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Chapter 1

Marker-Assisted Breeding in Wheat

Nana Vagndorf, Peter Skov Kristensen, Jeppe Reitan Andersen, Ahmed Jahoo and Jihad Orabi

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/intechopen.74724

Abstract

Selection is an integral component in plant breeding, which ensures the progressive values of the breeding material, in terms of yield and quality. However, selection is influenced by the environment in any given growing season. The observed phenotype is a product of the genotype (G), the environment (E), and/or genotype × environment (G×E). Therefore, phenotypic selection is not always the best predirector of the genotype. Therefore, an environment-independent method is preferred by the breeder. The development of molecular markers in plants has facilitated marker-assisted selection (MAS). MAS requires the establishment of correlation between a desired trait such as disease resistance and molecular marker(s). This can be obtained, e.g., by phenotyping a genetic mapping population followed by QTL analysis. Initially, this process was slow due to the laborious nature of the first DNA molecular marker system, such as restriction fragment length polymorphism (RFLP). Later, with the discovery of various marker systems amenable to automation and the development of genotyping techniques and instruments, MAS has become a standard procedure in plant breeding. In wheat breeding, MAS helped to accelerate the introgression of many genes that contribute to improve quality and resistance.

Keywords: wheat, marker-assisted breeding, molecular markers, wheat diseases, wheat quality

1. Introduction

Wheat is one of the most important sources of food worldwide. Data from FAOSTAT indicate that the need is still growing, indicated by the steadily increasing yield since 1961 (Figure 1). The need for an enhanced wheat production combined with stagnation in the area cultivated (Figure 1) leads to a demand for a more effective and higher yielding wheat production.
Marker-assisted selection (MAS) or molecular breeding offers an opportunity to accelerate the traditional breeding. Traditional breeding is based on phenotypic selection of genotypes obtained from crosses. Genotype × environment (G×E) interaction is a common problem including time-consuming and costly procedures of phenotyping. By employing molecular markers, desirable genes can be fixed in early generations of the breeding program. In addition, molecular markers are unaffected by environmental conditions and are detectable in all stages of the plant growth. Scientists and breeders across the world implement MAS in breeding programs [1].

2. Linkage and molecular markers

MAS is based on the concept of genetic linkage between loci. This describes the tendency of loci located closely together on the same chromosome being more likely to be inherited together in a recombination event during meiosis. Thus, two alleles located very close on the chromosome will almost always be inherited together.

Molecular markers are used in MAS to highlight a place on the chromosome close to or in a specific gene of interest. The technique is based on detecting different alleles (polymorphisms) between several individuals. Due to genetic linkage, the molecular marker will reveal if the linked allele is present or not in a line. Several types of molecular markers exist, depending on the type of polymorphism. In today’s MAS, markers detecting single nucleotide differences are usually employed.
3. Application of MAS in breeding for disease resistance in wheat

diseases

Plant diseases are a major constraint in wheat production and significant resources are allocated to control various diseases. The relatively long growing season of winter wheat renders it vulnerable to a range of diseases and breeding for disease resistance is generally thought to be the first line of defence [2]. Disease resistance is generally separated into quantitative and qualitative resistance. Qualitative resistance is most often controlled by a single gene and follows the gene-for-gene hypothesis. Thus, an R gene in the host can specifically interact with an Avr gene in the pathogen to induce a defence reaction in the host. Qualitative resistance often mediates a complete resistance response, whereas quantitative resistance is regarded as an incomplete or partial resistance. This type of resistance is usually mediated by several minor genes, which are designated as a quantitative trait locus (QTL) [3]. Following the development of MAS, targeted pyramiding of several resistance genes in single lines is now possible. In the following sections, three severe diseases of wheat and correlated resistance genes are described. Common to these diseases is that fungicides are becoming less efficient. Hence, more effective approaches are desired.

3.1. Septoria tritici blotch

One of the most important foliar diseases in wheat is Septoria tritici blotch (STB), caused by the fungus Zymoseptoria tritici formally known as Septoria tritici (anamorph) and Mycosphaerella graminicola L (teleomorph) [4]. STB is a devastating disease causing massive yield losses worldwide every year in wheat. Severe epidemics can reduce wheat yield by 35–50% [5]. Symptoms of the disease are chlorotic lesions on the leaf with black fruiting bodies containing fungal spores. Breeding strategies over the years have primarily focused on breeding for higher yield, in turn increasing the susceptibility towards STB [6]. Disease control can be performed by delaying sowing time, probably due to less time in the autumn for Z. tritici to infect seedlings and produce inoculum. Furthermore, the application of fungicides and implementation of resistant cultivars in breeding programs are widely used [5]. In previous years, several studies have identified STB resistance genes using molecular techniques. Stb1, Stb2 and Stb3 were the first qualitative genes for STB resistance to be named [7]. Prior to that, STB resistance was thought of as a quantitative, polygenic trait. Stb1 was mapped to the long arm of chromosome 5B in the cultivar Bulgariarg88 [8]. Stb2 was mapped to the short arm of chromosome 1B in the cultivar Veranopolis [9]. Additionally, Stb11 was mapped to the short arm of 1B [10]. However, no studies have included an allelism test of Stb2 and Stb11. Stb3 was mapped to the short arm of 7A in Israel493 [11]. Stb6 was mapped to the short arm of chromosome 3A in the cultivar Flame [12]. This gene is the only STB-resistant gene found to possess a gene-for-gene relationship, in which a specific R gene in the host interacts with an Avr gene in the pathogen. This was demonstrated in a study where Flame was found to confer specific resistance towards the Z. tritici isolate IPO323 [12]. This study conforms to the original gene-for-gene model proposed by Flor [13]. Stb6 was subsequently found to be one of the most abundant STB-resistant genes in European wheat [14]. In total, 18 Stb genes have been
identified and mapped using various molecular markers. Additionally, several QTL have been identified conferring STB resistance [7, 15]. Table 1 summarises major STB-resistance genes together with linked markers suitable for MAS. Additionally, several QTL have been identified conferring STB resistance [7, 15].

One of the more promising resistance genes identified in recent years is Stb16. This gene was identified in synthetic hexaploid wheat lines, which represent a rich source of variation [23]. Stb16 explained a high proportion of STB disease resistance and conferred resistance at the seedling stage to all tested Z. tritici isolates. Moreover, 20 tested isolates were all avirulent to this gene, indicating that Stb16 confers broad-spectrum resistance. If this is the case, Stb16 holds promise for future breeding of efficient and durable STB resistance.

In order to obtain the most resistant wheat variety, breeders should take a number of things into account. Since qualitative resistance genes often conform to the gene-for-gene hypothesis, they are readily overcome by the pathogen. Due to the high frequency of genetic recombination of Z. tritici, the specific recognition of R proteins by the host is lost [26]. Furthermore, the strong

<table>
<thead>
<tr>
<th>Resistance gene</th>
<th>Marker type</th>
<th>Marker name</th>
<th>Location</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stb1</td>
<td>SSR</td>
<td>Xbarc74, Xgwm335</td>
<td>5BL</td>
<td>[8]</td>
</tr>
<tr>
<td>Stb2</td>
<td>SSR</td>
<td>Xwmc406, Xbarc008</td>
<td>1BS</td>
<td>[9]</td>
</tr>
<tr>
<td>Stb3</td>
<td>SSR</td>
<td>Xwmc83</td>
<td>7AS</td>
<td>[11]</td>
</tr>
<tr>
<td>Stb4</td>
<td>SSR</td>
<td>Xgwm111, Xgwm44</td>
<td>7DS</td>
<td>[16]</td>
</tr>
<tr>
<td>Stb5</td>
<td>SSR</td>
<td>Xgwm44</td>
<td>7DS</td>
<td>[17]</td>
</tr>
<tr>
<td>Stb6</td>
<td>SSR</td>
<td>Xgwm369</td>
<td>3AS</td>
<td>[12]</td>
</tr>
<tr>
<td>Stb7</td>
<td>SSR</td>
<td>Xgwm160, Xwmc219, Xwmc319</td>
<td>4AL</td>
<td>[18]</td>
</tr>
<tr>
<td>Stb8</td>
<td>SSR</td>
<td>Xgwm146, Xgwm577</td>
<td>7BL</td>
<td>[19]</td>
</tr>
<tr>
<td>Stb9</td>
<td>SSR</td>
<td>Xhbg226, XksuF1b</td>
<td>2BL</td>
<td>[20]</td>
</tr>
<tr>
<td>Stb10</td>
<td>SSR</td>
<td>Xgwm848</td>
<td>1D</td>
<td>[21]</td>
</tr>
<tr>
<td>Stb11</td>
<td>SSR</td>
<td>Xbarc008</td>
<td>1BS</td>
<td>[22]</td>
</tr>
<tr>
<td>Stb12</td>
<td>SSR</td>
<td>Xwmc219, Xgw313</td>
<td>4AL</td>
<td>[21]</td>
</tr>
<tr>
<td>Stb13</td>
<td>SSR</td>
<td>Xwmc396</td>
<td>7BL</td>
<td>[19]</td>
</tr>
<tr>
<td>Stb14</td>
<td>SSR</td>
<td>Xwmc500, Xwmc632</td>
<td>3BS</td>
<td>Wheat gene catalogue</td>
</tr>
<tr>
<td>Stb16</td>
<td>SSR</td>
<td>Xgwm494</td>
<td>3DL</td>
<td>[23]</td>
</tr>
<tr>
<td>Stb17</td>
<td>SSR</td>
<td>Xhbg247</td>
<td>5AL</td>
<td>[23]</td>
</tr>
<tr>
<td>Stb18</td>
<td>SSR</td>
<td>Xgpw5176, Xgpw3087</td>
<td>6DS</td>
<td>[24]</td>
</tr>
<tr>
<td>StbWW</td>
<td>SSR</td>
<td>Xbarc119b</td>
<td>1BS</td>
<td>[25]</td>
</tr>
</tbody>
</table>

The name of the resistance gene, marker type, marker name, the location on the genome and the reference are indicated.

Table 1. An overview of the named and mapped genes for STB resistance.
selection pressure placed on the pathogens by one major resistance gene promotes the rise of new adapted races in the pathogen population [27]. An earlier study has proved that commercial cultivation of a highly resistant cultivar can result in loss of resistance towards STB. The intensive cultivation of the variety Gene in the 1990s in Oregon, US, resulted in resistance breakdown. Gene was found to be resistant to two specific isolates, which were avirulent to Stb6 and Stb10 [28]. Gradually, an adaptation of Z. tritici to one of the resistance genes occurred and the resistance was lost [26]. In general, it appears that most Z. tritici isolates used in earlier studies are virulent to almost all Stb genes [7]. This may indicate that Z. tritici easily can overcome single qualitative resistance genes. In contrast, the quantitative resistance is regarded as more durable. This is due to a lower selection pressure on the pathogen as a result of smaller resistance effects of individual QTL [3]. Furthermore, since quantitative resistance is often polygenic, the mutation of one gene does not necessarily break down disease resistance completely.

3.2. Fusarium head blight

Fusarium head blight (FHB) is an important disease in all wheat growing countries. Epidemics occur frequently, especially under seasons with regular rainfall [29]. The United States Department of Agriculture (USDA) has stated that FHB is the most devastating plant disease since the rust epidemics in the 1950s. FHB contaminates the grain with mycotoxins, in turn restricting its use for both animal and human consumption [30]. The disease is caused by several species of Fusarium; however, the predominant causal agent is the fungus Fusarium graminearum (teleomorph Gibberella zeae). The first symptoms of FHB on wheat plants occur shortly after flowering as diseased spikelets display premature bleaching. The bleaching usually spreads to the whole spike as the pathogen grows. When conditions are optimal for the pathogen, i.e., in a warm and moist environment, light pink coloured spores, called sporodochia, appear on individual spikelets. Later during the season, black fruiting bodies will appear. These are the sexual structures of the fungus, called perithecia. Disease progression results in shrinking and wrinkling of the grain inside the spike. As with the pathogen causing STB, F. graminearum produces both sexual and asexual spores: ascospores and macroconidia, respectively [30]. The major toxin produced by FHB in wheat is deoxynivalenol (DON). DON is a protein synthesis inhibitor also known as vomitoxin due to its negative impact on the digestive system of pigs. Several recommendations and restrictions have been made in order to keep DON levels sufficiently low in wheat for both animal and human consumption [31].

Chemical control and crop management are not sufficient to control FHB; thus, breeding resistant varieties plays a key role. Conventional breeding involves repeated testing of breeding lines under natural or artificial inoculations. This process is time-consuming, costly, and prone to influence by environment. Thus, it is relevant to supplement phenotypic selection with MAS for FHB resistance. [32]. FHB resistance is generally divided into three types: resistance to initial infection (type I), resistance to spreading of the pathogen in infected tissue (type II) and resistance to DON accumulation (type III) [33]. Several studies have demonstrated that FHB resistance is of quantitative nature [29]. Furthermore, the expression of resistance is highly dependent on the pathogen, the environment and the host [34], in turn complicating phenotypic selection. Several QTL for FHB resistance have been identified and
located during recent years [29]. The first QTL for type II resistance was identified in the spring wheat ‘Sumai 3’ on chromosome 3BS. This QTL was named Fhb1 and characterised by molecular markers [35–37]. Recently, Fhb1 was cloned from Sumai 3 and a pore-forming toxin-like (PFT) gene was found to confer FHB resistance [38]. Fhb1 has been found to reduce FHB disease severity tremendously and MAS is employed to incorporate the resistance in breeding programs [29]. A QTL, named Fhb2, on chromosome 6BS was found to confer type II FHB resistance [39, 40]. Additionally, Fhb4 was identified and located on chromosome 4B [41].

Table 2 lists all FHB-resistant genes identified by molecular markers. Currently, breeders are pyramiding Fhb1, Fhb2 and Fhb4 in single breeding lines to obtain optimal FHB resistance [34]. Several additional QTL have been identified and located in numerous studies [29].

<table>
<thead>
<tr>
<th>Resistance gene</th>
<th>Marker type</th>
<th>Marker name</th>
<th>Location</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fhb1</td>
<td>SSR</td>
<td>Xgwm493, Xgwm533</td>
<td>3BS</td>
<td>[42]</td>
</tr>
<tr>
<td>Fhb2</td>
<td>SSR</td>
<td>Xgwm133, Xgwm644</td>
<td>6BS</td>
<td>[40]</td>
</tr>
<tr>
<td>Fhb4</td>
<td>SSR</td>
<td>Xhbg226, Xgwm149</td>
<td>4B</td>
<td>[41]</td>
</tr>
<tr>
<td>Fhb5</td>
<td>SSR</td>
<td>Xgwm304, Xgwm415</td>
<td>5A</td>
<td>[43]</td>
</tr>
<tr>
<td>Fhb6</td>
<td>KASP</td>
<td>Wg1s_snp1</td>
<td>1AS</td>
<td>[44]</td>
</tr>
<tr>
<td>Fhb7</td>
<td>SSR</td>
<td>XsdauK66, Xcfa2240</td>
<td>7DS</td>
<td>[45]</td>
</tr>
</tbody>
</table>

Table 2. Overview of the FHB-resistant genes identified in wheat using molecular markers.

3.3. Wheat stripe rust (yellow rust)

Wheat stripe rust, mostly designated as ‘yellow rust’ (YR), causes major yield losses every year. The disease is caused by *Puccinia striiformis*, which belongs to the family *Pucciniaceae* of rust fungi. The most devastating epidemics occur in temperate areas with cool and humid summers or in warmer areas with cool nights. The fungus is heteroecious, i.e., it requires at least two hosts in order to proliferate. *P. striiformis* uses cereals as a primary host and *Berberis* spp. as a secondary host for sexual recombination. Typical, yellow stripes develop on the leaf in lesions. Spores continue to be produced as stripes spread longitudinally on the leaf. After the onset of senescence, *P. striiformis* will produce teliospores. Teliospores can infect the secondary host, *Berberis* spp., and initiate onset of pycnia infection of the *Berberis* leaf [46].

Breeding for YR resistance was initiated in 1905 by Biffen [47]. To date, more than 70 genes (*Yr* genes) conferring YR resistance have been identified [48]. Most of the catalogued genes confer seedling resistance, while relatively few confer adult plant resistance. In general, studies have shown that seedling resistance is conferred by single genes and the resistance is therefore easily overcome by the pathogen by mutations in virulence genes. Adult plant resistance is generally thought to be more durable [49]. High-temperature adult plant (HTAP) genes are expressed as the plants grow older and the weather becomes warmer [50]. HTAP genes confer a non-specific, quantitative resistance. Studies have proven that varieties with HTAP genes display resistance
to YR even after having been cultivated for 60 years [51]. Additionally, several studies have mapped QTL to all wheat chromosomes except chromosome 1D and 3A [49]. Commonly used resistance genes employed in wheat breeding programs include Yr18, Yr29 and Yr36 [52–54]. Yr36 is tightly linked to Gpc-B1, a high-protein gene, rendering varieties with Yr36 and Gpc-B1 useful in breeding for YR resistance and improved quality. Table 3 lists a selection of Yr genes that have been characterised and mapped with molecular markers suitable for MAS.

Several incidences have been reported where Yr genes have been classified as ineffective. Some of the most widely used resistance genes including Yr17 [62], Yr27 [63] and Yr31 [64] have recently lost resistance towards YR.

### 4. Marker-assisted wheat breeding for improving quality traits

Wheat is grown in large parts of the world and is used for animal feed or for a wide range of products such as pasta, biscuits, cakes and bread. The end-use quality differs greatly between wheat cultivars and is influenced by several traits, e.g., grain hardness, grain protein content, gluten content and composition and starch properties. Quality should therefore be an important focus in wheat breeding programs. However, wheat quality cannot be easily determined phenotypically, and different methods are preferred in different countries and industries. Methods for testing quality are typically time-consuming and costly and require relatively large amounts of grain, which is typically not available until late stages of breeding programs. Thus, markers for wheat quality traits can be very useful, as they enable screening of a high number of lines and can be used early in breeding programs [65, 66].

#### 4.1. Grain hardness

Grain hardness influences milling, flour and end-use properties of wheat. Flour from grain with hard endosperm texture has higher water absorption than flour from soft grain and is therefore preferred for bread-making. A soft endosperm texture leads to less starch granule damage.

<table>
<thead>
<tr>
<th>Resistance gene</th>
<th>Marker type</th>
<th>Marker name</th>
<th>Location</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yr5</td>
<td>SSR</td>
<td>Xgwm501</td>
<td>2BL</td>
<td>[55]</td>
</tr>
<tr>
<td>Yr7</td>
<td>SSR</td>
<td>Xgwm526</td>
<td>2BL</td>
<td>[56]</td>
</tr>
<tr>
<td>Yr15</td>
<td>SSR</td>
<td>Xbarc8, Xgwm493</td>
<td>1BS</td>
<td>[57]</td>
</tr>
<tr>
<td>Yr18</td>
<td>CAPS</td>
<td>Cssfr6</td>
<td>7D</td>
<td>[58]</td>
</tr>
<tr>
<td>Yr36</td>
<td>SSR</td>
<td>Xgwm508, Xbarc136</td>
<td>6BS</td>
<td>[54]</td>
</tr>
<tr>
<td>Yr60</td>
<td>SSR</td>
<td>Xwmc776</td>
<td>4AL</td>
<td>[59]</td>
</tr>
<tr>
<td>Yr76</td>
<td>SSR</td>
<td>Xwmc11, Xwmc332</td>
<td>6BS</td>
<td>[60]</td>
</tr>
<tr>
<td>Yr78</td>
<td>SNP</td>
<td>IWA7257</td>
<td>6BS</td>
<td>[61]</td>
</tr>
</tbody>
</table>

Table 3. A selection of the genes conferring YR resistance identified by molecular markers.
during the milling and consequently to lower water absorption, which is preferred in the production of biscuits and cakes. Grain hardness is primarily controlled by the Hardness locus on chromosome 5DS. This locus consists of three small genes: Pina-D1, Pinb-D1 (Puroindoline a/b) and grain softness protein-1 (Gsp-1). Wheat varieties with the wild-type alleles Pina-D1a and Pinb-D1a normally have soft grain, while deletions or other loss-of-function mutations in one or both Pin genes cause harder grain (Table 4) [67, 68]. Pinb-D1 mutations are positively associated with many quality traits, but the alleles are not equally useful in breeding for improved quality. Pinb-D1d has been reported to have a lower effect on gluten quality and loaf volume than the b- or c-allele [69]. Alleles of Pinb-D1 can be detected using PCR primers that target a specific mutation (Pinb-D1b), using a restriction enzyme on the amplified Pinb-D1 gene (Pinb-D1c), or by sequencing the amplified gene (Pinb-D1d-g) [67, 70, 71].

<table>
<thead>
<tr>
<th>Allele</th>
<th>Change in protein</th>
<th>Primer sequences, 5′–3′</th>
<th>PCR product</th>
<th>References</th>
</tr>
</thead>
</table>
| Pina-D1a | Wild-type | F: ATGAAGGCCCTCTTCCTCA  
R: TCACCAGTAATAGCCATAGTG | 448 bp | [73, 74] |
| Pinb-D1b | Large deletion | F: ATGAAGGCCCTCTTCCTCA  
R: TCACCAGTAATAGCCATAGTG | Null (0 bp) | [73, 74] |
| Pinb-D1a | Wild-type | F: ATGAAGACCTTATTCCTCA  
R: CTCATGCTCACAGCCGT | 240 bp | [70, 73] |
| Pinb-D1b | Gly to Ser  
pos. 46 | F: ATGAAGACCTTATTCCTCA  
R: CTCATGCTCACAGCCGT | 240 bp | [70, 73] |
| Pinb-D1c | Leu to Pro  
pos. 60 | F: ATGAAGACCTTATTCCTCA  
R: TCACCAGTAATAGCCACTGGGA | 448 bp* | [67, 73] |
| Pinb-D1d | Trp to Arg  
pos. 44 | F: TGCAAGGATTACGTGATGGA  
R: TCACCAGTAATAGCCACTGGGA | 300 bp for pyrosequencing | [67, 71] |
| Pinb-D1e | Trp to stop  
codon pos. 39 | F: TGCAAGGATTACGTGATGGA  
R: TCACCAGTAATAGCCACTGGGA | 300 bp for pyrosequencing | [71, 75] |
| Pinb-D1f | Trp to stop  
codon pos. 44 | F: TGCAAGGATTACGTGATGGA  
R: TCACCAGTAATAGCCACTGGGA | 300 bp for pyrosequencing | [71, 75] |
| Pinb-D1g | Cys to stop  
codon pos. 56 | F: TGCAAGGATTACGTGATGGA  
R: TCACCAGTAATAGCCACTGGGA | 300 bp for pyrosequencing | [71, 75] |

Wild type alleles confer soft endosperm; mutations confer hard endosperm. For additional alleles, see reviews [68, 72]. Digest with restriction enzyme PvuII to cut other alleles into 264 bp and 184 bp. Pinb-D1c is not cut.

Table 4. Alleles of Pina-D1 and Pinb-D1 and the change in amino acid sequence of the encoded protein.
4.2. Gluten

The characteristic viscoelastic properties of wheat dough are due to a network of gluten proteins that is formed when flour is mixed with water. Thus, gluten is a major factor contributing to wheat quality. High grain protein content is typically associated with high quality, since roughly 80% of the grain protein is gluten [76]. However, both the amount and the composition of gluten affect wheat quality. Gluten consists of two types of proteins: polymeric glutenins and monomeric gliadins. Glutenins can be classified as low or high molecular weight (LMW or HMW) subunits, while gliadins can be classified as α, β, γ or ω types [77, 78]. The most important HMW glutenins, LMW glutenins, and gliadins are encoded by the Glu-1, Glu-3 and Gli-1 loci, respectively (Table 5). HMW glutenins generally have the largest impact on wheat quality. Each of the three Glu-1 loci comprises two genes that can encode an x- or a y-type HMW subunit. In hexaploid wheat, only three to five of the HMW subunits are expressed (zero to two from Glu-A1, one to two from Glu-B1, and two from Glu-D1) [79]. The Glu-1 alleles with the largest positive effect on baking quality are Glu-D1d, Glu-A1a or Glu-Alb and Glu-B1al [80, 81]. SDS-PAGE electrophoresis can be used to screen varieties for their HMW glutenin proteins. DNA markers have also been developed to discriminate between different alleles of Glu-1, Glu-3 and Gli-1 loci [82, 83]. For Glu-A1 and Glu-D1, KASP markers are available that can be used to select varieties with the optimal alleles [84]. Each of the Glu-3 loci (Glu-A3, Glu-B3 and Glu-D3) contains several linked genes, and many alleles have been found for all three loci [85–89]. Markers are available for individual alleles of Glu-A3 and Glu-B3, and multiplex PCR can be used to screen for certain combinations of alleles simultaneously [87]. However, the alleles of Glu-3 loci with the largest effects are not consistent across studies [90–92]. The exact effects of the individual alleles on wheat quality traits are challenging to determine, since they can be influenced by genetic background, environment and G×E interactions [91, 93]. Furthermore, the alleles can have both additive effects and epistatic interactions [94, 95]. Ref. [93] showed that the d-allele of Glu-B3 might increase the positive effects of the HMW loci Glu-B1i and Glu-D1d. The Glu-A3b or d-allele and Glu-B3b, d- or g-allele can possibly be used for improving dough strength and extensibility [90–92]. Glu-B3h has been reported to be positively associated with wheat quality in some lines and negatively associated in other lines. This discrepancy is possibly due to linkage with different Gli-B1 alleles [90]. The Gli-1 loci encode γ and ω gliadins and are linked to the Glu-3 loci [96], while Glu-2 loci encode α and β gliadins and are located on chromosome 6AS, 6BS and 6DS [78]. Overview of markers (including primer sequences) for more alleles of Glu loci and other quality genes can be found in [82].

4.3. Wheat-rye translocation and falling number

The wheat-rye translocation 1BL.1RS has been employed in many breeding programs as it carries resistance genes against powdery mildew and rusts. Markers for the resistance genes can be used to test for the absence or presence of the translocation in wheat varieties [100]. Alternatively, markers for Glu-B3 or Gli-B1 might be used (Table 6), since many wheat varieties with the 1BL.1RS translocation do not have these two loci, but instead can have the rye secalin locus Sec-1 [96]. Therefore, wheat quality can be negatively affected by the translocation [101]. Additionally, the 1BL.1RS translocation can have a negative effect on falling number. Falling number is an indirect measure of α-amylase enzyme activity. The α-amylases are encoded by
<table>
<thead>
<tr>
<th>Locus</th>
<th>Chr. arm</th>
<th>Primer sequences, 5′–3′</th>
<th>PCR product</th>
<th>References</th>
</tr>
</thead>
</table>
| Glu-A1 | 1AL      | FAM: AAGTGTTAATCTTCCGCAACA  
Vic: AAGTGTTAACTTCCGCAACG  
Common: GGCCCTGAGATAGTGAAACC | Glu-A1a or Glu-A1b  
Vic: Glu-A1c | [84, 97] |
| Glu-B1 | 1BL      | F: ACCTGCTCAAGCTTTGGTTC  
R: GATTGGTGTTGATACAGG | Glu-B1al: 447 bp  
Others: 0 bp | [98] |
| Glu-D1 | 1DL      | FAM: ATAGTATGAAACCTGTCGGAG  
Vic: ATAGTATGAAACCTGTCGGAGC  
Common: TACTAAAAGGTATTACCCAAGTGTAACCT | Glu-D1a or others  
Vic: Glu-D1d | [84, 99] |
| Glu-A3 | 1AS      | F: TCTCAGTGCAGCCAAACAA  
R: GGTAGGGAGGCGAGAGGCGAG  
F: TCTCAGTGCAGCCAAACAA  
R: TGGGGTTGGGAGACACATA  
F: CACCATGAAGACCTTCCTCA  
R: CACCATGAAGACCTTCCTCA  
F: CCAAGAAATACTAGTTAACACTAGTC  
R: GTTGGGTTGGGAAACAA | Glu-A3b: 894 bp  
Others: 0 bp | [86, 87] |
| Glu-B3 | 1BS      | F: ATCATGTTAAGACTGATAG  
R: CATGGTGCCACTTCTTCTC  
F: CACCATGAAGACCTTCCTCA  
R: CACCATGAAGACCTTCCTCA  
F: CCAAGAAATACTAGTTAACACTAGTC  
R: GTTGGGTTGGGAAACAA | Glu-B3b: 1549 bp  
Others: 0 bp | [88] |
| Glu-A3 | 1AS      | F: TTCAGATGCAGCCAAACAA  
R: TGGGGTTGGGAGACACATA | Glu-A3d: 967 bp  
Others: 0 bp | [86, 87] |
| Glu-B3 | 1BS      | F: ATGTCAGTCGGGATCAGTAC  
R: TGGGGTTGGGAGACACATA | Glu-B3d: 662 bp  
Others: 0 bp | [88] |
| Glu-B3 | 1BS      | F: CACCATGAAGACCTTCCTCA  
R: CACCATGAAGACCTTCCTCA  
F: CCAAGAAATACTAGTTAACACTAGTC  
R: GTTGGGTTGGGAAACAA | Glu-B3g: 853 bp  
Others: 0 bp | [88] |

Favourable alleles are marked in bold.

Table 5. Important HWM and LMW glutenin loci, their chromosomal location and primer sequences for detection of alleles with positive effects on wheat quality.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Primer sequences, 5′–3′</th>
<th>PCR product</th>
<th>References</th>
</tr>
</thead>
</table>
| Glu-B1 | F: TGATCTGGCCACAAAGGGA  
(1BL.1RS) C: TATGGTGCACCACTTCTGTCGAG  
R: CATCCCATGCGGCCAGTTAGTGCAG | Glu-B1.1: 369 bp  
Glu-B1.2 or 1BL.1RS: 0 bp  
Glu-B1.2: 397 bp  
Glu-B1.1 or 1BL.1RS: 0 bp | [96] |
| Rht-D1 | F: GTTGGGAGGCGGAGAGGCGAG  
R: CATCCCATGCGGCCAGTTAGTGCAG | Rht-D1b: 237 bp  
Rht-D1a: 0 bp | [106] |
| wbm    | F: CCGTCAACAAGATTTACAGGGTTG  
R: TTATGGATCTTATGTTCTGTTG | High wbm expression: 961 bp  
Others: 0 bp | [103] |
| Gpc-B1 | F: TCTCAGAAGGCGGAGAGGAGACA  
R: TCTCCTCACATCACTACAGCA | Gpc-B1: 122 bp  
No Gpc-B1: 126 bp | [105] |

Favourable alleles are marked in bold.

Table 6. Additional loci influencing wheat quality traits.
the loci α-Amy-1, α-Amy-2 and α-Amy-3 located on the homoeologous chromosome groups 6, 7 and 5, respectively. High falling number reduces the risk of pre-harvest sprouting, which has a considerable negative impact on quality. Environmental conditions around the time of harvest influence falling number, but it is also influenced genetically. The b-allele of the Rht-D1 (reduced height) gene on chromosome 4D is correlated with increased falling number [102].

4.4. Other genes for improving quality

Ref. [103] identified a gene, wheat bread making (wbm), that was highly expressed in developing seeds of wheat varieties with good bread-making quality. Polymorphisms in the promoter region sequence were identified between good- and poor-quality varieties. The allele identified in the good quality varieties was positively associated with gluten and bread-making quality in CIMMYT (The International Maize and Wheat Improvement Center) germplasm [104].

Genes from wild wheat relatives might also be used for improving quality in modern cultivars. Backcrossing can be used to transfer the genes into breeding material. In this case, MAS is useful since offspring containing the desired genes easily can be detected, and linkage drag can be reduced. One example of such a gene is Gpc-B1 (grain protein content), which was found in wild emmer (Triticum turgidum L. ssp. dicoccoides). This gene has been used for increasing grain protein content in both durum and common wheat [105]. Markers tightly linked to Gpc-B1 were identified, but require digestion with restriction enzymes. Therefore, [105] recommends the use of the marker shown in Table 6 for MAS, although it is not completely linked to Gpc-B1.

5. Conclusion and perspectives

Trait-linked DNA markers have been identified for numerous traits in wheat, including disease resistance and grain quality. Employing such markers in MAS offers several advantages to wheat breeding compared to conventional phenotypic selection and laborious analysis of grain quality. These advantages include the fixation of desirable traits at an early stage of the breeding program and marker-assisted backcrossing in order to transfer agronomically important genes from wild relatives to cultivated wheat.

In addition, DNA markers are neutral to both environment and tissue type. Thus, they can be employed at any plant developmental stage and independent on environmental conditions during selection. This is particularly relevant for selection for disease resistance. DNA markers further offer the possibility for targeted pyramiding of several resistance genes, a task impossible by phenotypic selection due to complex host-pathogen interactions. To secure durable resistance, it is important to combine qualitative and quantitative resistance in a given line. Here, molecular markers can be used to combine both resistances.

As DNA markers have been correlated to numerous traits, they can be employed to combine, e.g., resistance and grain quality in the early generations. Consequently, DNA markers are being employed in early generations to select for several traits, in turn reducing the number of lines entering replicated, multi-location trials. Similarly, the number of samples for laboratory analysis of grain quality can be reduced. In effect, the application of MAS can lead to an
optimisation of resources demanded by any given breeding program, allowing the breeder to focus phenotypic selection on highly multi-genic traits, difficult to handle with MAS, e.g., yield.

Following developments in technologies and statistical genetics, the application of DNA markers in breeding is rapidly changing. While MAS has been employed to select for traits controlled by one/few genes, genomic selection will allow accurate selection for traits affected by numerous genes.

Once genomic selection has been validated in breeding programs, it can be implemented in combination with MAS. This will further improve selection efficiency and accuracy for disease resistance and quality parameters as well as for multi-genic traits such as yield.

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