In cases of populations with a *Hordeum spontaneum* parent, the contribution of the exotic allele to the QTL was calculated. Only if the QTL was mapped with the HA, a direct contribution from a single parent can be assigned to the QTL effect. The most coinciding QTL were detected for plant height, yield and above ground biomass. No QTL could be validated for leaf senescence (AUDPC) or water status and water loss, measured with the THz-Sensor. Each trait will be discussed below.

4.5.1 Days to heading

Heading date is a critical trait for adaption to different environments and cultivation areas. It is the result of the interaction of different environmental factors and genes, including vernalization, photoperiodic response or earliness *per se*. Most QTL mapping populations in the past used a cross between a winter and spring barley, to investigate the vernalization and photoperiodic genes. The parents of the MAGIC population are all spring barley, with the exception of Ragusa, which can be assigned as a semi-type. Therefore, out of the classical studied flowering genes only *Vrn-H3* could be of interest in the MAGIC population. The QTL QDhe.MAGIC.HA-7H.a was mapped with both approaches to the short arm of chromosome 7H. This position corresponded to the barley vernalization gene *Vrn-H3* (Laurie et al., 1995; Yan et al., 2006), which was confirmed among others by Schmalenbach et al. (2009) (QHea.S42IL-7H.a) and mapped recently to chromosome 7H, 28.8 cM, by Comadran et al. (2012). QDhe.MAGIC.HA-7H.a (QDhe.MAGIC.BA-7H.a) for days to heading corresponded to the gene *HvGI*, mapped by Wang et al. (2010). Ten unique QTL for days to heading were detected in the MAGIC population.

4.5.2 Plant height

The most QTL could be confirmed for the trait plant height, which is a well a studied trait in barley. QPlh.MAGIC.HA-1H.a could be confirmed by Schmalenbach et al. (2009) to Qhei.S4IL-1H.a and QPlh.MAGIC.HA-2H.b to QHt.StMo-2H.2 was mapped by Hayes et al. (1993) on chromosome 2H. One QTL on chromosome 3H, QPlh.MAGIC.HA-3H.a (QPlh.MAGIC.BA-3H.a), coincided with a QTL detected by Baum et al. (2003), PH.3H-4, and Pasam et al. (2012), QTL7_PHT. A second QTL on 3H, QPlh.MAGIC.BA-3H.b coincided with the dwarfing gene *swd1/denso* from Laurie et al. (1995), which was detected in several studies. The QPlh.MAGIC.HA-3H.b (QPlh.MAGIC.BA-3H.c) coincided with QTL QTL.9_PHT and QTL QPlh.MAGIC.HA-6H.a matched with QTL17_PHT, both mapped by Pasam et al. (2012). The QTL QPlh.MAGIC.HA-7H.a (QPlh.MAGIC.BA-7H.a) for plant height was confirmed by a mapped QTL von Korff et al. (2008) (Qhei.S42.-7H.b). Three unique QTL for plant height were mapped in the MAGIC population.

4.5.3 Grain yield and yield components

Grain yield is well known as a complex trait, especially in interaction with drought conditions. It has always been one of the most important breeding goals and therefore is a well studied trait. Dissecting the complex trait grain yield into components which may be under simpler genetic control has been one of the approaches to understand the trait. Therefore, in this study not

only grain yield was analysed, but as well above ground biomass, flower abortion, number of ears, number of kernels per ear and the thousand kernel weight.

Above ground biomass (ABG)

Five QTL for above ground biomass coincided with known QTL from literature; one QTL from the MAGIC population, QAgb.MAGIC.BA-5H.b matched with BYnb.5H-4 mapped by Baum et al. (2003). Three QTL, QAgb.MAGIC.HA-3H.a, QAgb.MAGIC.BA-4H.b and QAgb.MAGIC.HA-4H.b (QAgb.MAGIC.BA-4H.c) were already mapped in von Korff et al. (2006) as Qmas.S42-3H.a, Qmas.S42-4H.a and Qmas.S42-4H.b. respectively.

The first marker*treatment interaction QTL QAgb.MAGIC.HA-1H.a (QAgb.MAGIC.BA-1H.a) detected for above ground biomass was confirmed by the QTL BYnb.1H-1 in the study from Baum et al. (2003), in which a set of AB-QTL RILs were phenotyped under two rain fed levels, based on the location of the research station. In the AB-QTL study, the exotic allele from *Hordeum spontaneum* had a positive effect of the biomass under drought conditions. The marker*treatment effect in the MAGIC population was detected by both approaches. Under well watered conditions, the allele from Ragusa had the biggest effect on the above ground biomass, enhancing it by 0.6 g/plant compared to the modern variety Barke. But under terminal drought conditions, the positive effect to produce high amount of biomass was assigned to the genotype Ackermanns Bavaria, which had the highest effect on the trait. Seventeen additional QTL were mapped in the MAGIC population, which were not mentioned in barley literature before.

Flower abortion (FA) number of ears (NE), number of kernels (NK) and thousand kernel weight (TKW)

One QTL, QFla.MAGIC.HA-2H.a (QFla.MAGIC.BA-2H.a), matched via BLASTn of the most significant SNP marker sequence with the *vrs1* gene for row-type (Komatsuda et al., 2007). The detected QTL QNke.MAGIC.HA-2H.a (QNke.MAGIC.BA-2H.a) and QTkw.MAGIC.HA-2H.b (QTkw.MAGIC.BA-2H.a) were mapped at the same position and therefore confirm the *vrs1* gene as well. The QTL for number of kernels, QNke.MAGIC.HA-2H.a (QNke.MAGIC.BA-2H.a), mapped in the MAGIC population on chromosome 2H, 144.2 cM had main marker and marker*treatment interaction effects and was mapped parallel with both approaches. This QTL coincided with detected QTL by Comadran et al. (2011) under drought environments.

A second QTL for number of kernels, QNke.MAGIC.HA-4H.a (QNke.MAGIC.BA-4H.a) matched with the region of the gene *int-c* (Waugh et al., 2009) and coincided with a QTL mapped by

Comadran et al. (2011) in the association panel. All these allelic effects pointed out the influence of row type number to these traits. One QTL in the MAGIC population, QNep.MAGIC.HA-5H.a (QNep.MAGIC.BA-5H.a), for number of ears, as a component trait for yield, was mapped by von Korff et al. (2006) as the QTL Qear.S42-5H.a and as SNP 11_20553 by Comadran et al. (2011) at the beginning of the short arm of chromosome 5H. Besides the one QTL for TKW mentioned above all remaining QTL mapped in the MAGIC DH-lines for TKW were mapped in other populations as well.

The main marker and marker*treatment interaction effect in the MAGIC population, QTkw.MAGIC.HA-2H.a, was mapped as QTL4_TGW by Pasam et al. (2012), and as a interaction effect with drought environment as tkw_br (bPb_4875) by Varshney et al. (2012), who tested an association panel on two contrasting experimental sites in Syria, concerning the amount of rainfall. Three more allele effects for thousand kernel weight, QTkw.MAGIC.HA-4H.a, QTkw.MAGIC.HA-5H.a (QTkw.MAGIC.BA-5H.a) and QTkw.MAGIC.HA-6H.a were detected on 4H, 5H and 6H, all coincided with QTL mapped by Baum et al. (2003) (KW.4H-3) on 4H, Pillen et al. (2003) (QTgw.pil-5H.4), Pasam et al. (2012) (QTL16_TGW) and Forster et al. (2004) (TGW*) on 5H and Forster et al. (2004) on 6H (TGW). QTkw.MAGIC.BA-6H.a mapped in the MAGIC population by the BA coincided with the QTL Qkw-tera_6H.a by von Korff et al. (2008), BCD348B by Teulat et al. (2001b) and KW.6H-2 by Baum et al. (2003) on 6H. One unique QTL was mapped in the MAGIC population for flower abortion, three unique ones for number of ears. The QTL mapped for number of kernels and thousand kernel weight were all mapped in literature before.

For grain yield, five QTL could be confirmed with known QTL from literature. The QTL QYld.MAGIC.HA-5H.b coincided with Qyld.S42-5H.b detected by von Korff et al. (2006), HvUDPGPPxYLD by Pillen et al. (2003), CDO344 by Teulat et al. (2001b), GY.5H-4 by Baum et al. (2003) and Forster et al. (2004) on chromosome 5H. The second one, QYld.MAGIC.BA-7H.b on chromosome 7H, matched with QTL S5D, A5D, T5D detected by Comadran et al. (2008) and WG380 Teulat et al. (2001b). One QTL for marker*treatment interaction, QYld.MAGIC.BA-1H.a was located on chromosome 1H and coincided with a QTL for grain yield detected by Talame et al. (2004) in a doubled haploid population from Barke and HOR11508, a wild barley accession, grown under water deficit in three Mediterranean countries. For all three locations, the allele from Barke increased the yield in his study. The QTL in the MAGIC population was only detected with the BA; a favourable parent for that trait cannot be assigned, neither with the raw data. The second QTL for marker*treatment interaction, QYld.MAGIC.BA-4H.a, coincided with a QTL from Comadran et al.

(2008) (T4D) and Talame et al. (2004) (E33M60-130), where again Barke carried the favourable allele at the location of the QTL. Again in the MAGIC population the QTL was detected by the BA, no particular parent of the crossing can be addressed. Another QTL for a marker*treatment interaction detected on chromosome 6H, QYld.MAGIC.HA-6H.a coincided with a QTL for grain yield by Talame et al. (2004). Once more, in his study Barke carried the favourable allele at the position. Barke was the parent carrying the favourable allele under well watered conditions in the MAGIC population as well, leading to a grain yield of 6.1 g/plant. But under terminal drought conditions the positive allelic effect was inherited from the parent Ackermanns Bavaria.

The allele effects are not comparable between the studies, but the position on the chromosome for an effect on yield under drought conditions is repeatable, that is the benefit of all the studies conducted under drought conditions. Nine unique QTL were detected for grain yield.

The traits AUDPC, DGF and the one evaluated with the THz-sensor were never discussed in literature so far. Therefore, the QTL for these traits mapped in the MAGIC population are unique.

Table 23: List of detected QTL in the MAGIC DH-lines that coincide with genes and QTL from literature

Trait	QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	Candidate genes/QTL	Reference
Above ground biomass (AGB)								
	QAgb.MAGIC.HA-1H.a	QAgb.MAGIC.BA-1H.a	1	37.1	36.4-50.3	I	BYnb.1H-1	Baum et al., 2003
	QAgb.MAGIC.HA-3H.a		3	168.9	168.9	M	Qmas.S42-3H.a	von Korff et al., 2006
		QAgb.MAGIC.BA-4H.b	4	105.2	105.2	M	Qmas.S42-4H.a	von Korff et al., 2006
	QAgb.MAGIC.HA-4H.b	QAgb.MAGIC.BA-4H.c	4	163.6	155.5-163.6	M	Qmas.S42-4H.b	von Korff et al., 2006
		QAgb.MAGIC.BA-5H.b	5	80.5	53.4-80.5	M	BYnb.5H-4	Baum et al., 2003
Days to heading (DHE)								
	QDhe.MAGIC.HA-3H.a		3	56.8	54.2-56.8	M	HvGl	Wang et al., 2010
							QTL8_HD	Pasam et al., 2012
	QDhe.MAGIC.HA-7H.a	QDhe.MAGIC.BA-7H.a	7	32.7	30.7-32.7	M	*Vrn-H3*	Yan et al., 2004
Flower abortion (FA)								
	QFla.MAGIC.HA-2H.a	QFla.MAGIC.BA-2H.a	2	144.2	142.8-144.2	M	*vrs1*	BLASTn
Number of ears (NE)								
	QNep.MAGIC.HA-5H.a	QNep.MAGIC.BA-5H.a	5	0.0	0.0	M	Qear.S42-5H.a	von Korff et al., 2006
							SNP 11_20553	Comadran et al., 2008
Number of kernels (NK)								
	QNke.MAGIC.HA-2H.a	QNke.MAGIC.BA-2H.a	2	144.2	144.2	M/I	*vrs1*	Comadran et al., 2011
	QNke.MAGIC.HA-4H.a	QNke.MAGIC.BA-4H.a	4	33.7	33.7-34.1	M	region of int-c	Comadran et al., 2011
Plant height (PLH)								
	QPlh.MAGIC.HA-1H.a		1	76.0	70.5-76.0	M	Qhei.S4IL-1H.a	Schmalenbach et al., 2008
	QPlh.MAGIC.HA-2H.b		2	154.6	154.6	M	QHt.StMo-2H.2	Hayes et al., 1993
	QPlh.MAGIC.HA-3H.a	QPlh.MAGIC.BA-3H.a	3	73.7	73.7-74.6	M	PH.3H-4	Baum et al., 2003
							QTL7_PHT	Pasam et al., 2012
		QPlh.MAGIC.BA-3H.b	3	134.6	134.6-145.6	M	*sdw1/denso*	Laurie et al., 1995
	QPlh.MAGIC.HA-3H.b	QPlh.MAGIC.BA-3H.c	3	161.6	161.6-168.9	M	QTL.9_PHT	Pasam et al., 2012
	QPlh.MAGIC.HA-6H.a		6	108.4	101.9-110.7	M	QTL17_PHT	Pasam et al., 2012
							PH	Forster et al., 2003
	QPlh.MAGIC.HA-7H.a	QPlh.MAGIC.BA-7H.a	7	36.9	33.5-36.9	M	Qhei.S42.-7H.b	von Korff et al., 2006
Thousand kernel weight (TKW)								
	QTkw.MAGIC.HA-2H.a		2	42,6	29.9-42.6	M/I	QTL4_TGW	Pasam et al., 2012
							tkw_br (bPb_4875)	Varshney et al., 2012
	QTkw.MAGIC.HA-2H.b	QTkw.MAGIC.BA-2H.a	2	141.7	147.7	M	*vrs1*	Comadran et al., 2011
	QTkw.MAGIC.HA-4H.a		4	102,4	98.7-102.4	M	KW.4H-3	Baum 2003

Trait	QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	Candidate genes/QTL	Reference
	QTkw.MAGIC.HA-5H.a	QTkw.MAGIC.BA-5H.a	5	206.3	206.3-213.8	M	QTgw.pil-5H.4	Pillen et al., 2003
							QTL16_TGW	Pasam et al., 2012
							TGW*	Forster et al., 2003
		QTkw.MAGIC.BA-6H.a	6	64.6	64.6	M	Qkw-tera_6H.a	von Korff et al., 2008
							KW.6H-2	Baum et al., 2003
							BCD348B	Teulat et al., 2001b
	QTkw.MAGIC.HA-6H.a		6	82,2	82.2-91.3	M	TGW	Forster et al., 2003
Grain yield (YLD)								
		QYld.MAGIC.BA-1H.a	1	36.4	36.4	I	GY	Talame et al., 2004
	QYld.MAGIC.HA-4H.a	QYld.MAGIC.BA-4H.a	4	10.6	10.6	M/I	T4D	Comadran et al., 2008
							E33M60-130	Talame et al., 2004
	QYld.MAGIC.HA-5H.b		5	80.5	80.5	M	Qyld.S42-5H.b	von Korff et al., 2006
							HvUDPGPPxYLD	Pillen et al., 2004
							CDO344	Teulat et al., 2001
							GY.5H-4	Baum et al., 2003
							GY	Forster et al., 2003
	QYld.MAGIC.HA-6H.a		6	147.3	146.1-147.9	I	GY	Talame et al., 2004
		QYld.MAGIC.BA-7H.b	7	217.6	216.4-236.8	M	S5D, A5D, T5D	Comadran et al., 2008
							WG380	Teulat et al., 2001

Underscored genes/QTL and references correspond to drought environments.

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] CentiMorgan range from the first to the last significant marker in a QTL

[e] A putative QTL was assumed in a vicinity of a marker locus, if the marker main effect (M) or /and marker*treatment interaction (I) was significant with $P<0.05$ or $P<0.001$, depending on the trait of interest.

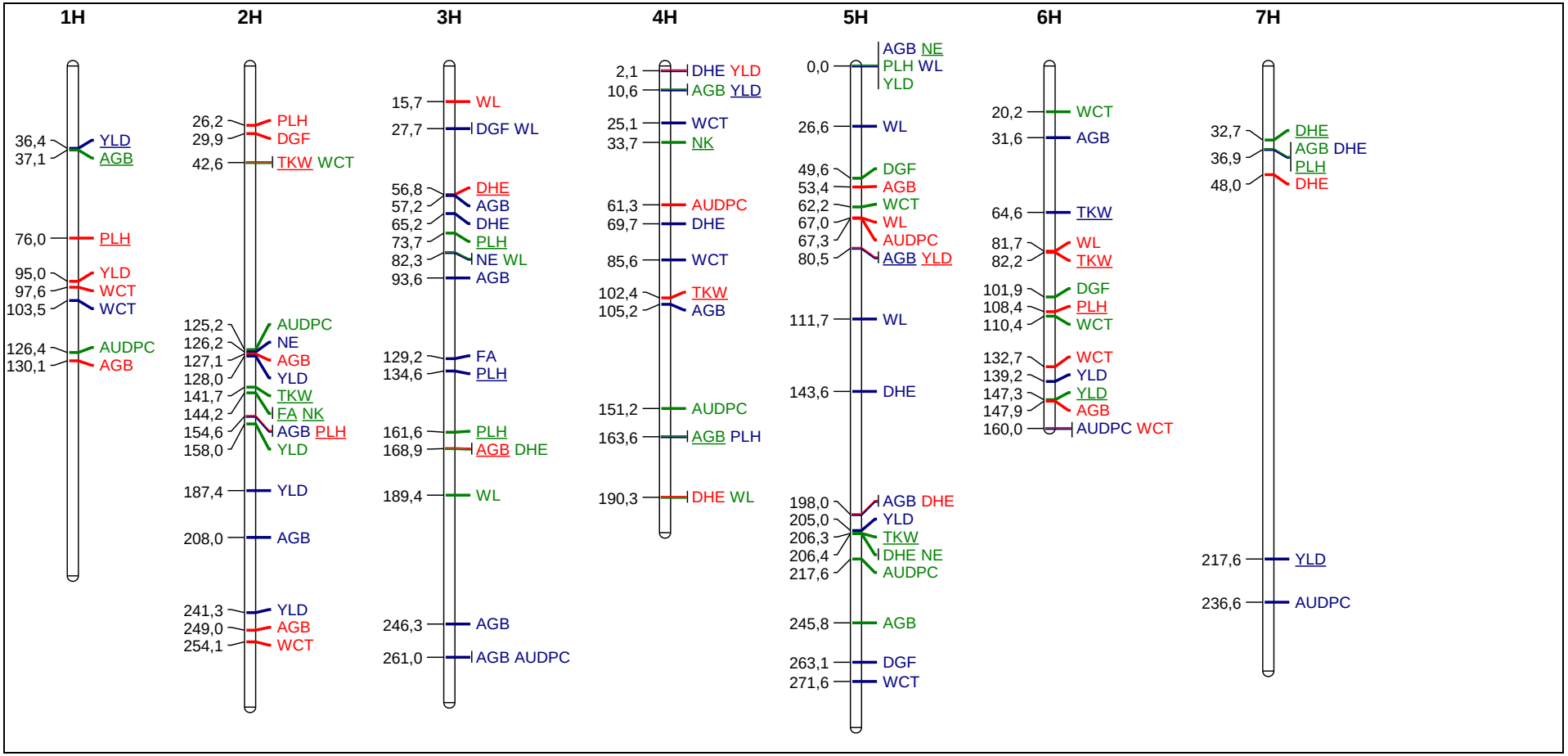

Fig. 14: Genetic map of QTL coinciding with QTL or genes known from literature (underscored).
QTL mapped with the BA are written in blue, QTL mapped with the HA in red.

4.6 Genotype and treatment interaction – drought tolerance

Yield was and still is the traditional target of breeding programs and breeding for high yielding genotypes under drought stress environments is even more challenging. Therefore, yield and yield components were investigated in 534 MAGIC DH-lines for ten different traits in the polytunnel in 2011 and 2012 under two water treatments (well watered and terminal drought), as well as for two traits, WCT and WL, evaluated with the THz-sensor to detected the water status in leaves. The results from the ANOVA (Table 11) documented, that the traits DHE and FA had no significant treatment effects as well as genotype*treatment effects. Therefore, no marker*treatment interaction was calculated for these traits in the QTL mapping approaches. The remaining eight traits were tested among the main marker effect for the marker*treatment interaction effects as well. Only five of the traits, AGB, AUDPC, NK, TKW and YLD, had significant marker*treatment interaction allele effects.

The most marker*treatment interaction allele effects were mapped in the traits AGB, nine out of 27 QTL effects were significant for marker*treatment interaction. One QTL was mapped with both approaches, QAgb.MAGIC.HA-1H.a and QAgb.MAGIC.BA-1H.a, (chromosome 1H, 37.1 cM), two more were mapped with the HA, six were mapped with the BA. The allelic effects estimated by the BA for the marker*treatment interaction were rather low; the reason was already explained in chapter 4.3. For three QTL in AGB, QAgb.MAGIC.BA-1H.a, QAgb.MAGIC.BA-5H.a and QAgb.MAGIC.BA-6H.a the effect under terminal drought conditions was estimated to 0, which means no allelic effect between the parents was detected under drought conditions. Interestingly, one of this QTL (QAgb.MAGIC.BA-1H.a) was detected with the HA (QAgb.MAGIC.HA-1H.a) as well, and in contrast to the BA the approach was able to detect an allelic effect under terminal drought as well. The HA addressed the allele effect under the two treatments to different parents, under well watered to Ragusa (13.1 g) and Heils Franken (11.7 g), and under terminal drought to Barke (6.8 g) and Heils Franken (6.6 g). First, this result showed the advantage of the HA over the BA concerning the information content and detecting of differences between the parents. Second, the high information content from the HA enabled to identify different favourable alleles under different watering conditions. The allele from Ragusa was not able to produce high amounts of above ground biomass under terminal drought conditions although it clearly had the highest impact under well watered conditions. This pattern of difference of the allelic effect between the watering conditions of the same trait was detected for eight out of ten marker*treatment interactions with the HA. Only the allelic effects for marker*interaction of NK, QNke.MAGIC.HA-2H.a, and TKW, QTkw.MAGIC.HA-2H.a, were constant under both treatments, the highest NK was assigned to the allele from Ragusa and the lowest NK to Ackermanns Bavaria. For TKW, the lowest weight was

inherited from Ragusa, the highest from Barke. The allelic effects for QNke.MAGIC.HA-2H.a and QTkw.MAGIC.HA-2H.a under terminal drought were smaller than under well watered conditions. This result implied that the allelic effect from Ragusa was strong enough to have a significant impact on the trait, under well watered and terminal drought conditions. On the other hand, the results implied that the selection environment for a trait like NK and TKW would be irrelevant to the selection successes for this trait under drought.

Two out of ten mapped QTL for AUDPC had a marker*treatment interaction. Pflugs Intensiv was the parent inheriting the allele for high leaf senescence under both treatments for the QTL mapped to 5H; QAuc.MAGIC.HA-5H.b and QAuc.MAGIC.BA-5H.a. Reduced leaf senescence under well watered and terminal drought conditions is a favourable trait in crops. The good phenotypic performance of Barke under controlled conditions caved in under drought, the allele from Ragusa performed the lowest AUDPC under drought conditions. Only 1/5 of the detected QTL for AUDPC interacted with water treatment. For a trait like AUDPC, which is a selection criterion for the ability of a plant to tolerate water limitation in the breeding process, a higher number of QTL with marker*treatment interaction was expected.

Five QTL with marker*treatment interaction effect were mapped out of 14 QTL for grain yield. Here as well a higher number of interaction effects were expected. The effects mapped with the BA were quite small, especially for the effect under terminal drought, ranging from 0 g at QTL QYld.MAGIC.BA-1H.a to -0.10 g at QYld.MAGIC.BA-4H.a. The effects calculated with the HA were slightly higher, settled between 0.2 g (QYld.MAGIC.HA-6H.a) and 0.3 g (QYld.MAGIC.HA-2H.a). This implied not only the higher power of the approach using haplotype blocks, it also showed that the performance of all parents to drought tolerance for grain yield was rather low. There was no outstanding allelic effect for grain yield under drought stress discovered.

Eight QTL for marker*treatment interaction were investigated with multiple mean comparisons. The QTL for AGB, AUDPC and YLD had in common, that no significant differences were detected between the parental means under terminal drought. Only the QTL concerning number of kernels (QNke.MAGIC.HA-2H.a) and thousand kernel weight (QTkw.MAGIC.HA-2H.a) had significant differences between the parents under terminal drought conditions. These significant differences showed the same pattern as under well watered conditions, the mean of Ragusa was significantly different to the mean of the other parents. The remaining parents differed not from each other. Under this circumstances Ragusa could be named drought tolerant concerning number of kernels and thousand kernel weight. Unfortunately, the effect of significant differences between the mean of Ragusa and the remaining parents relied on the spike morphology of Ragusa. It was the only six

rowed barley of all parents and therefore had a significant higher amount of kernels and a significant lower thousand kernel weight. These results were expected. As Comadran et al. (2011) mentioned the 2- and 6-rowed barley phenotypes are under control of two major genes (Komatsuda and Mano, 2002) both of which have already been cloned. *Vrs1* on the long arm of chromosome 2H (Pourkheirandish et al., 2007) and *int-c* on the short arm of chromosome 4H (Waugh et al. 2009). The QTL QNke.MAGIC.HA-2H.a with its position on 2H, 144.2 cM matched with the gene *vrs1* (Pourkheirandish et al., 2007) and therefore cannot be named an improving QTL under terminal drought. The QTL QTkw.MAGIC.HA-2H.a was mapped as well by Pasam et al. (2012) as QTL4_TGW and Varshney et al. (2012) as tkw_br (bPb_4875), but did not coincide with any gene mapped before. Therefore, the QTL QTkw.MAGIC.HA-2H.a can be named as an improving QTL for thousand kernel weight under drought with a positive allelic effect derived from parent Barke.

However, under well watered conditions the parental means for all detected marker*treatment interactions were significantly different from each other and depending on the trait clustered in different groups. The parental means at QYld.MAGIC.HA-2H.a clustered in four groups, where the mean of Ragusa had the greatest amount of yield/plant and was significantly different to the variety Barke. This effect might be dependent on the fact that Ragusa is six rowed barley landrace and has a higher number of kernels and therefore could have a high yield. The second QTL for yield investigated for multiple comparisons, QYld.MAGIC.HA-6H.a, showed with five clusters significant differences between the parents within the well watered conditions. This signified that the parents differed a lot for the trait yield between each other. This implied that the genetic potential between the parents concerning yield is quite different and that they were well chosen as parents for the MAGIC population. But the multiple comparisons between the parents under terminal drought conditions revealed no significant differences, except for the two QTL for NK and TKW mentioned above.

Except for the QTL QTkw.MAGIC.HA-2H.a and QNke.MAGIC.HA-2H.a no significant allelic effect under terminal drought conditions could be detected. This could be due to the starting time, the duration and severity of the terminal drought. The average yield reduction was around 45% between well watered and terminal drought conditions. In dependence on Blum (2006), who defines severe drought stress as a yield reduction of more than 70% compared to yield under well watered conditions, the applied drought stress would be defined as a moderate water shortage. Yield under more moderate water shortage reflects closely yield under favourable conditions (Blum 2006). Therefore the applied drought stress might not have been severe enough to target the drought tolerant genetic regions. The choice of parents could be a second drawback for the detection of QTL under drought conditions. The eight parents differed significantly for all traits under well watered

conditions as seen in Table 8. Only for the traits AUDPC, DGF and YLD no significant differences were detected under terminal drought conditions, a higher QTL potential under terminal drought conditions was expected. The MAGIC population was not established with the only perspective of QTL mapping under terminal drought. None of the genotypes was a drought tolerant genotype per definition. They were chosen due to their contribution to German plant breeding.

Table 24: List of QTL with marker*treatment interaction effects for binary and haplotype approach

								Binary approach	Haplotype approach							
Trait	**QTL-name HA[a]**	**QTL-name BA[a]**	**Chr[b]**	**Pos[c]**	**Genetic interval[d]**	**Effect[e]**	**treat**	**Diff BA[f]**	**AB**	**AD**	**B**	**HF**	**HH**	**PI**	**R**	**Parental[g]**
Above ground biomass (AGB)																
	QAgb.MAGIC.HA-1H.a	QAgb.MAGIC.BA-1H.a	1H	37.1	36.4-50.3	I	ww	0.6	12.9	.	12.5	11.7	12.6	.	13.1	1.4
							td	0.0	6.8	.	6.8	6.6	6.7	.	6.6	0.3
		QAgb.MAGIC.BA-2H.b	2H	208.0	204.8-208.0	I	ww	0.6								
							td	-0.1								
	QAgb.MAGIC.HA-2H.b		2H	249.0	241.3-251.2	I	ww		12.6	.	13.3	12.1	12.1	.	12.9	1.2
							td		6.6	.	6.8	6.9	6.8	.	6.7	0.3
		QAgb.MAGIC.BA-3H.c	3H	246.3	246.3	I	ww	0.4								
							td	-0.1								
		QAgb.MAGIC.BA-3H.d	3H	261.0	261.0	I	ww	0.5								
							td	-0.2								
		QAgb.MAGIC.BA-5H.a	5H	0.0	0.0	I	ww	-0.4								
							td	0.0								
		QAgb.MAGIC.BA-5H.c	5H	198.0	191.3-198.0	M/I	ww	0.7								
							td	0.1								
		QAgb.MAGIC.BA-6H.a	6H	31.6	31.6	I	ww	-0.8								
							td	0.0								
	QAgb.MAGIC.HA-6H.a		6H	147.9	139.2-160.0	I	ww		12.2	12.8	12.5	11.7	11.8	.	13.1	1.4
							td		6.8	6.7	6.6	6.8	6.5	.	6.9	0.5
Leaf senescence (AUDPC)																
	QAuc.MAGIC.HA-5H.b	QAuc.MAGIC.BA-5H.a	5H	217.6	217.6	I	ww	-2.7	35.7	36.8	34.1	36.3	38.4	38.8	37.5	4.6
							td	0.4	65.5	65.8	65.9	65.2	66.2	69.3	64.2	5.1
		QAuc.MAGIC.BA-7H.a	7H	236.6	236.6	I	ww	-1.4								
							td	1.5								
Number of kernels (NK)																
	QNke.MAGIC.HA-2H.a	QNke.MAGIC.BA-2H.a	2H	144.2	144.2	M/I	ww	13.9	19.2	.	19.7	20.2	.	.	33.7	14.5
							td	6.9	16.0	.	16.0	16.6	.	.	22.4	6.4
Plant height (PLH)																
	QPlh.MAGIC.HA-3H.a	QPlh.MAGIC.BA-3H.a	3H	73.7	73.7-74.6	I	ww	7.7								
							td	3.6								

Trait	QTL-name HA[a]	QTL-name BA[a]	Chr[b]	Pos[c]	Genetic interval[d]	Effect[e]	treat	Binary approach Diff BA[f]	Haplotype approach AB	AD	B	HF	HH	PI	R	Parental[g]
Thousand kernel weight (TKW)																
	QTkw.MAGIC.HA-2H.a		2H	42.6	29.9-42.6	M/I	ww		51.4		52.3	51.2			37.5	14.8
							td		47.7		48.3	48.0			38.1	10.2
Grain yield (YLD)																
		QYld.MAGIC.BA-1H.a	1H	36.4	36.4	I	ww	0.3								
							td	0.0								
	QYld.MAGIC.HA-2H.a	QYld.MAGIC.BA-2H.b	2H	158.0	154.6-170.5	M/I	ww	0.5	5.7	.	5.2	5.7	5.4	.	6.8	1.6
							td	0.1	2.9	.	2.7	2.9	3.0	.	2.9	0.3
		QYld.MAGIC.BA-2H.d	2H	241.3	241.3	I	ww	0.5								
							td	0.1								
	QYld.MAGIC.HA-4H.a	QYld.MAGIC.BA-4H.a	4H	2.1	0-10.64	M/I	ww	-0.4								
							td	-0.1								
	QYld.MAGIC.HA-6H.a		6H	147.3	146.1-147.9	I	ww		5.6	5.6	6.0	5.3	5.2	.	5.9	0.8
							td		2.9	2.8	2.9	2.8	2.8	.	2.9	0.2

[a] QTL names consist of the qualifier "Q", the trait abbreviation, the population name, the approach name, the chromosomal location and a consecutive character to discriminate two or more QTL per chromosome.

[b] Chromosomal localisation of the marker.

[c] Position of the most significant SNP marker in cM

[d] CentiMorgan range from the first to the last significant marker in a QTL

[e] A putative QTL was assumed in a vicinity of a marker locus, if the marker main effect (M) or /and marker*treatment interaction (I) was significant with $P<0.05$ or $P<0.001$, depending on the trait of interest

[f] Difference between the mean effect of allele 0 and allele 1

[g] Difference between the mean effect of the two most contrasting parents

Treat=water treatment: ww=well watered; td=terminal drought.

AB=Ackermanns Bavaria, AD=Ackermanns Danubia, B=Barke, HF=Heils Franken, HH=Heines Hanna, PF=Pflugs Intensiv, R=Ragusa

4.7 Epistasis in the MAGIC population

In this study, diallelic epistatic interactions were calculated using a model which tested all pairwise marker combinations. The analysis demonstrated that epistatic interactions play an important role in quantitative traits. The calculation of epistatic effects was conducted with the binary approach and resulted into 23 significant interactions for eight phenotypic traits. From all 46 mapped genomic positions within the epistatic effects, only twelve were mapped as main marker allelic effects with the multi-locus analysis of the binary QTL mapping approach. In many studies, only epistatic effects were tested between loci with significant main marker effects. The determination of epistatic interaction in this study was specially designed to test all marker*marker interaction. The result in Table 25 illustrates, that a large number of significant epistatic interactions would be undiscovered, as already mentioned by von Korff et al. (2010), and Li et al. (1997).

The most epistatic interactions were detected in the trait DHE. A reduction of DHE from 2.9 to 7.2 days was detected by the combination of the favourable alleles in different epistatic interactions. A "hotspot" region was the interaction between chromosome 7H, 30.5-36.9 cM and chromosome 5H, 206.4 cM. Three out of seven epistatic effects for DHE were mapped to this positional combination and explain the strongest effects among the seven interactions. Interestingly, two epistatic effects (DHE_4, DHE_5) were mapped with different SNP markers to 7H, position wise only 0.2 cM apart and 5H, 206.4 cM. Both of these epistatic effects were strong, resulting in reduced DHE by 5.3 (DHE_4) and 7.2 (DHE_5) days Fig. 15. But the favourable combinations of alleles varied. The favourable allele combination to reduce the DHE for DHE_4 was marker1=1 (1=more frequent allele) marker2=0 (0=less frequent allele), whereas DHE_5 required for the reduction of DHE a marker combination of 1/1. The third close by epistatic effect, DHE_6, showed the same pattern concerning the favourable allele like DHE_4, mapped to position of a main marker effect determined by the BA at chromosome 7H, 36.9 cM. Due to the binary QTL mapping approach a particular parent could not be assigned in this epistatic effect, but the raw data results clarified the avoidance of the alleles from parent Ragusa in concern with early DHE.

Two epistatic effects clustered for two traits, NK_2 and FA_4. The position for the first marker differed by 0.5 cM, 7H, 217.3 cM and 7H, 217.8 cM, respectively. The position of the second marker was exactly the same, 2H, 125.2 cM. The high number of sterile flowers was inherited by the parent Ragusa, with a significant higher number of flower abortion compared to the remaining parents. The unfavourable and less frequent allele was inherited by Ragusa. This explained the combination of alleles (1/1) for the epistatic effect for the lowest number of fertile abortion. The epistatic interaction for NK at the same locus for the first marker preferred the allele from Ragusa for a high number of kernels. Ragusa, due to its six-row-type inherited the tendency to produce a

high number of kernels. However, it was evident from the raw data, that favourable allele for an increase of NK for the second marker was not addressed to Ragusa or Heils Franken. A more precise conclusion cannot be made with the binary approach.

The trait flower abortion (FA) resulted only in two main marker effects mapped with the binary approach (Table 22). But four significant epistatic effects were mapped for this trait; all mapped with stronger effects than the main marker allele effect from QTL mapping. This suggested that epistatic effects play a large role in certain agronomic traits and enable the understanding and dissection of complex traits. The genetic position for both markers of the epistatic interaction of FA_1 were mapped closely together, further analysis is required to verify the results.

Four epistatic interaction effects were mapped for the estimation of the water content (WCT) of leaves. All of the interaction effects were greater than the main marker effects mapped with the binary approach. Cluster of epistatic effects for WCT with other traits was not discovered.

To my knowledge the work from von Korff et al. (2010) was the only one till now working on epistatic interaction in yield components. The two way epistatic interaction was conducted in a BC_2DH population S42, a cross between Scarlett and the Israeli wild barley accession ISR42-8, for heading date, plant height and yield. None of the epistatic effects mapped in the MAGIC population could be confirmed by the results from von Korff et al. (2010) for days to heading and plant height.

Table 25: Significant M1*M2 epistatic interactions determined with the BA in the MAGIC DH-lines

	SNP marker1		SNP marker2		Allele combination				
Name[a]	chr[b]	pos[c]	chr[b]	pos[c]	00[d]	01[d]	10[d]	11[d]	Diff[e]
AUDPC_1	4H	152.6	3H	145.6	64.5	50.9	53.1	50.5	13.9
DGF_1	7H	130.9	3H	56.8	36.6	38.9	37.7	37.8	2.3
DHE_1	3H	70.8	3H	58.6	55.3	58.2	57.6	57.1	3.0
DHE_2	4H	179.7	4H	69.7	59.4	55.5	57.4	57.3	3.9
DHE_3	5H	170.5	5H	143.6	57.5	58.9	58.1	56.0	2.9
DHE_4	7H	30.5	5H	206.4	56.3	60.9	55.6	57.1	5.3
DHE_5	7H	30.7	5H	206.4	63.4	56.8	58.3	56.2	7.2
DHE_6	7H	36.9	5H	206.4	55.1	60.8	54.8	57.1	6.1
DHE_7	7H	130.9	3H	161.6	57.7	58.6	60.5	56.4	4.1
FA_1	2H	144.2	2H	142.8	29.9	19.1	2.8	2.3	27.6
FA_2	3H	111.5	2H	144.2	35.4	24.1	2.1	2.2	33.3
FA_3	6H	87.3	2H	147.7	35.2	10.9	4.1	2.6	32.6
FA_4	7H	217.8	2H	125.2	33.6	9.8	8.1	2.9	30.6
NK_1	6H	139.2	2H	147.7	22.0	28.3	17.8	19.0	10.4
NK_2	7H	217.3	2H	125.2	25.0	32.5	18.2	18.3	14.3
PLH_1	3H	56.8	3H	43.9	90.3	82.0	87.5	86.6	8.3

	SNP marker1		SNP marker2		Allele combination				
Name[a]	**chr**[b]	**pos**[c]	**chr**[b]	**pos**[c]	**00**[d]	**01**[d]	**10**[d]	**11**[d]	**Diff**[e]
PLH_2	6H	113.4	3H	70.8	87.7	88.8	87.7	82.2	6.6
TKW_1	2H	144.2	2H	8.2	49.9	48.9	45.2	48.6	4.6
TKW_2	6H	147.3	2H	137.3	48.8	42.9	50.2	48.8	7.2
WCT_1	3H	207.1	2H	208.0	80.8	71.9	70.9	76.8	9.9
WCT_2	3H	246.3	3H	208.2	75.4	72.7	71.9	78.6	6.7
WCT_3	5H	143.6	3H	207.1	81.3	70.9	77.0	77.1	10.4
WCT_4	7H	217.3	2H	259.4	76.8	73.1	66.6	78.2	11.7

[a] Name of epistatic interaction for each trait
[b] Chromosomal location of interacting loci
[c] Genetic position in cM of interacting loci
[d] The four possible allele combinations at the two interacting loci, where 0 represents the less frequent allele in the population and 1 represents the more frequent allele in the population.
[e] = Difference between the effects from more and less frequent allele
Chromosomal and genetic positions are underscored if mapped as significant main marker effects in the QTL approach.

The results from the MAGIC population demonstrate that epistatic interactions play an important role in agronomic performance in barley. Although the position of the epistatic interaction did not coincide with the ones from von Korff et al. (2010), the importance of interactions of gene regions in the genome is worshiped in both, the MAGIC population and the S42 population, in contrast to the results from (Xu and Jia, 2007), who demonstrated that the contribution of epistatic interactions to genetic variation of quantitative characters was insignificant.

These differences might derive from different mapping populations and different mapping programs. The MAGIC DH-lines consist of small fragments of the parental genotypes, due to the crossing scheme of the population. With the multi-locus analysis and cross validation implemented in the mapping approach a precise and accurate mapping of the epistatic effects can be fulfilled.

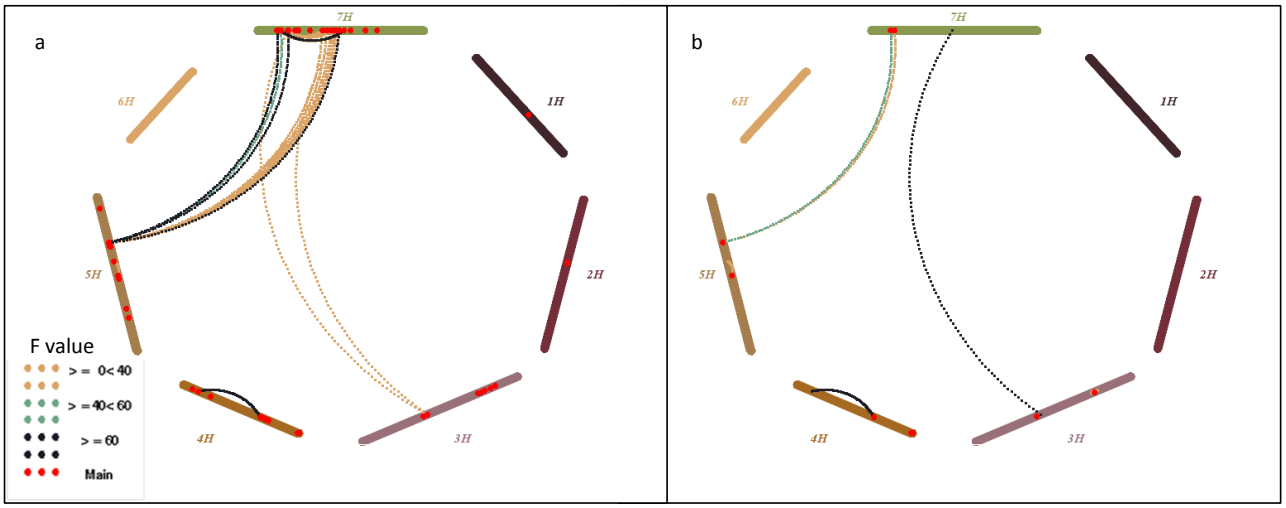

Fig. 15: Epistatic interaction for DHE, exemplary.
a) Represent all epistatic interaction before the use of multi-locus analysis. b) After the implementation of multi-locus analysis and cross validation. Main markers from QTL mapping approach are marked in red. The colours clarify the strength of the epistatic interaction.

4.8 Combination of positive allele effects

Within each trait

The combination of positive QTL of the same trait in one DH-line was analysed for both mapping approaches separately. For the BA five traits had no positive (FA) or only one positive allelic effect (AUDPC, DGF, NE, NK) and therefore combination of positive QTL in DH-lines could not be calculated. DH-lines with all positive combination could be identified for three of seven traits, DHE, PLH and TKW. But approximately half of the identified DH-lines did not confirm to the expected phenotype. These results were based on the binary code and on the fact that the mean for the allele 0 and allele 1 was assembled of more than one parent. Therefore, the means of the alleles were biased and the power of the binary approach in a multi-parent mapping population was low. DH-lines and the number of combined positive effects are listed in Table 26.

Table 26: DH-lines with combined positive allele effects estimated with the BA within traits

Trait[a]	DH-line[b]	Mean[c]	Population mean[d]	No of positive QTL[e]	No of combined positive QTL[f]
AGB	390	11.9	9.6	5	4
DHE	171	49.0	56.9	4	4
PLH	16	63.5	85.8	2	2
TKW	549	53.8	48.3	2	2
WL	76	1.6	5.1	4	3
WCT	86	88.3	75.5	5	4
YLD	145	5.1	4.2	5	4

[a] AGB (above ground biomass), DHE (days to heading), PLH (plant height), TKW (thousand kernel weight), WCT=water content in leaves after 96 hours without irrigation, WL= water loss, difference in water content within the leaves between 0 and 96 hours of no irrigation, YLD (grain yield)
[b] Number of DH-line
[c] Mean of the DH-line for each trait over both water conditions
[d] Mean of the all MAGIC DH-lines over both watering conditions
[e] Number of positive allelic effects detected in each trait
[f] Number of positive allelic effects combined in the selected DH-line

The traits for water content (WCT) and water loss (WL) evaluated with the THz-sensor were tested for their correlation to yield. The DH-lines that combined positive allele effects for the traits WCT were investigated for their phenotypic performance of yield, especially under terminal drought conditions. No difference in yield, under well watered and terminal drought conditions, were identified between DH-lines that carry a combination of positive allelic effects for WCT and DH-lines that carry no positive effect for the trait. The same accounts for the trait WL.

In contrast, only two traits (FA and NK) showed one positive effect under estimation with the haplotype approach and were neglected for the analysis. Due to the mapping approach the positive effects were directly assigned to one parent. For the determination of favourable DH-lines the combination of the positive parental alleles was investigated. DH-lines that combined all positive effects were not detected. Therefore, the effects were ranked, starting with the strongest effect and the DH-lines analysed for QTL combination. Only for the trait NE all positive effects could be detected in DH-lines, in case of PLH only two of eight positive effects were detected in DH-lines. But the results for the phenotypic mean in Table 27 illustrated that even with a low number of positive effects within a DH-line good candidate DH-lines were detected.

Table 27: DH-lines with combined positive allele effects estimated with the HA within traits

Trait[a]	DH-line[b]	Mean[c]	Population mean[d]	No of positive QTL[e]	No of combined positive QTL[f]
AGB	70	10.7	9.6	4	3
AUDPC	31	47.2	51.1	5	2
DHE	196	45.0	56.9	4	3
DGF	3	24.5	38.7	3	2
NE	168	8.6	4.4	2	2
PLH	44	66.0	85.8	8	2
TKW	70	56.1	48.3	4	2
WL	460/443	0/0	5.1	6	2
WCT	550	86.0	75.5	7	3
YLD	408	4.8	4.2	4	2

[a] AGB (above ground biomass), AUDPC (area under drought progress curve), DHE (days to heading), NE (number of ears), PLH (plant height), TKW (thousand kernel weight), WCT=water content in leaves after 96 hours without irrigation, WL= water loss, difference in water content within the leaves between 0 and 96 hours of no irrigation, YLD (grain yield)
[b] Number of DH-line
[c] Mean of the DH-line for each trait over both water conditions
[d] Mean of the all MAGIC DH-lines over both watering conditions
[e] Number of positive allelic effects detected in each trait
[f] Number of positive allelic effects combined in the selected DH-line

The advantage of the HA is obvious when comparing the two mapping approaches. Positive allelic effects were detected with the HA for a higher number of traits. The best performing DH-line differed between the approaches for every trait. No DH-line was detected with both approaches. But candidate DH-lines were assigned and can be evaluated in upcoming projects.

Across the traits

Concerning the results from the BA, only a small number of DH-lines combined the fraction of the strongest effect from all traits. DH-line 429 combined six of twelve positive effects and showed better performance compared to the population mean at ten traits. Fig. 16 showed the performance of the phenotypic values of two contrasting MAGIC DH-lines and the population mean. The DH-line 429 performed better at most traits than the population mean. Therefore the DH-line 429 is recommended as a candidate line for breeding purpose.

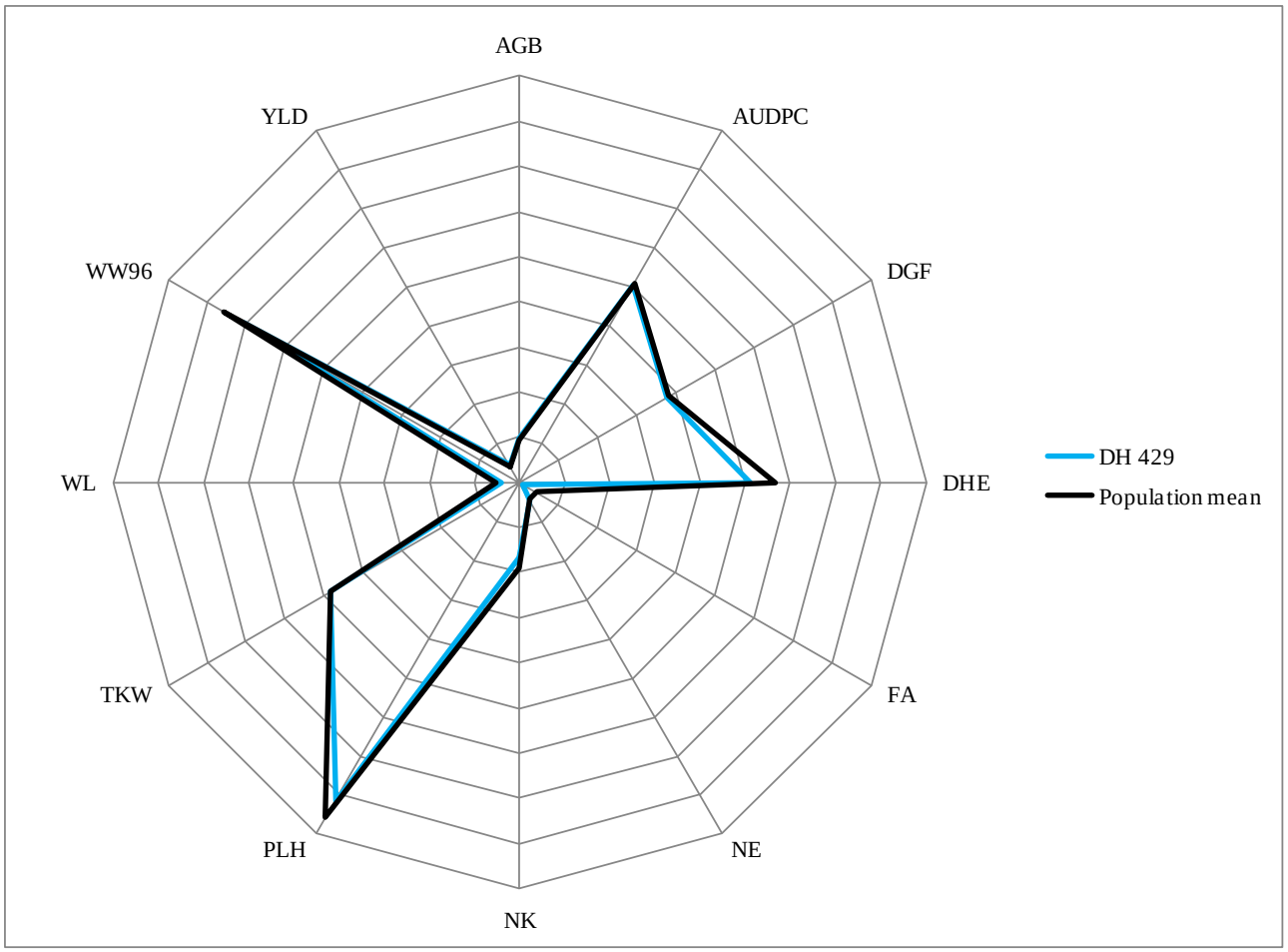

Fig. 16: Radar chart of the MAGIC DH-line 429 (blue) and the MAGIC population mean (black) for the phenotypic mean resulting from the BA at twelve traits. (WW96=WCT)

For the results from the HA approach, only two DH-lines (145 and 161) were detected which carried the combination of six positive effects within their genome. DH-line 145 was the only one that showed a better mean performance than the population mean for all these traits, for which it carried the positive allelic effect. In addition three more traits had a higher phenotypic mean than the population mean without being inherited by the parent with the strongest allelic effect. The outranging of DH-line 145 over the population mean is shown in Fig. 17.

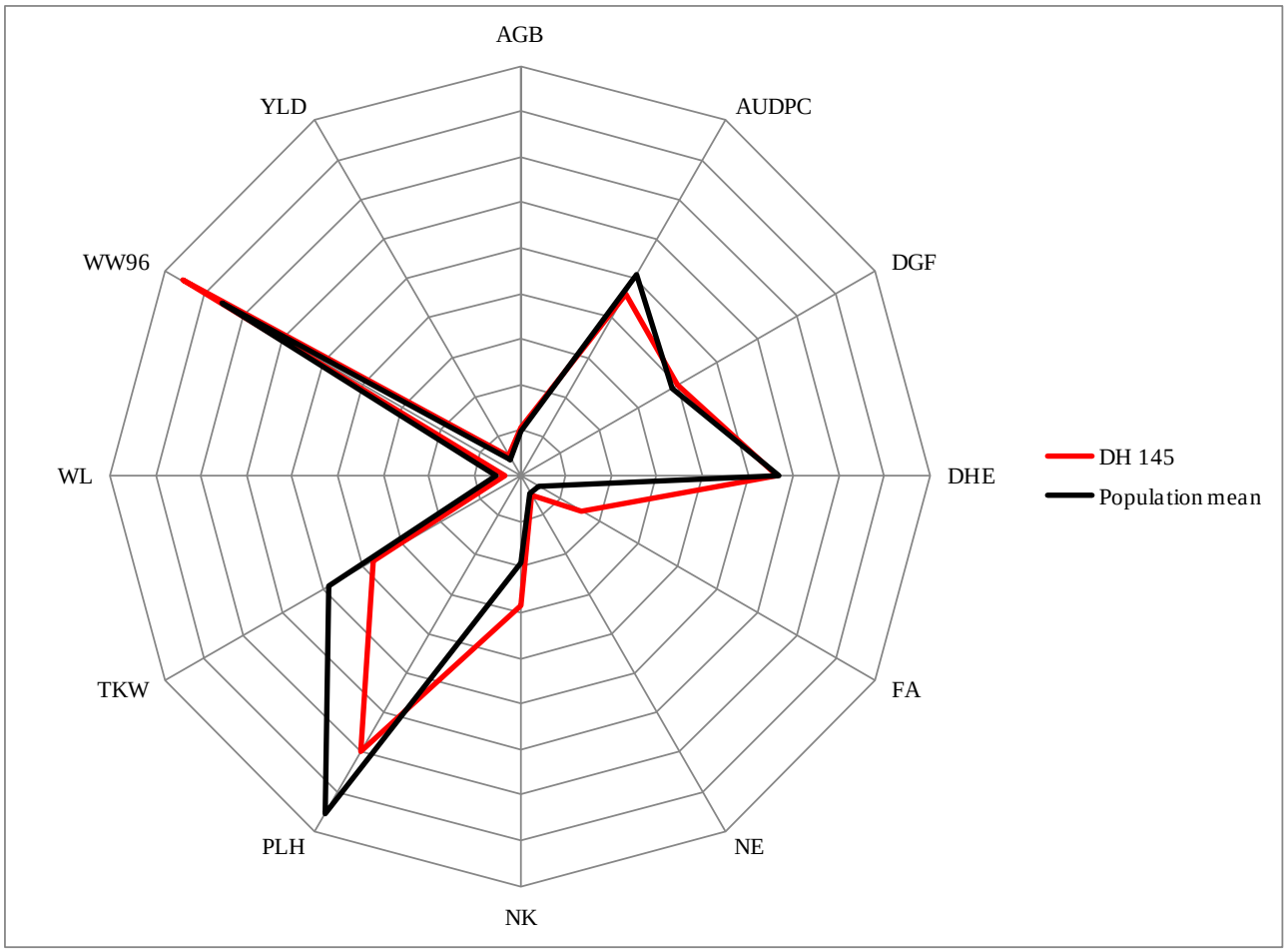

Fig. 17: Radar chart from the results from HA for DH-line 145 (red) and population mean (black) for twelve traits. (WW96=WCT)

A comparison between the two DH-lines chosen with the BA and the HA, DH 429 and DH 145, respectively showed an overall better phenotypic performance of DH-line 145 (Fig. 18). As illustrated in the figure DH-line 145 had a better phenotypic performance in more than half of the traits (AGB, AUDPC, NK, PLH, WL, WCT and YLD).

The analysis of the MAGIC population with haplotype approach enabled to pick the best performing DH-line out of 534 lines.

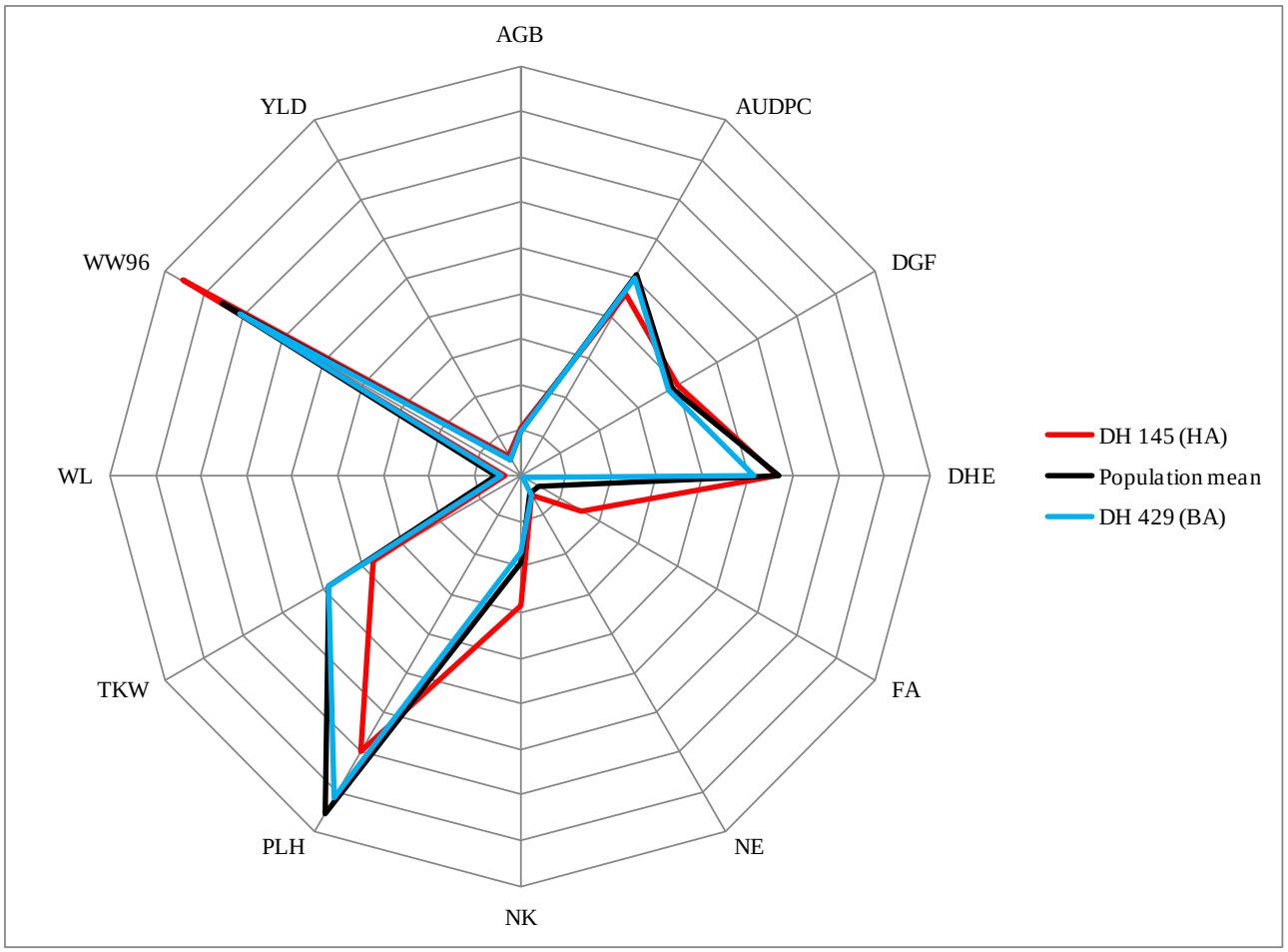

Fig. 18: Comparison of the two DH-lines chosen by BA (DH 429 in blue) and HA (DH 145 in red) as best performing DH-lines with multiple allelic effects for twelve phenotypic traits. (WW96=WCT)

4.9 MAGIC population as mapping population

To answer the question if a MAGIC population in general enables a higher amount of detected QTL is difficult. This definitely depends on the mapping population but as well on the number of genotypes under investigation and especially the mapping program which was used. In this study a quite conservative mapping approach was used, with different barriers, the multi-locus analysis, cross validation and conservative p-values. Therefore, the detected QTL in this study are hardly false positive QTL. But it is not always a question of the amount of mapped QTL, but of the precision. In simulation studies it has been demonstrated, that a fixed population of 1000 MAGIC individuals is sufficient to map a single additive locus that accounts for 5% of the phenotypic variation to within 0.96 cM distance (Valder et al., 2006). Kover et al. (2009) used 527 MAGIC lines of Arabidopsis derived from 19 founders and mapped with a precise resolution several QTL for germination and bolting time. The same population was used to study flowering time in 275 MAGIC lines by Ehrenreich et al. (2009). Based on the precise results from this pioneer

populations, several multi-parent populations are being created right now, including the one in Arabidopsis (Kover et al., 2009) and wheat (Huang et al. 2012), one in winter wheat (http://www.niab.com/pages/id/93/MAGIC_Populations_in_Wheat) and in rice (Bandillo et al., 2010, Leung et al., 2011). Unfortunately, the multi-parent populations differ in their crossing schemes and are not easily comparable.

However, the statistical complexity in the analysis of MAGIC populations is far higher than compared to bi-parental mapping population. But in the combination of the two mapping approaches discussed in this thesis and the use of the SAS 9.2 QTL mapping program, the complex statistical needs can be negotiated. This is shown in the results, especially in the outcome from the calculation of the epistatic interaction. To my knowledge there is no publication including so many strong epistatic interaction in barley. This is one huge advantage of the MAGIC population, which enables through a high number of crossover events (Broman, 2005) a dissection of epistatic interactions of complex traits. It might be highly probable to obtain useful MAGIC DH-lines combining favourable value of agronomic traits, which might directly be used in breeding programs.

5. Summary and Conclusion

The MAGIC DH-lines investigated in this research showed no population structure within the DH-lines and enabled with a strong decay of LD a precise mapping of genetic regions of interest. The terminal drought treatment applied in the early developmental stages of barley resulted in significant differences for the traits of interest between the well watered and the stress scenario.

The search for genetic regions with an influence on yield and yield components on the traits evaluated in this work was successful. QTL with main marker effects and marker*treatment interaction effects were discovered for twelve traits with two different mapping approaches. The two approaches mapped 35 allelic effects simultaneously. Both approaches showed advantages and drawbacks, the strength of the allelic effect was greater when calculated with the HA and the real parental allelic effect could be calculated only with the haplotype approach. But the binary approach was able to locate the region of interest in much smaller genetic intervals.

The comparison of the detected QTL with the known ones from literature revealed new genetic regions of interest for each investigated trait. Especially a gene region with association to days to heading on chromosome 5H, 206.4 cM, is of superior interest. The sequence of the most significant SNP marker matched with the sequence of a predicted protein in a databse, which regulates the phyto hormone auxin.

The output of allele effects for marker*treatment interaction was rather low. Multi comparisons between the parental allelic mean for the haplotype approach revealed only two genetic regions, QNke.MAGIC.HA-2H.a and QTkw.MAGIC.HA-2H.a, with significant differences between the parental allelic mean. Of these QTL QTkw.MAGIC.HA-2H.a can be named as a QTL with positive effect under terminal drought conditions, derived from parent Barke.

The use of the THz-sensor to determine water content in leaves is one of the novelties of this research project. Differences between the parents were detected; Ackermanns Danubia had the highest water content in leaves after five days of drought. Pflugs Intensiv was the most stable parent concerning water content under drought. QTL for water content and water holding capability were detected in the MAGIC population. No correlation of THz values with phenotypic values of yield or yield related trait was discovered, but clustering of QTL from water content and yield on 1H and 6H, with thousand kernel weight on 2H and with leaf senescence on 6H. Clusters for water holding capability were mapped on 5H with yield and biomass and with leaf senescence.

Not only epistatic interactions between main markers but between all possible markers were conducted and detected. The strength of the allelic effect was higher than the main marker effect, e.g. one epistatic interaction explained the reduction of DHE by 7.2 days. The results for epistatic interactions demonstrated the value of the interaction of gen regions in the agronomic performance

in barley. But they also explain the value of the MAGIC population, which enabled the detection of small genetic fragments with a high number of recombination during the crossing process.

In general, a MAGIC population comprised new challenging assignment to QTL mapping. Almost no commercial statistical programs that handle multi-parent populations are available. The application of a haplotype QTL mapping approach is contemporary and enables the direct investigation of multi-parent populations. But due to the mentioned drawbacks I recommend a routine use of both mapping approaches for QTL mapping, the binary and haplotype approach. Results from this study can be used as a starting block, the genetic map and the haplotype probability of each parent to be inherited to the offspring has to be pursued in the future. The MAGIC population proofed its importance as genetic resource and will be an ideal tool for investigating inheritance and interactions of genetic regions.

6. References

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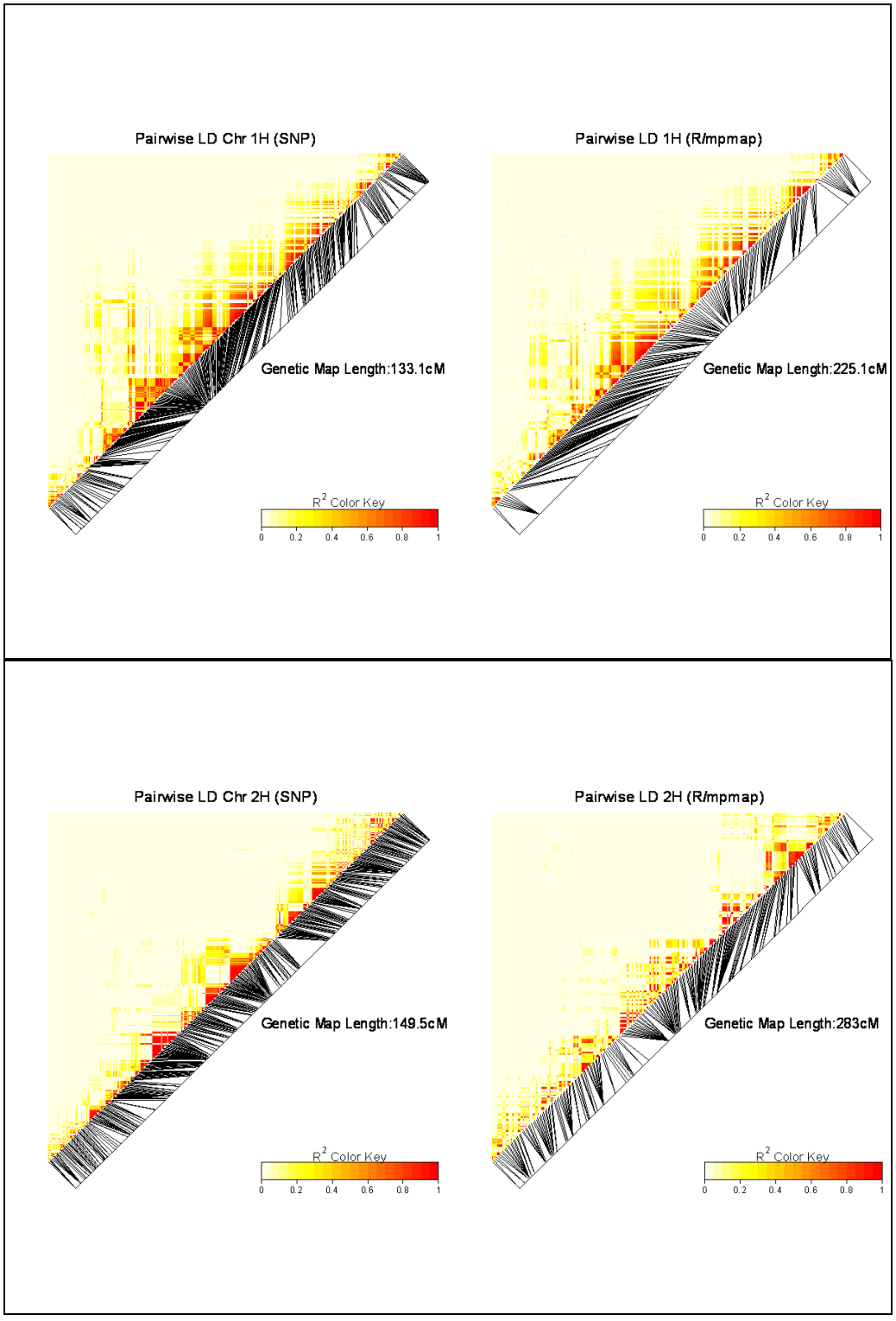
7. List of figures

8. List of tables

9. List of abbreviations

AFLP	Amplified fragment length polymorphism
AIC	Advanced intercross
AMPRIL	Arabidopsis multi-parent recombinant inbreed line
ANOVA	Analysis of variance
B.C.E.	Before common era
BAC	Bacterial artificial chromosome
bp	Base pair
cM	CentiMorgan
CW	Continuous wave
DArT	Diversity array technology
DAS	Days after sowing
DH	Double haploid
DNA	Deoxyribonucleic acid
EST	Expressed sequence tag
FAO	Food and agriculture organization
Gb	Gigabase
GBS	Genotyping by sequencing
HS	Heterogeneous stock
LD	Linkage disequilibrium
LOD	Logarithm of the odds
LTR	Long terminal repeat retrotransposons
MAF	Minor allele frequency
MAGIC	Multi-parent advanced generation intercross
Mb	Mega base
MHz	Megahertz
NAM	nested associated mapping
NIL	Near isogenic line
OPA	Illumina oligo pool assay
PCA	Principal component analysis
QTL	Quantitative trait loci
RAPD	Random amplified polymorphic DNA
REML	Restricted maximum likelihood
RFLP	Restriction fragment length polymorphism
RIL	Recombinant inbred line
SNP	Single nucleotide polymorphisms
SNV	Single nucleotide variants
SSR	Single sequence repeat
td	Terminal drought
TDS	Time domain spectroscopy
THz	TeraHertz
ww	Well watered

10. Appendix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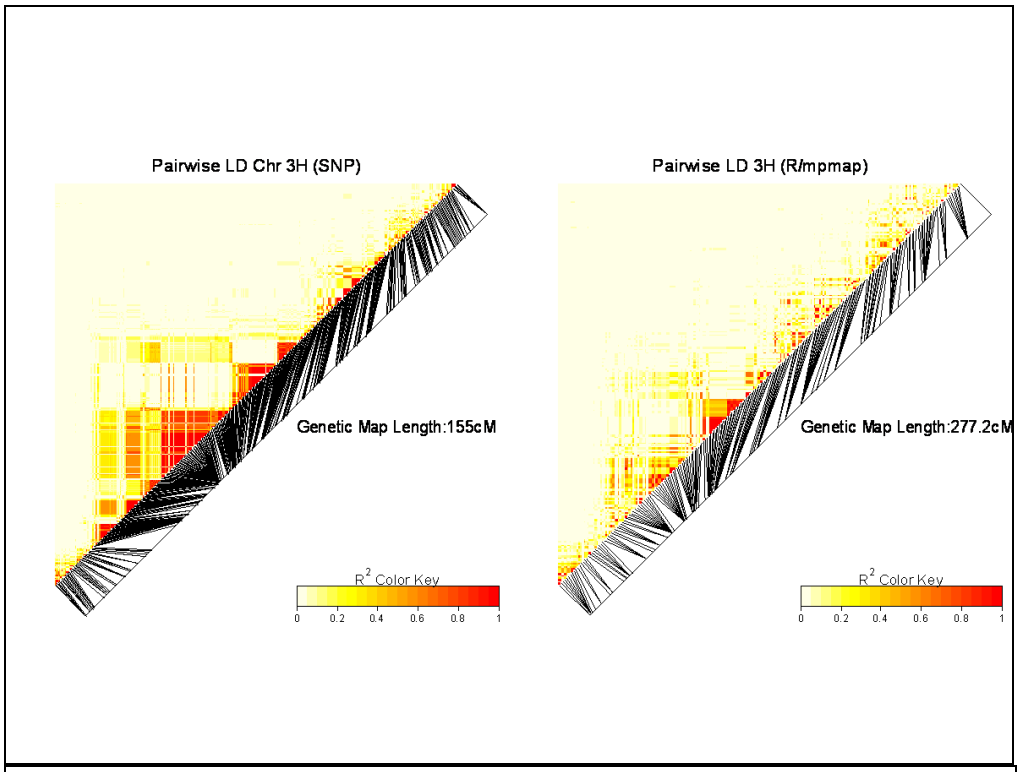
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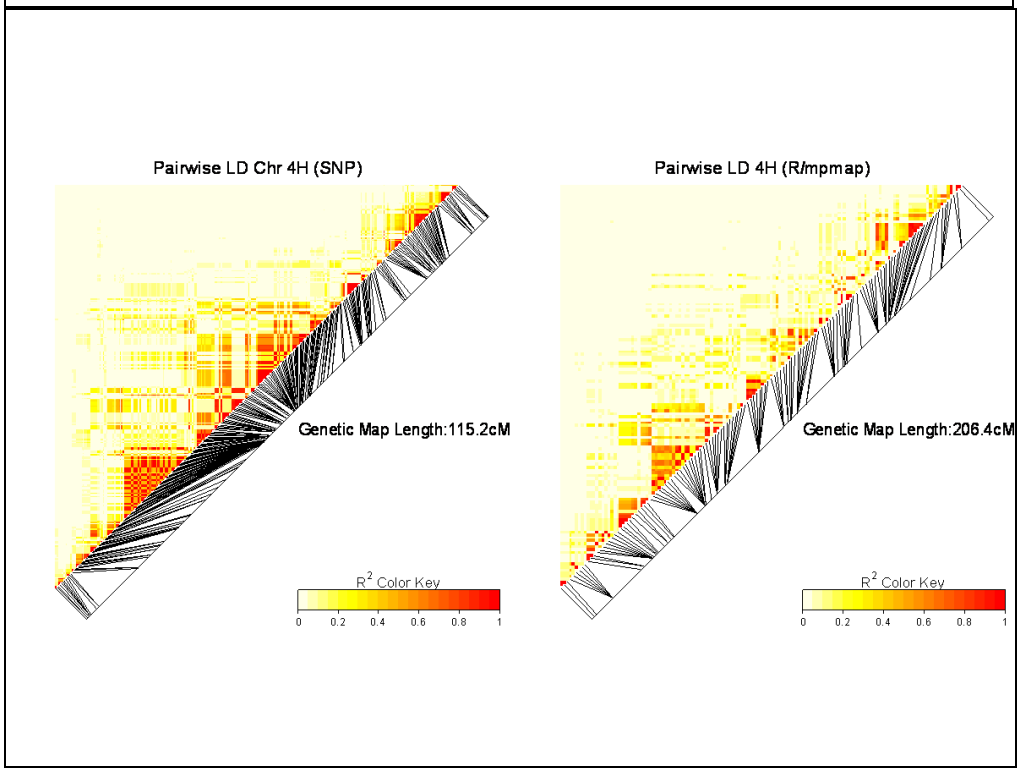
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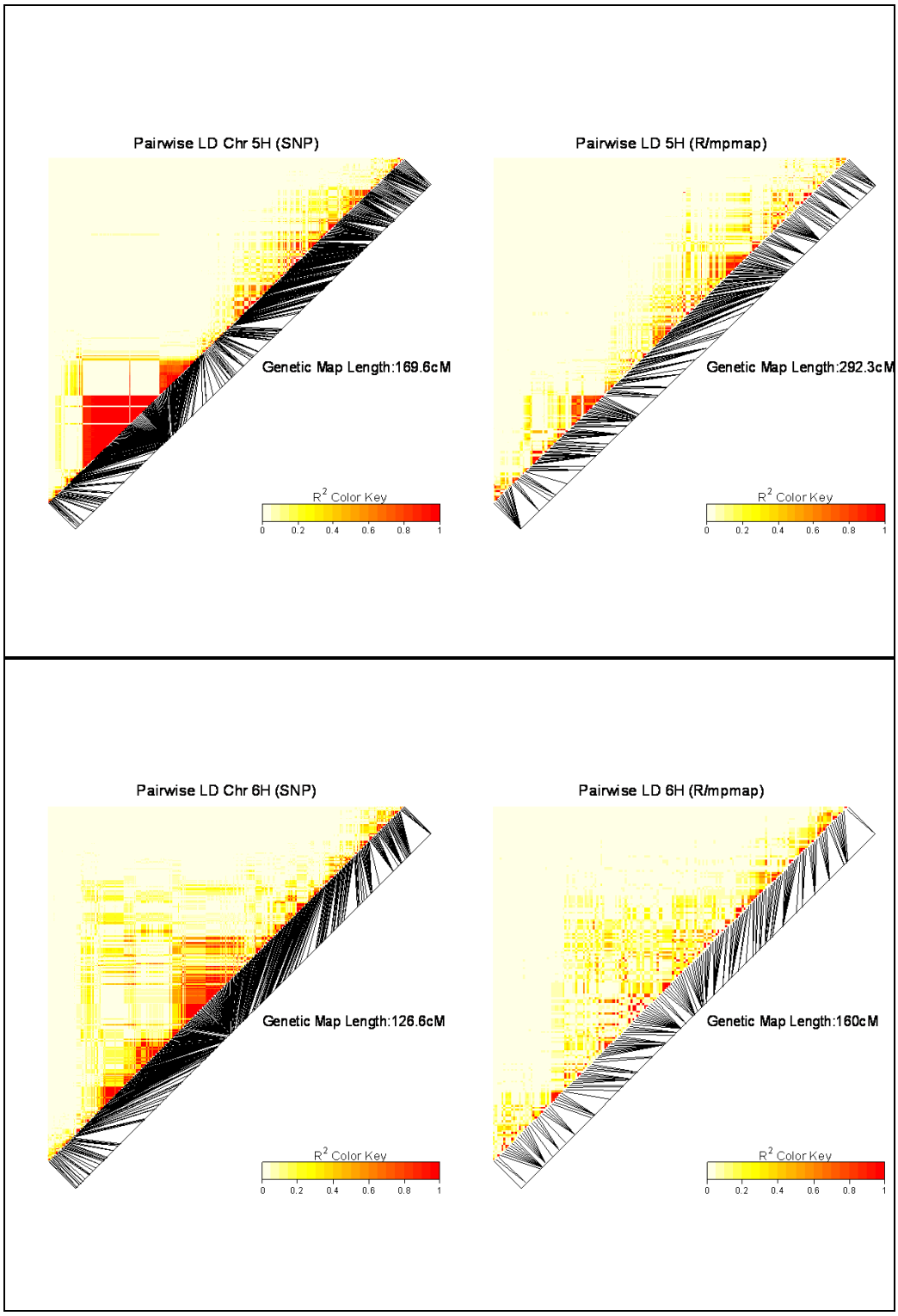
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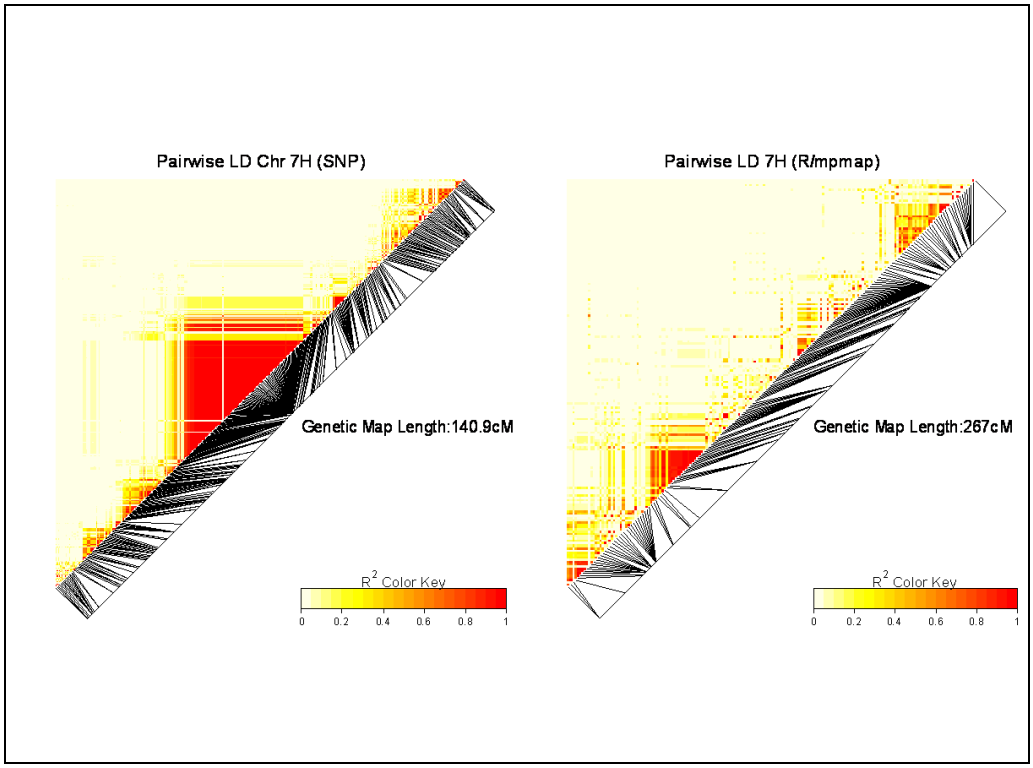

Appendix 1: Heat maps of linkage disequilibrium for each chromosome and each approach.
SNP=Binary approach, R/mpmap=Haplotype approach

Appendix 2: List of SNP markers with their locus name and chromosome and position in cM constructed from R/mpMap

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_11011	1H	0,0	12_11011	12_0233	12_11011	931-681	1_1011
12_30918	1H	0,0	12_30918	12_1144	12_30918	SCRI_abc15612_01_1	3_0918
11_20502	1H	13,4	11_20502	11_0481	3220-723	3220-723	2_0502
11_21174	1H	13,4	11_21174	11_1079	6949-895	6949-895	2_1174
11_21226	1H	13,4	11_21226	11_1126	7372-1253	7372-1253	2_1226
SCRI_RS_148560	1H	13,4					
SCRI_RS_148733	1H	13,4					
SCRI_RS_130592	1H	13,4					
SCRI_RS_205669	1H	13,4					
SCRI_RS_120053	1H	36,4					
12_30969	1H	37,1	12_30969	12_1184	12_30969	SCRI_bbc15015_01_164	3_0969
11_10419	1H	37,1	11_10419	11_0453	3101-111	3101-111	1_0419
11_21067	1H	50,3	11_21067	11_0992	6195-2137	6195-2137	2_1067
12_30715	1H	50,3	12_30715	12_0994	12_30715	U32_7636_1701	3_0715
SCRI_RS_184274	1H	58,1					
11_20712	1H	58,1	11_20712	11_0683	4226-570	4226-570	2_0712
SCRI_RS_119312	1H	61,6					
SCRI_RS_157757	1H	70,5					
12_30948	1H	70,5	12_30948	12_1166	12_30948	SCRI_bbc04473_01_2	3_0948
11_20371	1H	70,5	11_20371	11_0346	2496-1916	2496-1916	2_0371
12_30241	1H	70,5	12_30241	12_0726	12_30241	ABC15164_2_387	3_0241
SCRI_RS_124926	1H	75,4					
SCRI_RS_14227	1H	75,4					
11_10760	1H	75,9	11_10760	11_0879	5346-1587	5346-1587	1_0760
SCRI_RS_152464	1H	76,0					
11_10030	1H	76,0	11_10030	11_0042	10922-503	10922-503	1_0030
SCRI_RS_155382	1H	76,0					
12_31276	1H	76,0	12_31276	12_1385	12_31276	U35_19740_954	3_1276
SCRI_RS_189483	1H	76,0					
12_10506	1H	76,0	12_10506	12_0118	12_10506	3640-2807	1_0506
12_11169	1H	76,0	12_11169	12_0284	12_11169	ABC07427-1-1-329	1_1169
11_10764	1H	76,4	11_10764	11_0883	5381-1950	5381-1950	1_0764
SCRI_RS_140837	1H	76,4					
11_21134	1H	76,4	11_21134	11_1052	6720-641	6720-641	2_1134
11_20855	1H	76,4	11_20855	11_0819	5019-879	5019-879	2_0855
11_20514	1H	83,5	11_20514	11_0491	3277-446	3277-446	2_0514
11_11287	1H	83,5	11_11287	11_1422	ABC11913-1-1-104	ABC11913-1-1-104	1_1287
12_30336	1H	89,3	12_30336	12_0773	12_30336	U32_11789_202	3_0336
11_10526	1H	89,3	11_10526	11_0579	3710-852	3710-852	1_0526
11_11064	1H	89,3	11_11064	11_1326	ABC02639-1-4-370	ABC02639-1-4-370	1_1064
11_20660	1H	89,3	11_20660	11_0629	4020-643	4020-643	2_0660
SCRI_RS_221759	1H	92,9					
12_30683	1H	92,9	12_30683	12_0975	12_30683	U32_7097_198	3_0683
11_10985	1H	92,9	11_10985	11_1229	8613-278	8613-278	1_0985
11_10075	1H	92,9	11_10075	11_0112	1294-473	1294-473	1_0075
SCRI_RS_165811	1H	95,0					
SCRI_RS_11615	1H	95,0					
SCRI_RS_160545	1H	95,0					
11_10275	1H	95,0	11_10275	11_0307	2314-1412	2314-1412	1_0275
SCRI_RS_199178	1H	95,0					
SCRI_RS_132461	1H	95,0					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_153733	1H	95,0					
11_10933	1H	95,0	11_10933	11_1162	7800-594	7800-594	1_0933
SCRI_RS_153434	1H	97,6					
12_30350	1H	97,6	12_30350	12_0782	12_30350	U32_12209_166	3_0350
SCRI_RS_109060	1H	97,6					
11_21217	1H	97,6	11_21217	11_1117	7284-710	7284-710	2_1217
11_21053	1H	101,6	11_21053	11_0982	6118-595	6118-595	2_1053
12_30710	1H	101,8	12_30710	12_0992	12_30710	U32_7545_543	3_0710
11_10520	1H	101,8	11_10520	11_0571	3689-1101	3689-1101	1_0520
11_20798	1H	102,0	11_20798	11_0776	4716-1205	4716-1205	2_0798
11_10259	1H	103,5	11_10259	11_0295	2265-363	2265-363	1_0259
11_20810	1H	103,9	11_20810	11_0788	4793-777	4793-777	2_0810
11_21333	1H	104,0	11_21333	11_1218	8486-1964	8486-1964	2_1333
SCRI_RS_56976	1H	106,8					
SCRI_RS_1445	1H	106,8					
SCRI_RS_100503	1H	106,8					
SCRI_RS_145305	1H	109,1					
SCRI_RS_192779	1H	109,4					
SCRI_RS_121978	1H	113,4					
12_30821	1H	113,4	12_30821	12_1059	12_30821	OSU_Aglu3_536	3_0821
SCRI_RS_152795	1H	113,4					
SCRI_RS_130666	1H	113,4					
SCRI_RS_182431	1H	114,4					
11_21361	1H	114,6	11_21361	11_1243	8743-197	8743-197	2_1361
11_20095	1H	115,7	11_20095	11_0071	1190-86	1190-86	2_0095
SCRI_RS_2945	1H	115,7					
SCRI_RS_237999	1H	116,4					
SCRI_RS_118785	1H	116,8					
SCRI_RS_138118	1H	122,0					
11_10617	1H	122,0	11_10617	11_0672	4178-1592	4178-1592	1_0617
11_10043	1H	122,0	11_10043	11_0059	11603-445	11603-445	1_0043
SCRI_RS_159201	1H	122,0					
11_20229	1H	122,0	11_20229	11_0194	1670-369	1670-369	2_0229
SCRI_RS_132028	1H	122,8					
12_31179	1H	123,6	12_31179	12_1315	12_31179	U35_17286_433	3_1179
11_20432	1H	123,6	11_20432	11_0413	2877-867	2877-867	2_0432
11_21431	1H	123,6	11_21431	11_1295	9638-619	9638-619	2_1431
11_10002	1H	123,6	11_10002	11_0004	10070-1435	10070-1435	1_0002
11_11367	1H	123,6	11_11367	11_1461	ABC16273-1-1-48	ABC16273-1-1-48	1_1367
SCRI_RS_181239	1H	123,6					
SCRI_RS_157039	1H	126,4					
SCRI_RS_133886	1H	126,7					
SCRI_RS_188360	1H	127,6					
12_10166	1H	127,8	12_10166	12_0034	12_10166	1770-1477	1_0166
SCRI_RS_160234	1H	127,8					
11_21126	1H	127,8	11_21126	11_1046	6655-978	6655-978	2_1126
11_20290	1H	129,1	11_20290	11_0254	2036-1027	2036-1027	2_0290
SCRI_RS_138527	1H	129,3					
11_20990	1H	129,3	11_20990	11_0937	5772-1176	5772-1176	2_0990
SCRI_RS_125339	1H	129,3					
11_10686	1H	130,1	11_10686	11_0766	4665-882	4665-882	1_0686
SCRI_RS_156208	1H	130,1					
11_20121	1H	130,1	11_20121	11_0098	12492-541	12492-541	2_0121
12_30742	1H	130,6	12_30742	12_1008	12_30742	U32_825_2405	3_0742

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_9158	1H	132,1					
11_20434	1H	132,1	11_20434	11_0415	2881-935	2881-935	2_0434
SCRI_RS_166168	1H	132,1					
SCRI_RS_181353	1H	132,5					
11_20550	1H	134,2	11_20550	11_0516	3404-2470	3404-2470	2_0550
11_10830	1H	134,2	11_10830	11_0999	6250-1056	6250-1056	1_0830
SCRI_RS_162524	1H	134,4					
11_10006	1H	134,4	11_10006	11_0011	1016-376	1016-376	1_0006
SCRI_RS_135092	1H	134,4					
11_10433	1H	134,4	11_10433	11_0473	3201-603	3201-603	1_0433
11_21373	1H	134,4	11_21373	11_1251	8867-459	8867-459	2_1373
SCRI_RS_157246	1H	135,4					
SCRI_RS_121048	1H	135,4					
11_20475	1H	135,4	11_20475	11_0451	3087-1763	3087-1763	2_0475
SCRI_RS_197263	1H	135,4					
12_31163	1H	135,4	12_31163	12_1303	12_31163	U35_1704_1053	3_1163
SCRI_RS_188218	1H	135,4					
11_10396	1H	135,4	11_10396	11_0425	2935-1634	2935-1634	1_0396
11_11277	1H	139,6	11_11277	11_1419	ABC11290-sfp44-06	ABC11290-sfp44-06	1_1277
SCRI_RS_194371	1H	139,6					
12_31319	1H	139,6	12_31319	12_1415	12_31319	U35_21782_494	3_1319
SCRI_RS_199689	1H	139,6					
11_20169	1H	142,0	11_20169	11_0143	14371-423	14371-423	2_0169
11_10522	1H	142,2	11_10522	11_0575	3702-982	3702-982	1_0522
11_20754	1H	142,2	11_20754	11_0733	4499-1364	4499-1364	2_0754
11_10357	1H	142,4	11_10357	11_0387	2711-234	2711-234	1_0357
11_20840	1H	142,4	11_20840	11_0805	4927-1340	4927-1340	2_0840
SCRI_RS_235724	1H	143,1					
SCRI_RS_130139	1H	143,6					
SCRI_RS_188909	1H	146,7					
SCRI_RS_136856	1H	146,7					
SCRI_RS_235968	1H	147,4					
SCRI_RS_189168	1H	147,4					
SCRI_RS_171501	1H	150,1					
SCRI_RS_213675	1H	154,5					
12_20187	1H	154,5	12_20187	12_0428	12_20187	1498-596	2_0187
11_10111	1H	154,5	11_10111	11_0157	1497-628	1497-628	1_0111
SCRI_RS_106754	1H	154,5					
SCRI_RS_154528	1H	154,5					
12_10905	1H	154,5	12_10905	12_0209	12_10905	7389-555	1_0905
SCRI_RS_143810	1H	156,5					
SCRI_RS_175646	1H	156,5					
SCRI_RS_192730	1H	156,5					
SCRI_RS_238125	1H	156,5					
11_21392	1H	159,7	11_21392	11_1265	9105-497	9105-497	2_1392
SCRI_RS_224392	1H	159,7					
11_11481	1H	159,7	11_11481	11_1508	ConsensusGBS0361-5	ConsensusGBS0361-5	1_1481
SCRI_RS_169881	1H	159,7					
SCRI_RS_216088	1H	159,7					
BK_01	1H	159,7					
11_20021	1H	175,0	11_20021	11_0023	10360-563	10360-563	2_0021
SCRI_RS_155997	1H	175,0					
11_20908	1H	175,0	11_20908	11_0868	5283-1090	5283-1090	2_0908
SCRI_RS_170110	1H	175,3					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_147611	1H	175,3					
SCRI_RS_155758	1H	175,3					
11_20220	1H	179,1	11_20220	11_0185	1625-303	1625-303	2_0220
11_10854	1H	179,1	11_10854	11_1036	6547-1363	6547-1363	1_0854
SCRI_RS_159031	1H	179,1					
SCRI_RS_165588	1H	179,1					
SCRI_RS_120481	1H	190,2					
SCRI_RS_127646	1H	190,2					
11_10586	1H	190,2	11_10586	11_0632	4027-1814	4027-1814	1_0586
11_21140	1H	190,2	11_21140	11_1057	677-411	677-411	2_1140
11_21038	1H	210,3	11_21038	11_0972	6026-1949	6026-1949	2_1038
12_11443	1H	215,1	12_11443	12_0368	12_11443	ConsensusGBS0103-1	1_1443
11_20383	1H	215,1	11_20383	11_0358	2572-986	2572-986	2_0383
SCRI_RS_162628	1H	215,1					
SCRI_RS_10956	1H	215,1					
11_10590	1H	215,1	11_10590	11_0641	4057-2114	4057-2114	1_0590
SCRI_RS_199945	1H	215,1					
11_10443	1H	215,1	11_10443	11_0487	3263-2865	3263-2865	1_0443
12_30934	1H	215,1	12_30934	12_1158	12_30934	SCRI_bbc01078_01_1	3_0934
12_10693	1H	217,8	12_10693	12_0167	12_10693	472-1376	1_0693
11_20138	1H	217,8	11_20138	11_0119	13095-187	13095-187	2_0138
SCRI_RS_176006	1H	217,8					
SCRI_RS_175218	1H	217,8					
11_20772	1H	217,8	11_20772	11_0748	4592-118	4592-118	2_0772
SCRI_RS_196025	1H	225,1					
SCRI_RS_166806	2H	0,0					
SCRI_RS_139708	2H	0,0					
SCRI_RS_135585	2H	4,3					
SCRI_RS_184395	2H	4,3					
SCRI_RS_133377	2H	7,7					
SCRI_RS_169758	2H	7,7					
SCRI_RS_192463	2H	7,7					
SCRI_RS_165171	2H	8,2					
SCRI_RS_136200	2H	8,2					
SCRI_RS_122	2H	8,2					
SCRI_RS_168604	2H	8,2					
SCRI_RS_88391	2H	8,2					
12_10592	2H	8,2	12_10592	12_0138	12_10592	4063-677	1_0592
SCRI_RS_159503	2H	8,2					
SCRI_RS_231057	2H	8,2					
SCRI_RS_141564	2H	8,2					
SCRI_RS_10642	2H	10,0					
SCRI_RS_141753	2H	10,0					
SCRI_RS_155957	2H	12,2					
SCRI_RS_213799	2H	12,4					
SCRI_RS_204158	2H	20,6					
SCRI_RS_209516	2H	20,6					
SCRI_RS_144545	2H	20,6					
SCRI_RS_188511	2H	20,6					
SCRI_RS_152744	2H	20,6					
SCRI_RS_153226	2H	20,8					
SCRI_RS_192440	2H	21,2					
SCRI_RS_226348	2H	25,6					
12_31284	2H	25,6	12_31284	12_1393	12_31284	U35_20027_279	3_1284

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_231889	2H	25,7					
SCRI_RS_159228	2H	25,7					
SCRI_RS_141771	2H	25,9					
12_30155	2H	26,2	12_30155	12_0678	12_30155	ABC10887_1_461	3_0155
SCRI_RS_194812	2H	26,2					
11_20394	2H	27,5	11_20394	11_0378	2646-1277	2646-1277	2_0394
SCRI_RS_131218	2H	27,8					
SCRI_RS_150590	2H	28,0					
SCRI_RS_153672	2H	28,0					
SCRI_RS_143250	2H	28,0					
SCRI_RS_153693	2H	29,9					
12_31169	2H	29,9	12_31169	12_1308	12_31169	U35_17139_286	3_1169
SCRI_RS_12516	2H	37,3					
11_21261	2H	38,0	11_21261	11_1158	7747-1056	7747-1056	2_1261
SCRI_RS_115905	2H	38,9					
11_10180	2H	42,6	11_10180	11_0224	1865-396	1865-396	1_0180
SCRI_RS_155612	2H	42,6					
SCRI_RS_115892	2H	42,6					
11_21187	2H	42,6	11_21187	11_1088	7032-201	7032-201	2_1187
SCRI_RS_140819	2H	42,6					
11_10891	2H	42,6	11_10891	11_1099	7144-973	7144-973	1_0891
SCRI_RS_182371	2H	42,6					
SCRI_RS_5552	2H	42,6					
SCRI_RS_126877	2H	42,6					
11_21366	2H	49,2	11_21366	11_1247	8787-1459	8787-1459	2_1366
11_21304	2H	49,5	11_21304	11_1195	816-265	816-265	2_1304
SCRI_RS_212932	2H	53,8					
11_20173	2H	55,4	11_20173	11_0146	1447-464	1447-464	2_0173
11_10648	2H	55,4	11_10648	11_0718	4410-284	4410-284	1_0648
SCRI_RS_174935	2H	56,3					
11_10837	2H	60,8	11_10837	11_1009	6338-682	6338-682	1_0837
11_21388	2H	60,8	11_21388	11_1261	9060-471	9060-471	2_1388
SCRI_RS_10398	2H	60,8					
SCRI_RS_155546	2H	62,6					
SCRI_RS_194318	2H	67,5					
SCRI_RS_14801	2H	67,5					
SCRI_RS_237094	2H	67,5					
SCRI_RS_239231	2H	67,5					
SCRI_RS_221843	2H	67,5					
11_21096	2H	67,5	11_21096	11_1016	6384-866	6384-866	2_1096
SCRI_RS_147210	2H	67,5					
SCRI_RS_122681	2H	67,5					
11_11015	2H	67,5	11_11015	11_1281	946-2500	946-2500	1_1015
SCRI_RS_106444	2H	67,5					
11_10525	2H	77,2	11_10525	11_0578	3709-716	3709-716	1_0525
12_30042	2H	77,2	12_30042	12_0605	12_30042	ABC05679_1_681	3_0042
11_10399	2H	85,7	11_10399	11_0430	2964-382	2964-382	1_0399
11_11073	2H	87,3	11_11073	11_1333	ABC03253-1-2-279	ABC03253-1-2-279	1_1073
SCRI_RS_198148	2H	89,6					
12_30432	2H	91,0	12_30432	12_0829	12_30432	U32_2438_479	3_0432
SCRI_RS_154981	2H	91,2					
11_10342	2H	91,6	11_10342	11_0379	2651-1774	2651-1774	1_0342
11_10909	2H	91,6	11_10909	11_1131	7489-442	7489-442	1_0909
SCRI_RS_144776	2H	91,6					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_153531	2H	99,3					
SCRI_RS_171029	2H	99,4					
SCRI_RS_229103	2H	103,8					
11_10602	2H	119,4	11_10602	11_0654	411-495	411-495	1_0602
11_10070	2H	119,4	11_10070	11_0105	1275-734	1275-734	1_0070
12_30853	2H	119,4	12_30853	12_1091	12_30853	OSU_HVCBF8C_923	3_0853
11_20039	2H	119,4	11_20039	11_0035	10719-459	10719-459	2_0039
SCRI_RS_170235	2H	119,4					
11_20669	2H	119,4	11_20669	11_0637	4049-233	4049-233	2_0669
SCRI_RS_100054	2H	119,4					
SCRI_RS_237688	2H	119,4					
11_20585	2H	119,4	11_20585	11_0548	3576-2715	3576-2715	2_0585
SCRI_RS_163975	2H	119,4					
11_20960	2H	119,4	11_20960	11_0912	5573-1170	5573-1170	2_0960
11_20947	2H	119,7	11_20947	11_0899	5499-1430	5499-1430	2_0947
11_21166	2H	120,0	11_21166	11_1076	6911-866	6911-866	2_1166
11_21110	2H	120,0	11_21110	11_1030	6510-1430	6510-1430	2_1110
11_21144	2H	120,0	11_21144	11_1061	6804-1197	6804-1197	2_1144
11_21156	2H	120,0	11_21156	11_1070	6852-506	6852-506	2_1156
SCRI_RS_198848	2H	124,8					
11_21078	2H	124,8	11_21078	11_1001	6280-1098	6280-1098	2_1078
SCRI_RS_219568	2H	124,8					
11_21251	2H	125,2	11_21251	11_1148	7660-476	7660-476	2_1251
SCRI_RS_150266	2H	125,2					
SCRI_RS_6727	2H	125,2					
SCRI_RS_16024	2H	125,2					
SCRI_RS_16995	2H	125,2					
SCRI_RS_9469	2H	125,2					
11_10196	2H	125,2	11_10196	11_0239	1946-698	1946-698	1_0196
SCRI_RS_133539	2H	125,2					
SCRI_RS_156323	2H	125,2					
SCRI_RS_134812	2H	125,2					
11_10823	2H	125,2	11_10823	11_0981	6117-1507	6117-1507	1_0823
SCRI_RS_171032	2H	125,2					
SCRI_RS_235860	2H	126,2					
SCRI_RS_166540	2H	126,7					
11_21242	2H	127,1	11_21242	11_1135	7549-782	7549-782	2_1242
SCRI_RS_154398	2H	127,4					
SCRI_RS_116694	2H	127,7					
SCRI_RS_165795	2H	127,7					
SCRI_RS_171038	2H	128,0					
11_11533	2H	128,8	11_11533	11_1535	ConsensusGBS0705-1	ConsensusGBS0705-1	1_1533
SCRI_RS_139193	2H	137,3					
12_31424	2H	137,3	12_31424	12_1473	12_31424	U35_4325_1058	3_1424
12_10936	2H	137,3	12_10936	12_0215	12_10936	7804-582	1_0936
11_20080	2H	137,3	11_20080	11_0058	11591-265	11591-265	2_0080
SCRI_RS_180028	2H	141,7					
11_10475	2H	141,7	11_10475	11_0531	3469-1152	3469-1152	1_0475
11_21351	2H	141,7	11_21351	11_1231	8632-1809	8632-1809	2_1351
SCRI_RS_138463	2H	141,7					
11_21037	2H	141,7	11_21037	11_0971	6024-1095	6024-1095	2_1037
11_10214	2H	141,7	11_10214	11_0248	2020-539	2020-539	1_0214
SCRI_RS_4930	2H	142,8					
11_10287	2H	144,2	11_10287	11_0320	2371-950	2371-950	1_0287

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_30897	2H	144,2	12_30897	12_1127	12_30897	OSU_VRS1_HvHox1_260	3_0897
SCRI_RS_137263	2H	144,2					
SCRI_RS_160958	2H	144,2					
11_11250	2H	144,2	11_11250	11_1407	ABC10472-1-2-247	ABC10472-1-2-247	1_1250
SCRI_RS_196270	2H	144,2					
11_10876	2H	145,2	11_10876	11_1065	682-767	682-767	1_0876
SCRI_RS_159484	2H	145,2					
SCRI_RS_150494	2H	145,2					
11_20923	2H	145,2	11_20923	11_0880	5347-585	5347-585	2_0923
11_11307	2H	147,4	11_11307	11_1430	ABC12856-1-1-77	ABC12856-1-1-77	1_1307
11_10138	2H	147,4	11_10138	11_0188	1635-691	1635-691	1_0138
SCRI_RS_195164	2H	147,5					
12_10649	2H	147,7	12_10649	12_0154	12_10649	4419-1392	1_0649
11_21175	2H	147,7	11_21175	11_1080	6951-875	6951-875	2_1175
SCRI_RS_142188	2H	147,7					
11_10429	2H	154,6	11_10429	11_0467	3180-1771	3180-1771	1_0429
11_10731	2H	154,6	11_10731	11_0830	5088-59	5088-59	1_0731
11_10988	2H	154,6	11_10988	11_1234	866-442	866-442	1_0988
SCRI_RS_109266	2H	154,6					
12_31506	2H	154,6	12_31506	12_1518	12_31506	U35_6860_433	3_1506
SCRI_RS_200033	2H	158,0					
SCRI_RS_129178	2H	158,0					
SCRI_RS_209218	2H	158,0					
SCRI_RS_116193	2H	158,0					
SCRI_RS_179555	2H	158,0					
SCRI_RS_15119	2H	158,0					
SCRI_RS_172136	2H	158,0					
SCRI_RS_119718	2H	158,0					
11_10329	2H	158,0	11_10329	11_0366	2592-1237	2592-1237	1_0329
SCRI_RS_170209	2H	158,0					
SCRI_RS_161281	2H	158,0					
SCRI_RS_151056	2H	158,0					
SCRI_RS_13386	2H	158,0					
SCRI_RS_206020	2H	158,0					
SCRI_RS_134252	2H	168,0					
SCRI_RS_223897	2H	168,2					
11_20681	2H	168,6	11_20681	11_0650	4100-1047	4100-1047	2_0681
SCRI_RS_173017	2H	170,5					
11_10072	2H	170,5	11_10072	11_0106	1283-332	1283-332	1_0072
11_20293	2H	170,6	11_20293	11_0258	2052-792	2052-792	2_0293
11_21346	2H	170,9	11_21346	11_1227	8586-1221	8586-1221	2_1346
11_21099	2H	176,1	11_21099	11_1020	6419-1680	6419-1680	2_1099
SCRI_RS_158072	2H	177,5					
12_20027	2H	177,5	12_20027	12_0410	12_20027	10503-360	2_0027
12_20518	2H	185,9	12_20518	12_0471	12_20518	3294-439	2_0518
SCRI_RS_152664	2H	185,9					
SCRI_RS_918	2H	187,4					
SCRI_RS_15537	2H	187,4					
11_11236	2H	187,4	11_11236	11_1398	ABC09941-1-1-100	ABC09941-1-1-100	1_1236
11_10376	2H	187,4	11_10376	11_0403	2822-739	2822-739	1_0376
SCRI_RS_181112	2H	187,4					
11_20895	2H	187,7	11_20895	11_0854	5211-1755	5211-1755	2_0895
12_10447	2H	192,6	12_10447	12_0100	12_10447	3292-418	1_0447
11_10714	2H	192,6	11_10714	11_0802	4879-1560	4879-1560	1_0714

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_31461	2H	194,5	12_31461	12_1490	12_31461	U35_5285_326	3_1461
11_10566	2H	194,5	11_10566	11_0607	3910-1648	3910-1648	1_0566
11_10625	2H	204,1	11_10625	11_0687	4240-749	4240-749	1_0625
SCRI_RS_136379	2H	204,8					
SCRI_RS_154954	2H	208,0					
12_20183	2H	208,0	12_20183	12_0426	12_20183	1486-1515	2_0183
SCRI_RS_134241	2H	208,0					
SCRI_RS_11645	2H	208,0					
SCRI_RS_132586	2H	214,0					
SCRI_RS_151556	2H	218,0					
SCRI_RS_142593	2H	218,0					
12_30598	2H	218,0	12_30598	12_0926	12_30598	U32_5408_830	3_0598
SCRI_RS_155689	2H	218,0					
SCRI_RS_238606	2H	223,1					
SCRI_RS_151349	2H	237,6					
SCRI_RS_610	2H	237,6					
11_10404	2H	237,6	11_10404	11_0438	3000-1074	3000-1074	1_0404
SCRI_RS_154176	2H	237,6					
SCRI_RS_164608	2H	237,6					
SCRI_RS_12444	2H	237,6					
11_20366	2H	241,3	11_20366	11_0340	2464-1228	2464-1228	2_0366
SCRI_RS_157504	2H	241,3					
SCRI_RS_209551	2H	241,3					
SCRI_RS_124541	2H	241,3					
12_30678	2H	241,3	12_30678	12_0972	12_30678	U32_7077_588	3_0678
SCRI_RS_142314	2H	241,3					
SCRI_RS_168629	2H	249,0					
11_21274	2H	249,0	11_21274	11_1168	7826-869	7826-869	2_1274
11_20994	2H	251,2	11_20994	11_0939	5784-213	5784-213	2_0994
11_10791	2H	254,1	11_10791	11_0927	570-1376	570-1376	1_0791
SCRI_RS_230497	2H	254,3					
SCRI_RS_8671	2H	259,4					
SCRI_RS_10006	2H	264,2					
SCRI_RS_161636	2H	264,2					
SCRI_RS_155544	2H	264,2					
SCRI_RS_195051	2H	264,2					
11_10085	2H	264,2	11_10085	11_0127	1344-930	1344-930	1_0085
11_20590	2H	266,6	11_20590	11_0553	3608-2133	3608-2133	2_0590
SCRI_RS_116590	2H	266,6					
SCRI_RS_171198	2H	270,3					
SCRI_RS_211291	2H	271,9					
11_21181	2H	271,9	11_21181	11_1085	6990-661	6990-661	2_1181
SCRI_RS_138320	2H	271,9					
SCRI_RS_175216	2H	271,9					
SCRI_RS_139106	2H	271,9					
SCRI_RS_236521	2H	271,9					
12_30378	2H	283,0	12_30378	12_0799	12_30378	U32_14697_157	3_0378
11_10886	3H	0,0	11_10886	11_1090	7044-705	7044-705	1_0886
11_10112	3H	0,2	11_10112	11_0158	1499-290	1499-290	1_0112
11_20858	3H	0,6	11_20858	11_0822	5029-1423	5029-1423	2_0858
SCRI_RS_1804	3H	0,6					
11_20252	3H	0,6	11_20252	11_0217	1831-241	1831-241	2_0252
12_31409	3H	0,6	12_31409	12_1464	12_31409	U35_3907_2125	3_1409
SCRI_RS_132388	3H	0,6					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_20595	3H	0,6	11_20595	11_0557	3646-1984	3646-1984	2_0595
SCRI_RS_173491	3H	1,6					
11_11453	3H	3,9	11_11453	11_1494	ConsensusGBS0194-1	ConsensusGBS0194-1	1_1453
11_20529	3H	8,0	11_20529	11_0500	3344-1147	3344-1147	2_0529
SCRI_RS_184857	3H	8,0					
SCRI_RS_239142	3H	14,4					
12_10103	3H	15,7	12_10103	12_0020	12_10103	1453-346	1_0103
SCRI_RS_97417	3H	15,7					
SCRI_RS_192352	3H	15,7					
11_20742	3H	23,4	11_20742	11_0720	4443-1835	4443-1835	2_0742
SCRI_RS_214280	3H	25,5					
11_10565	3H	25,6	11_10565	11_0606	3906-558	3906-558	1_0565
SCRI_RS_155475	3H	27,7					
SCRI_RS_130264	3H	27,7					
SCRI_RS_153718	3H	27,7					
SCRI_RS_151808	3H	27,7					
SCRI_RS_177084	3H	27,7					
11_20794	3H	29,4	11_20794	11_0772	4701-2395	4701-2395	2_0794
11_10559	3H	39,0	11_10559	11_0603	3886-313	3886-313	1_0559
SCRI_RS_189757	3H	39,0					
SCRI_RS_144410	3H	39,0					
SCRI_RS_222975	3H	39,0					
SCRI_RS_4528	3H	43,9					
12_31475	3H	45,4	12_31475	12_1498	12_31475	U35_5532_765	3_1475
SCRI_RS_230486	3H	48,6					
SCRI_RS_119697	3H	48,6					
SCRI_RS_115045	3H	48,6					
11_11002	3H	48,6	11_11002	11_1258	9018-522	9018-522	1_1002
11_20193	3H	54,2	11_20193	11_0163	15141-257	15141-257	2_0193
SCRI_RS_211943	3H	54,2					
SCRI_RS_194531	3H	56,8					
SCRI_RS_6922	3H	56,8					
SCRI_RS_199987	3H	56,8					
12_30785	3H	56,8	12_30785	12_1039	12_30785	U32_9354_684	3_0785
11_20002	3H	56,8	11_20002	11_0002	10012-1239	10012-1239	2_0002
11_10224	3H	56,8	11_10224	11_0262	2066-1133	2066-1133	1_0224
SCRI_RS_124607	3H	56,8					
SCRI_RS_115423	3H	57,2					
SCRI_RS_231261	3H	57,2					
SCRI_RS_136959	3H	57,2					
SCRI_RS_237761	3H	57,2					
SCRI_RS_141171	3H	57,2					
11_21109	3H	57,2	11_21109	11_1029	6491-295	6491-295	2_1109
11_10672	3H	58,6	11_10672	11_0749	4593-2007	4593-2007	1_0672
SCRI_RS_1627	3H	65,2					
SCRI_RS_151299	3H	65,2					
11_10710	3H	65,2	11_10710	11_0795	4844-1737	4844-1737	1_0710
SCRI_RS_175314	3H	65,2					
11_20410	3H	65,2	11_20410	11_0394	2765-406	2765-406	2_0410
11_10601	3H	65,2	11_10601	11_0652	4105-1417	4105-1417	1_0601
12_30609	3H	65,2	12_30609	12_0933	12_30609	U32_5641_239	3_0609
12_31122	3H	65,2	12_31122	12_1281	12_31122	U35_15712_1129	3_1122
SCRI_RS_189045	3H	65,2					
SCRI_RS_219247	3H	65,2					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_10653	3H	65,2	11_10653	11_0724	4453-422	4453-422	1_0653
BK_08	3H	65,2					
11_20866	3H	66,5	11_20866	11_0827	5058-404	5058-404	2_0866
11_21129	3H	66,6	11_21129	11_1047	6681-314	6681-314	2_1129
11_11258	3H	66,7	11_11258	11_1410	ABC10667-1-1-288	ABC10667-1-1-288	1_1258
11_10005	3H	70,8	11_10005	11_0010	10126-999	10126-999	1_0005
11_10728	3H	70,8	11_10728	11_0823	5038-1035	5038-1035	1_0728
SCRI_RS_222102	3H	70,8					
SCRI_RS_155168	3H	70,8					
11_11191	3H	70,8	11_11191	11_1378	ABC08184-2-1-35	ABC08184-2-1-35	1_1191
11_10281	3H	71,0	11_10281	11_0315	2338-1572	2338-1572	1_0281
11_11086	3H	72,0	11_11086	11_1338	ABC04214-1-2-360	ABC04214-1-2-360	1_1086
SCRI_RS_135581	3H	72,0					
12_31372	3H	72,3	12_31372	12_1441	12_31372	U35_3151_1326	3_1372
SCRI_RS_229693	3H	73,7					
11_10380	3H	73,7	11_10380	11_0407	2838-663	2838-663	1_0380
11_21197	3H	73,7	11_21197	11_1096	7125-585	7125-585	2_1197
SCRI_RS_153148	3H	73,7					
11_20659	3H	73,7	11_20659	11_0628	4019-302	4019-302	2_0659
11_21120	3H	74,6	11_21120	11_1039	6573-369	6573-369	2_1120
SCRI_RS_137934	3H	79,6					
SCRI_RS_197825	3H	82,3					
SCRI_RS_161744	3H	82,3					
SCRI_RS_162931	3H	82,3					
SCRI_RS_104564	3H	82,3					
11_20778	3H	82,6	11_20778	11_0753	4618-1559	4618-1559	2_0778
SCRI_RS_144534	3H	82,8					
SCRI_RS_225522	3H	83,0					
11_20694	3H	83,3	11_20694	11_0662	4149-219	4149-219	2_0694
SCRI_RS_138291	3H	83,4					
11_20695	3H	83,9	11_20695	11_0663	4150-398	4150-398	2_0695
11_20877	3H	84,2	11_20877	11_0834	5128-1831	5128-1831	2_0877
SCRI_RS_10288	3H	84,5					
SCRI_RS_156056	3H	85,5					
11_21502	3H	86,6	11_21502	11_1445	ABC14384-1-1-53	ABC14384-1-1-53	2_1502
SCRI_RS_152371	3H	86,6					
SCRI_RS_142939	3H	86,6					
SCRI_RS_157479	3H	86,6					
SCRI_RS_231801	3H	86,6					
11_10335	3H	86,6	11_10335	11_0373	2616-2560	2616-2560	1_0335
11_21305	3H	86,6	11_21305	11_1197	8180-450	8180-450	2_1305
11_11394	3H	86,6	11_11394	11_1472	ABC19175-1-2-375	ABC19175-1-2-375	1_1394
SCRI_RS_13376	3H	86,6					
12_31346	3H	87,3	12_31346	12_1426	12_31346	U35_2539_392	3_1346
SCRI_RS_207408	3H	93,6					
12_30677	3H	93,6	12_30677	12_0971	12_30677	U32_7048_390	3_0677
11_21358	3H	93,6	11_21358	11_1240	8722-512	8722-512	2_1358
11_20093	3H	93,6	11_20093	11_0070	11832-415	11832-415	2_0093
SCRI_RS_223097	3H	93,6					
SCRI_RS_189039	3H	96,6					
SCRI_RS_202772	3H	96,6					
11_20115	3H	98,0	11_20115	11_0093	12280-797	12280-797	2_0115
SCRI_RS_171415	3H	98,0					
11_21163	3H	98,0	11_21163	11_1075	6883-203	6883-203	2_1163

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_219894	3H	98,0					
SCRI_RS_238157	3H	98,0					
11_20063	3H	98,0	11_20063	11_0050	11116-257	11116-257	2_0063
SCRI_RS_167410	3H	98,0					
SCRI_RS_146347	3H	98,0					
SCRI_RS_199922	3H	109,7					
SCRI_RS_138193	3H	111,5					
11_21294	3H	112,8	11_21294	11_1183	8020-87	8020-87	2_1294
12_30325	3H	112,8	12_30325	12_0768	12_30325	U32_10917_237	3_0325
SCRI_RS_826	3H	115,5					
11_11021	3H	115,5	11_11021	11_1294	963-386	963-386	1_1021
SCRI_RS_198609	3H	115,5					
SCRI_RS_159006	3H	116,0					
11_20136	3H	116,0	11_20136	11_0118	13081-199	13081-199	2_0136
11_21438	3H	116,0	11_21438	11_1299	9683-140	9683-140	2_1438
11_20999	3H	116,0	11_20999	11_0944	5797-777	5797-777	2_0999
SCRI_RS_146429	3H	129,2					
SCRI_RS_192761	3H	129,2					
11_20628	3H	129,2	11_20628	11_0593	3791-1525	3791-1525	2_0628
11_10515	3H	129,2	11_10515	11_0565	3674-1352	3674-1352	1_0515
12_30663	3H	134,6	12_30663	12_0964	12_30663	U32_6715_250	3_0663
SCRI_RS_235849	3H	134,6					
SCRI_RS_227472	3H	134,6					
SCRI_RS_231007	3H	134,6					
11_21381	3H	134,6	11_21381	11_1257	8984-579	8984-579	2_1381
SCRI_RS_115925	3H	134,6					
12_10344	3H	134,6	12_10344	12_0077	12_10344	2660-678	1_0344
12_30342	3H	134,6	12_30342	12_0777	12_30342	U32_12072_133	3_0342
11_21083	3H	145,6	11_21083	11_1003	6302-250	6302-250	2_1083
SCRI_RS_164704	3H	145,6					
11_20023	3H	145,6	11_20023	11_0025	1038-754	1038-754	2_0023
SCRI_RS_133339	3H	145,6					
12_30423	3H	145,6	12_30423	12_0823	12_30423	U32_2291_275	3_0423
11_10753	3H	145,6	11_10753	11_0864	5253-1318	5253-1318	1_0753
SCRI_RS_149566	3H	145,6					
SCRI_RS_114333	3H	145,6					
SCRI_RS_116542	3H	145,6					
11_20168	3H	145,6	11_20168	11_0142	1435-670	1435-670	2_0168
SCRI_RS_153519	3H	145,6					
12_30927	3H	145,6	12_30927	12_1153	12_30927	SCRI_aj420778_01_1	3_0927
SCRI_RS_14857	3H	145,6					
11_11330	3H	145,6	11_11330	11_1440	ABC13753-1-2-167	ABC13753-1-2-167	1_1330
SCRI_RS_163092	3H	153,0					
SCRI_RS_162929	3H	156,2					
SCRI_RS_3125	3H	156,8					
11_10312	3H	161,6	11_10312	11_0347	2500-1514	2500-1514	1_0312
SCRI_RS_131897	3H	161,6					
SCRI_RS_206510	3H	161,6					
SCRI_RS_121052	3H	161,6					
SCRI_RS_151711	3H	168,9					
12_31220	3H	168,9	12_31220	12_1343	12_31220	U35_18257_694	3_1220
12_30274	3H	168,9	12_30274	12_0741	12_30274	ABC19616_1_756	3_0274
12_31525	3H	168,9	12_31525	12_1530	12_31525	U35_835_1187	3_1525
11_11172	3H	168,9	11_11172	11_1370	ABC07496-pHv1343-02	ABC07496-pHv1343-02	1_1172

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_10754	3H	168,9	11_10754	11_0866	5260-462	5260-462	1_0754
11_20650	3H	168,9	11_20650	11_0615	3965-353	3965-353	2_0650
12_31238	3H	168,9	12_31238	12_1358	12_31238	U35_18691_432	3_1238
11_10867	3H	187,3	11_10867	11_1050	6716-823	6716-823	1_0867
SCRI_RS_146012	3H	187,3					
12_30960	3H	187,3	12_30960	12_1177	12_30960	SCRI_bbc09200_01_110	3_0960
12_30972	3H	189,4	12_30972	12_1185	12_30972	SCRI_bbc21998_01_388	3_0972
SCRI_RS_167755	3H	189,4					
11_20612	3H	191,2	11_20612	11_0581	3718-1026	3718-1026	2_0612
11_20527	3H	191,2	11_20527	11_0498	3340-1042	3340-1042	2_0527
11_20085	3H	191,2	11_20085	11_0063	11657-398	11657-398	2_0085
SCRI_RS_180027	3H	191,6					
SCRI_RS_13871	3H	191,6					
SCRI_RS_208297	3H	194,5					
12_31251	3H	195,5	12_31251	12_1366	12_31251	U35_19018_419	3_1251
11_20409	3H	200,2	11_20409	11_0393	2754-1027	2754-1027	2_0409
SCRI_RS_175038	3H	207,1					
SCRI_RS_194148	3H	207,1					
12_21386	3H	207,1	12_21386	12_0555	12_21386	9040-492	2_1386
SCRI_RS_167698	3H	207,1					
SCRI_RS_144559	3H	207,1					
SCRI_RS_14107	3H	207,1					
11_11436	3H	207,1	11_11436	11_1487	ConsensusGBS0038-2	ConsensusGBS0038-2	1_1436
SCRI_RS_169325	3H	208,2					
SCRI_RS_183550	3H	212,7					
SCRI_RS_231382	3H	220,7					
SCRI_RS_49693	3H	220,7					
11_10681	3H	220,7	11_10681	11_0760	4643-867	4643-867	1_0681
11_10570	3H	224,3	11_10570	11_0614	3949-1560	3949-1560	1_0570
SCRI_RS_180847	3H	224,3					
11_11410	3H	224,3	11_11410	11_1480	ABC36454-pHv2499-01	ABC36454-pHv2499-01	1_1410
11_21523	3H	229,7	11_21523	11_1500	ConsensusGBS0271-2	ConsensusGBS0271-2	2_1523
SCRI_RS_205592	3H	231,7					
SCRI_RS_115755	3H	231,7					
SCRI_RS_208633	3H	231,7					
11_21272	3H	231,7	11_21272	11_1166	7818-967	7818-967	2_1272
SCRI_RS_135155	3H	231,7					
SCRI_RS_189710	3H	231,7					
SCRI_RS_205957	3H	231,7					
SCRI_RS_172357	3H	231,7					
12_31500	3H	231,7	12_31500	12_1515	12_31500	U35_6520_551	3_1500
SCRI_RS_126369	3H	231,7					
11_10646	3H	241,5	11_10646	11_0716	4403-885	4403-885	1_0646
SCRI_RS_168360	3H	246,3					
SCRI_RS_173623	3H	246,3					
SCRI_RS_230023	3H	246,3					
11_10694	3H	246,3	11_10694	11_0780	4737-368	4737-368	1_0694
SCRI_RS_216141	3H	260,6					
SCRI_RS_128254	3H	260,6					
SCRI_RS_236603	3H	260,6					
11_20605	3H	261,0	11_20605	11_0567	3682-556	3682-556	2_0605
12_30736	3H	261,0	12_30736	12_1006	12_30736	U32_8179_620	3_0736
11_21267	3H	261,0	11_21267	11_1161	7782-410	7782-410	2_1267
SCRI_RS_203164	3H	261,0					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_143505	3H	261,0					
11_21362	3H	277,2	11_21362	11_1244	8752-523	8752-523	2_1362
SCRI_RS_164381	4H	0,0					
SCRI_RS_170785	4H	0,9					
12_31324	4H	2,1	12_31324	12_1417	12_31324	U35_21988_580	3_1324
SCRI_RS_150051	4H	10,6					
12_30764	4H	10,6	12_30764	12_1025	12_30764	U32_87_319	3_0764
SCRI_RS_13428	4H	10,6					
SCRI_RS_154517	4H	10,6					
11_21056	4H	10,6	11_21056	11_0983	6133-774	6133-774	2_1056
11_10208	4H	10,6	11_10208	11_0245	1996-652	1996-652	1_0208
SCRI_RS_12719	4H	25,1					
SCRI_RS_127657	4H	26,7					
SCRI_RS_162743	4H	26,8					
11_10113	4H	30,8	11_10113	11_0162	1513-514	1513-514	1_0113
SCRI_RS_105960	4H	30,8					
SCRI_RS_119628	4H	30,8					
11_10221	4H	30,8	11_10221	11_0259	2055-947	2055-947	1_0221
11_20210	4H	30,8	11_20210	11_0179	1593-1597	1593-1597	2_0210
SCRI_RS_157832	4H	30,8					
SCRI_RS_150585	4H	31,2					
SCRI_RS_180891	4H	31,8					
11_21070	4H	33,0	11_21070	11_0995	6208-987	6208-987	2_1070
11_20680	4H	33,2	11_20680	11_0649	4098-758	4098-758	2_0680
11_20606	4H	33,7	11_20606	11_0569	3687-271	3687-271	2_0606
11_20422	4H	34,1	11_20422	11_0406	2832-377	2832-377	2_0422
12_30863	4H	37,3	12_30863	12_1100	12_30863	OSU_HvPhyA_123	3_0863
SCRI_RS_228232	4H	38,8					
11_21122	4H	38,8	11_21122	11_1041	6589-1211	6589-1211	2_1122
SCRI_RS_145412	4H	40,8					
11_20012	4H	41,7	11_20012	11_0014	10255-529	10255-529	2_0012
SCRI_RS_220122	4H	42,3					
11_10048	4H	54,0	11_10048	11_0069	1180-70	1180-70	1_0048
SCRI_RS_128723	4H	54,0					
12_31462	4H	54,0	12_31462	12_1491	12_31462	U35_5294_1121	3_1462
SCRI_RS_168496	4H	54,0					
11_11207	4H	54,0	11_11207	11_1385	ABC08788-1-1-329	ABC08788-1-1-329	1_1207
11_10606	4H	54,0	11_10606	11_0660	4139-888	4139-888	1_0606
SCRI_RS_146174	4H	54,0					
SCRI_RS_146941	4H	54,0					
11_20289	4H	58,0	11_20289	11_0251	2028-1571	2028-1571	2_0289
SCRI_RS_150603	4H	58,0					
11_10946	4H	58,0	11_10946	11_1177	7942-948	7942-948	1_0946
SCRI_RS_181886	4H	58,0					
11_10639	4H	58,0	11_10639	11_0705	4336-2579	4336-2579	1_0639
11_11431	4H	58,0	11_11431	11_1483	ConsensusGBS0010-2	ConsensusGBS0010-2	1_1431
12_30455	4H	58,0	12_30455	12_0838	12_30455	U32_2772_898	3_0455
11_20906	4H	58,0	11_20906	11_0867	5273-894	5273-894	2_0906
12_30620	4H	58,7	12_30620	12_0938	12_30620	U32_5849_1360	3_0620
SCRI_RS_134620	4H	58,7					
11_11224	4H	61,3	11_11224	11_1394	ABC09432-1-1-160	ABC09432-1-1-160	1_1224
11_20610	4H	64,3	11_20610	11_0574	3699-1543	3699-1543	2_0610
SCRI_RS_195935	4H	64,3					
SCRI_RS_13552	4H	64,3					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_189180	4H	64,3					
11_20723	4H	64,3	11_20723	11_0697	4276-1082	4276-1082	2_0723
SCRI_RS_135365	4H	64,3					
11_20001	4H	68,2	11_20001	11_0001	1001-1187	1001-1187	2_0001
11_10881	4H	68,2	11_10881	11_1081	6954-861	6954-861	1_0881
12_31362	4H	68,2	12_31362	12_1436	12_31362	U35_2917_591	3_1362
SCRI_RS_143144	4H	69,7					
SCRI_RS_148392	4H	69,7					
11_10467	4H	69,7	11_10467	11_0520	3416-692	3416-692	1_0467
SCRI_RS_179438	4H	69,7					
SCRI_RS_155536	4H	69,7					
SCRI_RS_119778	4H	85,6					
SCRI_RS_157072	4H	85,6					
11_10432	4H	85,6	11_10432	11_0470	3190-644	3190-644	1_0432
11_10667	4H	85,6	11_10667	11_0740	454-1502	454-1502	1_0667
SCRI_RS_101389	4H	85,6					
12_30684	4H	85,6	12_30684	12_0976	12_30684	U32_7104_420	3_0684
12_31186	4H	85,6	12_31186	12_1320	12_31186	U35_17521_1003	3_1186
SCRI_RS_128974	4H	85,9					
SCRI_RS_225074	4H	98,7					
11_10093	4H	98,7	11_10093	11_0135	1385-827	1385-827	1_0093
SCRI_RS_147712	4H	98,7					
SCRI_RS_200957	4H	98,7					
SCRI_RS_179489	4H	100,9					
SCRI_RS_159159	4H	100,9					
11_10627	4H	101,7	11_10627	11_0689	424-423	424-423	1_0627
11_20451	4H	102,4	11_20451	11_0429	2955-452	2955-452	2_0451
SCRI_RS_89959	4H	102,4					
12_30328	4H	105,2	12_30328	12_0769	12_30328	U32_11103_408	3_0328
SCRI_RS_139806	4H	105,2					
SCRI_RS_143825	4H	105,2					
11_11513	4H	105,2	11_11513	11_1525	ConsensusGBS0589-1	ConsensusGBS0589-1	1_1513
SCRI_RS_219816	4H	105,2					
11_20670	4H	105,2	11_20670	11_0639	4051-1101	4051-1101	2_0670
SCRI_RS_140349	4H	110,1					
SCRI_RS_137903	4H	110,3					
11_20718	4H	124,5	11_20718	11_0690	4250-402	4250-402	2_0718
11_10723	4H	124,5	11_10723	11_0811	4986-1214	4986-1214	1_0723
11_20689	4H	124,5	11_20689	11_0657	4133-601	4133-601	2_0689
11_21151	4H	124,5	11_21151	11_1067	6841-637	6841-637	2_1151
SCRI_RS_129218	4H	124,5					
SCRI_RS_210971	4H	126,5					
12_10670	4H	129,0	12_10670	12_0161	12_10670	4555-499	1_0670
SCRI_RS_125524	4H	129,7					
SCRI_RS_184126	4H	129,7					
11_20197	4H	130,1	11_20197	11_0166	1523-1136	1523-1136	2_0197
11_10724	4H	130,4	11_10724	11_0812	4988-858	4988-858	1_0724
12_31246	4H	130,8	12_31246	12_1363	12_31246	U35_18847_967	3_1246
SCRI_RS_162410	4H	138,7					
SCRI_RS_168074	4H	146,9					
11_10588	4H	146,9	11_10588	11_0635	4039-1686	4039-1686	1_0588
SCRI_RS_157760	4H	146,9					
SCRI_RS_168399	4H	146,9					
11_20732	4H	146,9	11_20732	11_0709	4361-1867	4361-1867	2_0732

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_30539	4H	146,9	12_30539	12_0886	12_30539	U32_4329_198	3_0539
12_30554	4H	151,2	12_30554	12_0893	12_30554	U32_4613_499	3_0554
11_11470	4H	151,2	11_11470	11_1502	ConsensusGBS0288-1	ConsensusGBS0288-1	1_1470
SCRI_RS_197256	4H	151,2					
11_10510	4H	151,2	11_10510	11_0559	3652-872	3652-872	1_0510
SCRI_RS_121084	4H	152,6					
12_30718	4H	152,6	12_30718	12_0997	12_30718	U32_7764_707	3_0718
12_10271	4H	152,6	12_10271	12_0063	12_10271	2299-2992	1_0271
SCRI_RS_14487	4H	153,1					
SCRI_RS_188827	4H	153,1					
SCRI_RS_235688	4H	153,1					
11_20454	4H	153,1	11_20454	11_0435	299-163	299-163	2_0454
SCRI_RS_156130	4H	155,5					
SCRI_RS_167808	4H	155,6					
SCRI_RS_141803	4H	155,7					
SCRI_RS_10818	4H	155,7					
11_10334	4H	155,7	11_10334	11_0372	2614-1522	2614-1522	1_0334
11_21111	4H	155,7	11_21111	11_1032	6519-812	6519-812	2_1111
11_20515	4H	158,4	11_20515	11_0492	3282-555	3282-555	2_0515
12_31139	4H	158,4	12_31139	12_1290	12_31139	U35_16371_1353	3_1139
SCRI_RS_157611	4H	158,4					
SCRI_RS_148330	4H	163,6					
SCRI_RS_108369	4H	174,0					
11_11299	4H	179,7	11_11299	11_1428	ABC12417-1-1-46	ABC12417-1-1-46	1_1299
11_10611	4H	179,7	11_10611	11_0666	4160-1365	4160-1365	1_0611
SCRI_RS_9164	4H	179,7					
SCRI_RS_188829	4H	179,7					
11_10269	4H	190,3	11_10269	11_0305	2297-1250	2297-1250	1_0269
SCRI_RS_229116	4H	190,3					
SCRI_RS_151357	4H	204,6					
SCRI_RS_99965	4H	206,4					
11_20553	5H	0,0	11_20553	11_0521	3417-1451	3417-1451	2_0553
SCRI_RS_179411	5H	0,0					
SCRI_RS_109375	5H	0,0					
SCRI_RS_10929	5H	0,0					
12_30975	5H	0,0	12_30975	12_1188	12_30975	SCRI_gsp_0137	3_0975
SCRI_RS_141591	5H	0,0					
SCRI_RS_31797	5H	0,0					
12_30591	5H	0,0	12_30591	12_0919	12_30591	U32_5299_1659	3_0591
SCRI_RS_236640	5H	0,0					
SCRI_RS_214760	5H	0,0					
SCRI_RS_143952	5H	0,0					
SCRI_RS_179260	5H	0,0					
SCRI_RS_182131	5H	0,0					
SCRI_RS_149877	5H	0,0					
11_20206	5H	15,1	11_20206	11_0174	1582-63	1582-63	2_0206
SCRI_RS_155555	5H	15,1					
12_30714	5H	15,1	12_30714	12_0993	12_30714	U32_7632_376	3_0714
SCRI_RS_192396	5H	15,1					
SCRI_RS_98293	5H	23,9					
SCRI_RS_184564	5H	26,6					
11_20873	5H	28,8	11_20873	11_0829	5086-1239	5086-1239	2_0873
11_21426	5H	28,8	11_21426	11_1291	9608-371	9608-371	2_1426
SCRI_RS_194819	5H	28,8					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_11048	5H	28,8	11_11048	11_1319	ABC01741-1-4-299	ABC01741-1-4-299	1_1048
11_10688	5H	38,1	11_10688	11_0769	4684-775	4684-775	1_0688
11_20845	5H	49,6	11_20845	11_0809	4977-567	4977-567	2_0845
11_21391	5H	49,6	11_21391	11_1264	9100-978	9100-978	2_1391
SCRI_RS_175090	5H	49,6					
12_30654	5H	53,4	12_30654	12_0959	12_30654	U32_6548_1115	3_0654
11_20713	5H	53,4	11_20713	11_0685	4234-1944	4234-1944	2_0713
SCRI_RS_160471	5H	62,2					
11_20571	5H	62,2	11_20571	11_0538	3498-761	3498-761	2_0571
SCRI_RS_222345	5H	62,2					
12_21372	5H	62,2	12_21372	12_0553	12_21372	8865-547	2_1372
SCRI_RS_138727	5H	62,2					
SCRI_RS_189402	5H	62,2					
12_31155	5H	62,2	12_31155	12_1298	12_31155	U35_16881_1495	3_1155
11_20101	5H	62,2	11_20101	11_0078	12005-188	12005-188	2_0101
SCRI_RS_145275	5H	62,2					
11_10058	5H	62,2	11_10058	11_0088	1215-862	1215-862	1_0058
SCRI_RS_174091	5H	62,2					
SCRI_RS_157728	5H	65,4					
11_20766	5H	65,4	11_20766	11_0745	4570-591	4570-591	2_0766
SCRI_RS_133674	5H	67,0					
12_30707	5H	67,3	12_30707	12_0990	12_30707	U32_7514_744	3_0707
SCRI_RS_205508	5H	69,2					
12_31312	5H	69,2	12_31312	12_1411	12_31312	U35_21417_466	3_1312
11_10580	5H	72,3	11_10580	11_0625	3997-796	3997-796	1_0580
SCRI_RS_220645	5H	72,5					
SCRI_RS_166209	5H	80,5					
SCRI_RS_175087	5H	80,5					
SCRI_RS_171189	5H	80,5					
11_10621	5H	80,5	11_10621	11_0680	421-528	421-528	1_0621
12_30410	5H	80,5	12_30410	12_0818	12_30410	U32_2073_1148	3_0410
SCRI_RS_3114	5H	80,5					
11_20987	5H	80,5	11_20987	11_0931	5754-850	5754-850	2_0987
SCRI_RS_221999	5H	80,5					
SCRI_RS_205235	5H	80,5					
11_21065	5H	80,7	11_21065	11_0991	6184-200	6184-200	2_1065
SCRI_RS_13395	5H	86,8					
SCRI_RS_178739	5H	87,5					
11_11506	5H	88,1	11_11506	11_1522	ConsensusGBS0527-5	ConsensusGBS0527-5	1_1506
SCRI_RS_220101	5H	92,4					
11_20396	5H	92,4	11_20396	11_0381	2664-314	2664-314	2_0396
SCRI_RS_135425	5H	92,4					
11_21200	5H	92,4	11_21200	11_1098	7140-595	7140-595	2_1200
12_30515	5H	92,4	12_30515	12_0873	12_30515	U32_3899_1715	3_0515
11_21344	5H	92,4	11_21344	11_1225	8561-968	8561-968	2_1344
SCRI_RS_168185	5H	92,4					
SCRI_RS_165919	5H	92,4					
SCRI_RS_171243	5H	92,8					
SCRI_RS_147462	5H	93,1					
SCRI_RS_159056	5H	93,5					
12_30644	5H	93,5	12_30644	12_0953	12_30644	U32_6403_547	3_0644
SCRI_RS_209398	5H	94,3					
11_20306	5H	94,4	11_20306	11_0272	2146-2256	2146-2256	2_0306
11_20105	5H	95,0	11_20105	11_0082	12045-83	12045-83	2_0105

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_31183	5H	95,5	12_31183	12_1319	12_31183	U35_17419_413	3_1183
12_30538	5H	95,5	12_30538	12_0885	12_30538	U32_4304_3452	3_0538
SCRI_RS_114549	5H	95,5					
11_21121	5H	95,5	11_21121	11_1040	65-778	65-778	2_1121
11_20372	5H	97,1	11_20372	11_0348	2505-850	2505-850	2_0372
SCRI_RS_215787	5H	97,1					
SCRI_RS_119781	5H	97,4					
11_20236	5H	111,7	11_20236	11_0200	171-1301	171-1301	2_0236
SCRI_RS_160332	5H	111,7					
11_21001	5H	113,8	11_21001	11_0946	5799-578	5799-578	2_1001
SCRI_RS_166296	5H	113,8					
12_31427	5H	113,8	12_31427	12_1474	12_31427	U35_4373_471	3_1427
SCRI_RS_150410	5H	119,9					
11_20526	5H	120,6	11_20526	11_0497	3333-1209	3333-1209	2_0526
12_31271	5H	120,6	12_31271	12_1381	12_31271	U35_19573_1049	3_1271
SCRI_RS_11206	5H	131,5					
SCRI_RS_140487	5H	131,5					
SCRI_RS_212784	5H	131,5					
11_20850	5H	131,5	11_20850	11_0815	5004-375	5004-375	2_0850
SCRI_RS_146093	5H	131,5					
12_10408	5H	136,4	12_10408	12_0095	12_10408	3018-1012	1_0408
SCRI_RS_152347	5H	143,6					
11_21150	5H	143,6	11_21150	11_1066	6833-658	6833-658	2_1150
SCRI_RS_4923	5H	143,6					
SCRI_RS_140054	5H	143,6					
12_31417	5H	143,6	12_31417	12_1468	12_31417	U35_4145_1152	3_1417
12_21497	5H	153,4	12_21497	12_0578	12_21497	ABC11984-1-1-45	2_1497
SCRI_RS_235416	5H	153,4					
11_10578	5H	153,4	11_10578	11_0621	39-843	39-843	1_0578
SCRI_RS_158235	5H	153,4					
11_11350	5H	153,4	11_11350	11_1451	ABC14689-1-9-399	ABC14689-1-9-399	1_1350
11_21314	5H	153,4	11_21314	11_1203	8258-330	8258-330	2_1314
SCRI_RS_236569	5H	153,4					
12_30855	5H	153,4	12_30855	12_1093	12_30855	OSU_HVCBF9_988	3_0855
SCRI_RS_13960	5H	153,4					
12_30456	5H	153,4	12_30456	12_0839	12_30456	U32_2783_2471	3_0456
SCRI_RS_152849	5H	163,1					
11_11273	5H	165,5	11_11273	11_1416	ABC11221-1-3-410	ABC11221-1-3-410	1_1273
SCRI_RS_214241	5H	165,5					
SCRI_RS_157897	5H	167,2					
SCRI_RS_127785	5H	170,5					
SCRI_RS_206565	5H	170,5					
BK_22	5H	170,5					
11_21061	5H	184,5	11_21061	11_0987	6170-304	6170-304	2_1061
SCRI_RS_126419	5H	184,5					
SCRI_RS_231239	5H	191,3					
SCRI_RS_196437	5H	191,3					
SCRI_RS_2831	5H	191,3					
12_30524	5H	191,3	12_30524	12_0878	12_30524	U32_4034_1438	3_0524
SCRI_RS_162696	5H	191,3					
SCRI_RS_198525	5H	191,3					
SCRI_RS_182540	5H	191,5					
SCRI_RS_212515	5H	191,5					
SCRI_RS_195217	5H	191,5					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
12_30377	5H	198,0	12_30377	12_0798	12_30377	U32_14622_323	3_0377
SCRI_RS_189371	5H	198,0					
11_20347	5H	198,0	11_20347	11_0318	2352-277	2352-277	2_0347
SCRI_RS_150691	5H	198,0					
SCRI_RS_149088	5H	198,0					
11_20300	5H	198,0	11_20300	11_0266	211-259	211-259	2_0300
SCRI_RS_1501	5H	198,0					
11_20883	5H	198,4	11_20883	11_0841	5154-117	5154-117	2_0883
11_10805	5H	198,4	11_10805	11_0950	5844-1011	5844-1011	1_0805
SCRI_RS_165331	5H	198,5					
SCRI_RS_165569	5H	199,3					
SCRI_RS_150232	5H	199,8					
11_10705	5H	204,2	11_10705	11_0789	4795-782	4795-782	1_0705
SCRI_RS_78626	5H	204,5					
SCRI_RS_51000	5H	205,0					
11_20003	5H	205,0	11_20003	11_0003	10047-338	10047-338	2_0003
12_30611	5H	205,0	12_30611	12_0934	12_30611	U32_5714_470	3_0611
11_20188	5H	205,0	11_20188	11_0159	1501-353	1501-353	2_0188
11_10901	5H	205,0	11_10901	11_1121	7337-388	7337-388	1_0901
11_10820	5H	205,0	11_10820	11_0976	6054-1050	6054-1050	1_0820
11_21041	5H	205,0	11_21041	11_0974	603-72	603-72	2_1041
BK_17	5H	205,0					
11_21203	5H	205,5	11_21203	11_1102	7167-466	7167-466	2_1203
12_31237	5H	205,5	12_31237	12_1357	12_31237	U35_18649_1027	3_1237
SCRI_RS_166218	5H	206,3					
SCRI_RS_188785	5H	206,3					
12_30067	5H	206,3	12_30067	12_0622	12_30067	ABC07029_1_290	3_0067
SCRI_RS_130992	5H	206,3					
11_10095	5H	206,3	11_10095	11_0140	1394-1222	1394-1222	1_0095
SCRI_RS_188141	5H	206,3					
SCRI_RS_154144	5H	206,4					
11_10146	5H	206,4	11_10146	11_0198	1697-636	1697-636	1_0146
11_10783	5H	206,4	11_10783	11_0911	5571-640	5571-640	1_0783
SCRI_RS_166857	5H	210,5					
SCRI_RS_168544	5H	210,5					
SCRI_RS_4658	5H	210,5					
SCRI_RS_230112	5H	211,2					
SCRI_RS_148120	5H	211,7					
SCRI_RS_140356	5H	211,7					
SCRI_RS_149936	5H	211,7					
SCRI_RS_188572	5H	211,7					
12_30635	5H	213,8	12_30635	12_0947	12_30635	U32_6188_1308	3_0635
SCRI_RS_214130	5H	213,8					
11_20551	5H	213,8	11_20551	11_0518	3412-579	3412-579	2_0551
SCRI_RS_161534	5H	213,8					
11_10658	5H	213,8	11_10658	11_0731	447-88	447-88	1_0658
SCRI_RS_105705	5H	213,8					
12_30580	5H	215,4	12_30580	12_0911	12_30580	U32_5092_965	3_0580
SCRI_RS_208686	5H	215,7					
11_20568	5H	216,0	11_20568	11_0534	3477-1248	3477-1248	2_0568
12_30400	5H	216,1	12_30400	12_0811	12_30400	U32_1794_707	3_0400
SCRI_RS_225632	5H	216,5					
12_31206	5H	217,1	12_31206	12_1332	12_31206	U35_17942_828	3_1206
SCRI_RS_173583	5H	217,6					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_10217	5H	218,4	11_10217	11_0253	203-1128	203-1128	1_0217
SCRI_RS_161614	5H	218,5					
11_20104	5H	218,6	11_20104	11_0081	1204-1104	1204-1104	2_0104
SCRI_RS_13262	5H	218,6					
12_10904	5H	218,7	12_10904	12_0208	12_10904	7382-626	1_0904
SCRI_RS_138608	5H	218,7					
SCRI_RS_167426	5H	218,7					
SCRI_RS_138735	5H	219,9					
SCRI_RS_153575	5H	219,9					
11_10536	5H	219,9	11_10536	11_0586	3759-1385	3759-1385	1_0536
11_20560	5H	220,5	11_20560	11_0525	3443-1234	3443-1234	2_0560
SCRI_RS_230034	5H	222,6					
SCRI_RS_181376	5H	222,6					
11_20676	5H	224,7	11_20676	11_0646	407-259	407-259	2_0676
12_31165	5H	224,7	12_31165	12_1305	12_31165	U35_17121_1510	3_1165
SCRI_RS_155999	5H	225,3					
11_10363	5H	225,3	11_10363	11_0391	2746-1501	2746-1501	1_0363
SCRI_RS_235550	5H	225,5					
11_21077	5H	225,5	11_21077	11_1000	6260-183	6260-183	2_1077
12_30062	5H	225,5	12_30062	12_0618	12_30062	ABC06870_1_371	3_0062
SCRI_RS_157026	5H	225,7					
BK_04	5H	225,7					
SCRI_RS_168534	5H	233,6					
SCRI_RS_138029	5H	233,6					
12_30183	5H	233,6	12_30183	12_0693	12_30183	ABC11767_1_299	3_0183
11_21355	5H	233,6	11_21355	11_1236	8682-406	8682-406	2_1355
11_11497	5H	233,6	11_11497	11_1516	ConsensusGBS0451-1	ConsensusGBS0451-1	1_1497
SCRI_RS_173935	5H	233,6					
11_10336	5H	233,6	11_10336	11_0374	2617-1234	2617-1234	1_0336
SCRI_RS_204570	5H	233,6					
SCRI_RS_155322	5H	243,8					
11_20334	5H	244,5	11_20334	11_0303	2290-796	2290-796	2_0334
SCRI_RS_19741	5H	245,6					
12_30165	5H	245,6	12_30165	12_0683	12_30165	ABC11168_1_163	3_0165
11_20829	5H	245,6	11_20829	11_0799	485-1369	485-1369	2_0829
12_30666	5H	245,6	12_30666	12_0966	12_30666	U32_6903_1480	3_0666
SCRI_RS_123668	5H	245,6					
11_10161	5H	245,8	11_10161	11_0206	1761-804	1761-804	1_0161
11_20078	5H	245,8	11_20078	11_0057	11470-478	11470-478	2_0078
SCRI_RS_131479	5H	245,8					
11_20988	5H	245,8	11_20988	11_0932	5757-248	5757-248	2_0988
11_20826	5H	245,8	11_20826	11_0796	4845-123	4845-123	2_0826
SCRI_RS_102066	5H	245,8					
SCRI_RS_157318	5H	245,8					
11_10236	5H	245,8	11_10236	11_0271	2144-852	2144-852	1_0236
SCRI_RS_178615	5H	245,8					
SCRI_RS_134358	5H	253,6					
SCRI_RS_165835	5H	253,6					
11_20934	5H	254,3	11_20934	11_0888	5428-146	5428-146	2_0934
SCRI_RS_195241	5H	256,0					
11_10254	5H	256,5	11_10254	11_0290	2244-3247	2244-3247	1_0254
SCRI_RS_130982	5H	257,4					
SCRI_RS_192640	5H	260,1					
SCRI_RS_199694	5H	260,1					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_20536	5H	263,1	11_20536	11_0508	3362-644	3362-644	2_0536
SCRI_RS_199722	5H	263,1					
SCRI_RS_150686	5H	263,1					
SCRI_RS_203575	5H	263,1					
SCRI_RS_160831	5H	263,1					
12_20816	5H	263,5	12_20816	12_0498	12_20816	4810-1279	2_0816
12_11450	5H	271,6	12_11450	12_0371	12_11450	ConsensusGBS0152-1	1_1450
11_21138	5H	271,6	11_21138	11_1056	6761-490	6761-490	2_1138
SCRI_RS_131163	5H	271,6					
SCRI_RS_240083	5H	271,6					
SCRI_RS_179582	5H	271,6					
11_20022	5H	271,6	11_20022	11_0024	10386-329	10386-329	2_0022
SCRI_RS_145394	5H	271,6					
SCRI_RS_153933	5H	271,6					
SCRI_RS_13882	5H	273,5					
11_10778	5H	279,4	11_10778	11_0902	552-188	552-188	1_0778
11_10600	5H	279,4	11_10600	11_0651	4103-1386	4103-1386	1_0600
11_10736	5H	279,4	11_10736	11_0837	5145-1355	5145-1355	1_0736
SCRI_RS_194566	5H	279,4					
SCRI_RS_237948	5H	284,8					
SCRI_RS_239569	5H	284,8					
11_21155	5H	285,1	11_21155	11_1069	6851-867	6851-867	2_1155
11_21108	5H	285,1	11_21108	11_1028	6489-465	6489-465	2_1108
11_20786	5H	289,2	11_20786	11_0764	4658-1237	4658-1237	2_0786
12_30494	5H	291,1	12_30494	12_0859	12_30494	U32_3501_418	3_0494
11_10401	5H	291,1	11_10401	11_0434	2978-938	2978-938	1_0401
12_30360	5H	291,1	12_30360	12_0789	12_30360	U32_13213_63	3_0360
12_31292	5H	291,5	12_31292	12_1399	12_31292	U35_20347_823	3_1292
SCRI_RS_130320	5H	291,5					
SCRI_RS_190416	5H	292,3					
SCRI_RS_11024	5H	292,3					
SCRI_RS_232575	5H	292,3					
11_20132	5H	292,3	11_20132	11_0111	12925-332	12925-332	2_0132
SCRI_RS_168487	6H	0,0					
11_20232	6H	2,3	11_20232	11_0197	1692-742	1692-742	2_0232
SCRI_RS_153023	6H	2,3					
11_20262	6H	8,7	11_20262	11_0226	1872-1372	1872-1372	2_0262
11_20415	6H	9,3	11_20415	11_0399	2795-1707	2795-1707	2_0415
SCRI_RS_194048	6H	9,7					
SCRI_RS_8388	6H	9,7					
SCRI_RS_211856	6H	9,7					
11_21204	6H	9,7	11_21204	11_1107	7185-370	7185-370	2_1204
SCRI_RS_159124	6H	9,7					
SCRI_RS_164308	6H	9,7					
SCRI_RS_146663	6H	9,7					
11_20886	6H	11,1	11_20886	11_0844	5159-579	5159-579	2_0886
SCRI_RS_194023	6H	11,1					
SCRI_RS_153928	6H	11,1					
SCRI_RS_141842	6H	11,1					
SCRI_RS_202485	6H	11,1					
SCRI_RS_206183	6H	11,1					
SCRI_RS_207933	6H	14,1					
11_20294	6H	17,3	11_20294	11_0260	2057-412	2057-412	2_0294
SCRI_RS_129888	6H	17,3					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_202723	6H	17,3					
SCRI_RS_20187	6H	17,3					
SCRI_RS_139713	6H	20,2					
11_20493	6H	24,3	11_20493	11_0465	3178-1276	3178-1276	2_0493
SCRI_RS_167505	6H	24,3					
11_20315	6H	24,3	11_20315	11_0282	2188-425	2188-425	2_0315
11_10136	6H	24,3	11_10136	11_0186	1628-410	1628-410	1_0136
SCRI_RS_154426	6H	24,3					
SCRI_RS_222092	6H	31,6					
SCRI_RS_21695	6H	32,7					
12_30697	6H	33,2	12_30697	12_0984	12_30697	U32_7321_990	3_0697
12_30673	6H	33,2	12_30673	12_0969	12_30673	U32_6987_1361	3_0673
12_31308	6H	33,2	12_31308	12_1409	12_31308	U35_21048_1160	3_1308
11_10994	6H	33,2	11_10994	11_1249	885-104	885-104	1_0994
SCRI_RS_170814	6H	40,3					
SCRI_RS_154121	6H	44,2					
12_20463	6H	46,0	12_20463	12_0468	12_20463	3024-711	2_0463
SCRI_RS_235711	6H	46,2					
11_10939	6H	48,8	11_10939	11_1170	7848-441	7848-441	1_0939
11_10427	6H	48,8	11_10427	11_0464	3164-1386	3164-1386	1_0427
12_30361	6H	48,8	12_30361	12_0790	12_30361	U32_13368_432	3_0361
11_10494	6H	49,1	11_10494	11_0550	3580-331	3580-331	1_0494
11_10061	6H	49,5	11_10061	11_0089	12210-480	12210-480	1_0061
12_11455	6H	49,5	12_11455	12_0374	12_11455	ConsensusGBS0224-1	1_1455
12_30516	6H	49,5	12_30516	12_0874	12_30516	U32_3923_1371	3_0516
11_10799	6H	51,8	11_10799	11_0936	5771-91	5771-91	1_0799
SCRI_RS_213547	6H	51,8					
SCRI_RS_186520	6H	52,6					
SCRI_RS_157552	6H	52,6					
11_10220	6H	59,2	11_10220	11_0256	2047-850	2047-850	1_0220
11_20184	6H	59,4	11_20184	11_0155	1490-959	1490-959	2_0184
SCRI_RS_162581	6H	64,6					
11_10013	6H	64,6	11_10013	11_0027	1041-1441	1041-1441	1_0013
SCRI_RS_165041	6H	64,6					
SCRI_RS_222319	6H	64,6					
SCRI_RS_169672	6H	64,6					
11_20266	6H	64,6	11_20266	11_0233	1911-55	1911-55	2_0266
SCRI_RS_167	6H	64,6					
11_11147	6H	64,6	11_11147	11_1366	ABC06682-1-1-311	ABC06682-1-1-311	1_1147
SCRI_RS_155654	6H	65,5					
11_10355	6H	65,5	11_10355	11_0386	2702-284	2702-284	1_0355
11_10227	6H	65,5	11_10227	11_0265	210-450	210-450	1_0227
12_30857	6H	65,5	12_30857	12_1095	12_30857	OSU_HvCry2_1031	3_0857
11_11205	6H	69,2	11_11205	11_1383	ABC08769-1-1-205	ABC08769-1-1-205	1_1205
11_10461	6H	70,2	11_10461	11_0511	3378-619	3378-619	1_0461
12_30144	6H	70,2	12_30144	12_0667	12_30144	ABC10338_1_723	3_0144
SCRI_RS_206536	6H	70,2					
11_20636	6H	70,2	11_20636	11_0600	3865-103	3865-103	2_0636
SCRI_RS_130605	6H	72,3					
SCRI_RS_188520	6H	72,3					
12_30441	6H	72,3	12_30441	12_0832	12_30441	U32_2540_144	3_0441
11_21473	6H	72,3	11_21473	11_1343	ABC04676-1-1-59	ABC04676-1-1-59	2_1473
SCRI_RS_205256	6H	72,3					
SCRI_RS_118255	6H	72,3					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_222017	6H	72,3					
11_20329	6H	72,3	11_20329	11_0294	2259-488	2259-488	2_0329
11_21298	6H	72,3	11_21298	11_1186	8048-952	8048-952	2_1298
SCRI_RS_152393	6H	72,3					
SCRI_RS_165986	6H	72,3					
11_10455	6H	72,3	11_10455	11_0502	3348-395	3348-395	1_0455
SCRI_RS_154805	6H	72,3					
11_21124	6H	74,3	11_21124	11_1042	6593-185	6593-185	2_1124
SCRI_RS_231790	6H	74,5					
11_20682	6H	74,5	11_20682	11_0653	4109-90	4109-90	2_0682
12_30510	6H	77,7	12_30510	12_0870	12_30510	U32_3803_1334	3_0510
SCRI_RS_131341	6H	77,9					
12_30473	6H	78,0	12_30473	12_0845	12_30473	U32_3124_299	3_0473
SCRI_RS_195226	6H	78,3					
12_30802	6H	78,5	12_30802	12_1051	12_30802	U32_979_915	3_0802
11_20291	6H	78,6	11_20291	11_0255	2041-1317	2041-1317	2_0291
11_10040	6H	78,6	11_10040	11_0054	1140-1508	1140-1508	1_0040
SCRI_RS_204596	6H	78,6					
11_20673	6H	78,6	11_20673	11_0642	4064-1724	4064-1724	2_0673
11_11349	6H	78,6	11_11349	11_1450	ABC14687-1-4-344	ABC14687-1-4-344	1_1349
11_20468	6H	79,9	11_20468	11_0448	3048-1349	3048-1349	2_0468
SCRI_RS_147342	6H	81,7					
SCRI_RS_168455	6H	81,7					
SCRI_RS_138001	6H	81,7					
SCRI_RS_187343	6H	81,7					
SCRI_RS_145279	6H	81,7					
12_30133	6H	82,2	12_30133	12_0658	12_30133	ABC09903_1_265	3_0133
11_20746	6H	82,2	11_20746	11_0725	4454-1080	4454-1080	2_0746
12_30804	6H	82,6	12_30804	12_1052	12_30804	U32_9797_1113	3_0804
11_21069	6H	82,6	11_21069	11_0994	6205-683	6205-683	2_1069
11_21225	6H	83,5	11_21225	11_1125	7370-818	7370-818	2_1225
11_11067	6H	83,7	11_11067	11_1328	ABC02895-1-4-231	ABC02895-1-4-231	1_1067
SCRI_RS_206704	6H	83,7					
SCRI_RS_144892	6H	83,7					
SCRI_RS_170672	6H	83,9					
11_21014	6H	87,3	11_21014	11_0955	5873-880	5873-880	2_1014
11_20651	6H	87,3	11_20651	11_0617	397-288	397-288	2_0651
SCRI_RS_223224	6H	87,3					
11_20058	6H	87,3	11_20058	11_0047	11016-603	11016-603	2_0058
11_10635	6H	87,3	11_10635	11_0701	4313-482	4313-482	1_0635
12_30346	6H	87,3	12_30346	12_0780	12_30346	U32_12122_51	3_0346
11_20620	6H	87,3	11_20620	11_0589	3773-756	3773-756	2_0620
SCRI_RS_129756	6H	91,1					
SCRI_RS_137870	6H	91,3					
SCRI_RS_164341	6H	94,0					
SCRI_RS_12874	6H	94,0					
12_30626	6H	94,0	12_30626	12_0942	12_30626	U32_5968_585	3_0626
11_20784	6H	95,3	11_20784	11_0759	4642-1124	4642-1124	2_0784
11_10469	6H	95,3	11_10469	11_0524	3436-354	3436-354	1_0469
12_31088	6H	95,3	12_31088	12_1265	12_31088	U35_13855_365	3_1088
SCRI_RS_205971	6H	95,3					
SCRI_RS_170674	6H	95,3					
12_31250	6H	98,0	12_31250	12_1365	12_31250	U35_19005_402	3_1250
SCRI_RS_177093	6H	98,0					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_736	6H	101,9					
11_21025	6H	104,7	11_21025	11_0961	5926-798	5926-798	2_1025
SCRI_RS_149165	6H	105,0					
SCRI_RS_169374	6H	106,1					
SCRI_RS_164037	6H	106,3					
SCRI_RS_10932	6H	107,8					
SCRI_RS_184453	6H	108,0					
SCRI_RS_162589	6H	108,4					
11_20996	6H	110,4	11_20996	11_0941	578-587	578-587	2_0996
SCRI_RS_182637	6H	110,4					
11_10595	6H	110,4	11_10595	11_0647	4076-1056	4076-1056	1_0595
11_20972	6H	110,7	11_20972	11_0922	5684-601	5684-601	2_0972
SCRI_RS_124224	6H	110,7					
11_10734	6H	112,6	11_10734	11_0832	5124-1707	5124-1707	1_0734
SCRI_RS_120442	6H	112,6					
12_31432	6H	113,4	12_31432	12_1477	12_31432	U35_4470_378	3_1432
SCRI_RS_98225	6H	113,4					
SCRI_RS_151574	6H	118,2					
SCRI_RS_224910	6H	118,2					
11_10015	6H	118,2	11_10015	11_0028	10425-725	10425-725	1_0015
12_31044	6H	118,2	12_31044	12_1243	12_31044	UCI_Dhn7_1221	3_1044
SCRI_RS_8034	6H	118,2					
11_20036	6H	118,2	11_20036	11_0034	10687-540	10687-540	2_0036
11_20467	6H	118,2	11_20467	11_0447	3047-1400	3047-1400	2_0467
SCRI_RS_6720	6H	118,2					
SCRI_RS_189619	6H	124,4					
SCRI_RS_135063	6H	127,0					
SCRI_RS_213956	6H	127,0					
SCRI_RS_149269	6H	127,0					
SCRI_RS_169022	6H	132,7					
SCRI_RS_147455	6H	132,7					
SCRI_RS_162836	6H	132,7					
11_11534	6H	132,7	11_11534	11_1536	ConsensusGBS0708-6	ConsensusGBS0708-6	1_1534
SCRI_RS_131119	6H	132,7					
SCRI_RS_138295	6H	139,2					
11_20029	6H	139,2	11_20029	11_0030	10535-217	10535-217	2_0029
SCRI_RS_206827	6H	139,2					
11_20005	6H	139,2	11_20005	11_0005	1007-651	1007-651	2_0005
11_20211	6H	139,5	11_20211	11_0181	1597-158	1597-158	2_0211
SCRI_RS_152414	6H	146,1					
11_10828	6H	146,1	11_10828	11_0988	617-167	617-167	1_0828
11_10175	6H	147,3	11_10175	11_0219	1852-509	1852-509	1_0175
SCRI_RS_235672	6H	147,3					
SCRI_RS_10655	6H	147,3					
12_31283	6H	147,3	12_31283	12_1392	12_31283	U35_19999_392	3_1283
11_20687	6H	147,3	11_20687	11_0656	4126-1180	4126-1180	2_0687
11_21112	6H	147,3	11_21112	11_1033	6523-1691	6523-1691	2_1112
SCRI_RS_151280	6H	147,9					
11_20537	6H	160,0	11_20537	11_0509	3363-1795	3363-1795	2_0537
12_30956	6H	160,0	12_30956	12_1173	12_30956	SCRI_bbc07676_02_30	3_0956
11_10327	7H	0,0	11_10327	11_0364	2585-2901	2585-2901	1_0327
SCRI_RS_187827	7H	0,0					
SCRI_RS_219349	7H	0,0					
SCRI_RS_155795	7H	16,6					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_162708	7H	27,9					
SCRI_RS_164730	7H	28,2					
SCRI_RS_169904	7H	29,8					
SCRI_RS_125000	7H	30,1					
SCRI_RS_177253	7H	30,1					
SCRI_RS_219709	7H	30,1					
11_21326	7H	30,4	11_21326	11_1213	8390-328	8390-328	2_1326
11_20113	7H	30,4	11_20113	11_0091	12239-662	12239-662	2_0113
SCRI_RS_134872	7H	30,5					
11_21528	7H	30,7	11_21528	11_1507	ConsensusGBS0356-1	ConsensusGBS0356-1	2_1528
11_10772	7H	30,7	11_10772	11_0891	5467-1663	5467-1663	1_0772
SCRI_RS_171008	7H	30,7					
12_30752	7H	32,7	12_30752	12_1017	12_30752	U32_8480_522	3_0752
SCRI_RS_229041	7H	32,7					
11_21270	7H	32,7	11_21270	11_1164	7810-113	7810-113	2_1270
SCRI_RS_236651	7H	32,7					
SCRI_RS_137626	7H	33,5					
12_31305	7H	33,8	12_31305	12_1408	12_31305	U35_20926_243	3_1305
11_10726	7H	33,8	11_10726	11_0821	5028-1261	5028-1261	1_0726
SCRI_RS_230478	7H	33,8					
11_20975	7H	33,8	11_20975	11_0925	5695-922	5695-922	2_0975
SCRI_RS_129779	7H	36,9					
11_20126	7H	36,9	11_20126	11_0102	12701-485	12701-485	2_0126
12_30065	7H	36,9	12_30065	12_0621	12_30065	ABC06987_1_260	3_0065
12_10979	7H	36,9	12_10979	12_0227	12_10979	8548-1250	1_0979
SCRI_RS_149501	7H	36,9					
SCRI_RS_152122	7H	36,9					
12_30545	7H	36,9	12_30545	12_0890	12_30545	U32_4414_290	3_0545
SCRI_RS_187590	7H	36,9					
SCRI_RS_196063	7H	36,9					
12_30576	7H	36,9	12_30576	12_0909	12_30576	U32_5005_2035	3_0576
SCRI_RS_139962	7H	36,9					
11_11348	7H	48,0	11_11348	11_1449	ABC14535-1-1-75	ABC14535-1-1-75	1_1348
SCRI_RS_15864	7H	48,4					
11_20195	7H	48,4	11_20195	11_0165	1518-624	1518-624	2_0195
11_10153	7H	59,4	11_10153	11_0203	1735-1424	1735-1424	1_0153
SCRI_RS_12729	7H	59,4					
SCRI_RS_129686	7H	60,0					
SCRI_RS_195940	7H	65,6					
12_30496	7H	83,9	12_30496	12_0860	12_30496	U32_3530_642	3_0496
11_21178	7H	83,9	11_21178	11_1084	6975-1101	6975-1101	2_1178
SCRI_RS_140553	7H	103,4					
12_10369	7H	103,4	12_10369	12_0084	12_10369	2790-70	1_0369
12_30213	7H	103,4	12_30213	12_0708	12_30213	ABC13238_1_90	3_0213
11_20205	7H	103,4	11_20205	11_0173	1578-552	1578-552	2_0205
BK_03	7H	110,8					
11_10299	7H	117,0	11_10299	11_0333	2429-1929	2429-1929	1_0299
SCRI_RS_152074	7H	117,0					
11_20827	7H	117,0	11_20827	11_0797	4849-1248	4849-1248	2_0827
SCRI_RS_112718	7H	117,0					
11_20828	7H	121,2	11_20828	11_0798	4850-969	4850-969	2_0828
11_10370	7H	121,2	11_10370	11_0398	2792-749	2792-749	1_0370
SCRI_RS_207127	7H	121,2					
11_10055	7H	121,2	11_10055	11_0085	1212-890	1212-890	1_0055

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_20314	7H	124,8	11_20314	11_0281	2183-227	2183-227	2_0314
12_30563	7H	126,8	12_30563	12_0899	12_30563	U32_4768_190	3_0563
11_10073	7H	127,7	11_10073	11_0108	1290-729	1290-729	1_0073
SCRI_RS_150768	7H	130,7					
11_10721	7H	130,9	11_10721	11_0808	497-386	497-386	1_0721
SCRI_RS_169639	7H	130,9					
BK_07	7H	130,9					
12_31211	7H	138,3	12_31211	12_1337	12_31211	U35_18063_1739	3_1211
12_30419	7H	139,2	12_30419	12_0821	12_30419	U32_2166_347	3_0419
SCRI_RS_207246	7H	139,2					
SCRI_RS_181727	7H	149,6					
11_20485	7H	149,6	11_20485	11_0460	3140-491	3140-491	2_0485
SCRI_RS_225636	7H	149,6					
SCRI_RS_104566	7H	149,6					
SCRI_RS_127791	7H	149,6					
12_30806	7H	149,6	12_30806	12_1053	12_30806	U32_9828_126	3_0806
SCRI_RS_204256	7H	149,6					
SCRI_RS_193197	7H	149,6					
12_31440	7H	149,6	12_31440	12_1479	12_31440	U35_4712_928	3_1440
12_31294	7H	149,6	12_31294	12_1401	12_31294	U35_20364_468	3_1294
SCRI_RS_172243	7H	149,6					
SCRI_RS_168994	7H	152,5					
SCRI_RS_136586	7H	152,5					
SCRI_RS_124251	7H	152,5					
SCRI_RS_152752	7H	152,5					
11_10169	7H	173,5	11_10169	11_0214	1800-1101	1800-1101	1_0169
SCRI_RS_112204	7H	173,5					
11_20092	7H	173,5	11_20092	11_0068	1178-279	1178-279	2_0092
11_20247	7H	173,5	11_20247	11_0212	1789-782	1789-782	2_0247
SCRI_RS_1347	7H	173,5					
SCRI_RS_141732	7H	174,4					
SCRI_RS_182503	7H	174,4					
SCRI_RS_139808	7H	179,7					
SCRI_RS_162966	7H	179,7					
SCRI_RS_219260	7H	179,7					
SCRI_RS_150049	7H	191,1					
SCRI_RS_149645	7H	191,1					
SCRI_RS_223021	7H	191,8					
11_20192	7H	191,8	11_20192	11_0161	1511-545	1511-545	2_0192
12_10652	7H	191,8	12_10652	12_0156	12_10652	445-1199	1_0652
12_30362	7H	191,8	12_30362	12_0791	12_30362	U32_13417_246	3_0362
12_30797	7H	191,8	12_30797	12_1049	12_30797	U32_9614_416	3_0797
11_20103	7H	192,1	11_20103	11_0080	12027-128	12027-128	2_0103
SCRI_RS_127224	7H	193,2					
12_31261	7H	193,2	12_31261	12_1374	12_31261	U35_19382_606	3_1261
11_20495	7H	200,9	11_20495	11_0469	3187-1073	3187-1073	2_0495
SCRI_RS_179528	7H	203,1					
SCRI_RS_148318	7H	203,4					
11_10451	7H	204,1	11_10451	11_0494	3313-1443	3313-1443	1_0451
SCRI_RS_150053	7H	209,7					
11_10851	7H	210,8	11_10851	11_1031	6517-602	6517-602	1_0851
SCRI_RS_222330	7H	210,8					
12_31351	7H	211,3	12_31351	12_1428	12_31351	U35_2705_1795	3_1351
SCRI_RS_174285	7H	211,3					

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
11_10965	7H	216,4	11_10965	11_1209	8365-454	8365-454	1_0965
SCRI_RS_142007	7H	216,4					
12_21208	7H	216,4	12_21208	12_0543	12_21208	7208-468	2_1208
12_30368	7H	216,4	12_30368	12_0794	12_30368	U32_13527_471	3_0368
SCRI_RS_166511	7H	217,3					
11_20710	7H	217,3	11_20710	11_0677	4204-176	4204-176	2_0710
SCRI_RS_152931	7H	217,3					
11_20225	7H	217,3	11_20225	11_0192	1660-347	1660-347	2_0225
11_20722	7H	217,3	11_20722	11_0696	4275-1288	4275-1288	2_0722
SCRI_RS_152228	7H	217,3					
SCRI_RS_197190	7H	217,3					
SCRI_RS_160641	7H	217,3					
12_30329	7H	217,3	12_30329	12_0770	12_30329	U32_11227_239	3_0329
SCRI_RS_140096	7H	217,3					
12_10036	7H	217,6	12_10036	12_0007	12_10036	1116-409	1_0036
SCRI_RS_143373	7H	217,8					
12_20016	7H	217,8	12_20016	12_0409	12_20016	10308-451	2_0016
11_10894	7H	217,8	11_10894	11_1104	7172-1536	7172-1536	1_0894
11_10121	7H	217,8	11_10121	11_0170	1555-631	1555-631	1_0121
12_31350	7H	217,8	12_31350	12_1427	12_31350	U35_2649_795	3_1350
SCRI_RS_13615	7H	217,8					
11_11031	7H	217,8	11_11031	11_1309	984-583	984-583	1_1031
SCRI_RS_166323	7H	217,8					
12_31450	7H	217,8	12_31450	12_1486	12_31450	U35_5079_499	3_1450
SCRI_RS_139563	7H	217,8					
11_21229	7H	217,8	11_21229	11_1129	7397-854	7397-854	2_1229
SCRI_RS_1383	7H	217,8					
SCRI_RS_235853	7H	217,8					
SCRI_RS_155078	7H	217,8					
SCRI_RS_154069	7H	221,7					
SCRI_RS_157219	7H	222,0					
12_31374	7H	224,9	12_31374	12_1442	12_31374	U35_3205_2012	3_1374
11_10861	7H	224,9	11_10861	11_1043	6628-1302	6628-1302	1_0861
12_21328	7H	224,9	12_21328	12_0549	12_21328	8412-664	2_1328
11_20139	7H	227,7	11_20139	11_0120	13108-412	13108-412	2_0139
12_20241	7H	227,7	12_20241	12_0439	12_20241	1754-505	2_0241
11_11275	7H	227,7	11_11275	11_1417	ABC11252-1-2-254	ABC11252-1-2-254	1_1275
11_20962	7H	227,7	11_20962	11_0914	5595-297	5595-297	2_0962
SCRI_RS_120015	7H	227,7					
11_20117	7H	227,7	11_20117	11_0094	12368-207	12368-207	2_0117
11_20586	7H	229,2	11_20586	11_0549	3579-703	3579-703	2_0586
11_20847	7H	230,3	11_20847	11_0813	4991-1028	4991-1028	2_0847
SCRI_RS_130821	7H	230,3					
SCRI_RS_4604	7H	230,3					
12_30974	7H	230,3	12_30974	12_1187	12_30974	SCRI_bbc32814_01_394	3_0974
SCRI_RS_148742	7H	233,1					
SCRI_RS_174159	7H	233,7					
11_10687	7H	233,7	11_10687	11_0767	4671-856	4671-856	1_0687
11_10896	7H	233,7	11_10896	11_1106	7180-778	7180-778	1_0896
SCRI_RS_178933	7H	233,7					
11_10885	7H	236,3	11_10885	11_1087	7023-448	7023-448	1_0885
12_10677	7H	236,6	12_10677	12_0163	12_10677	4624-2108	1_0677
11_21160	7H	236,8	11_21160	11_1072	6868-595	6868-595	2_1160
11_10130	7H	236,8	11_10130	11_0178	1590-544	1590-544	1_0130

Locus name	Chr	Pos	BOPAMARK	BOPA	OLDNAME	POPA123S	POPA
SCRI_RS_151387	7H	237,7					
11_10797	7H	237,7	11_10797	11_0934	5764-430	5764-430	1_0797
12_30380	7H	241,6	12_30380	12_0801	12_30380	U32_1480_347	3_0380
SCRI_RS_126437	7H	241,6					
SCRI_RS_141470	7H	241,6					
SCRI_RS_132017	7H	244,0					
12_20832	7H	244,0	12_20832	12_0503	12_20832	4863-1723	2_0832
SCRI_RS_140746	7H	244,0					
SCRI_RS_220680	7H	244,0					
11_10843	7H	244,0	11_10843	11_1021	6433-124	6433-124	1_0843
11_11440	7H	244,0	11_11440	11_1489	ConsensusGBS0084-1	ConsensusGBS0084-1	1_1440
12_30593	7H	244,0	12_30593	12_0921	12_30593	U32_5362_853	3_0593
11_10174	7H	244,0	11_10174	11_0218	1847-1745	1847-1745	1_0174
SCRI_RS_158599	7H	245,2					
SCRI_RS_169268	7H	267,0					

[a] Name of SNP given by Germinate iSelect
[b] linkage group in the MAGIC population
[c] genetic position in the MAGIC population constructed with R/mpMap

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