The seed storage proteins (SSPs) of cultivated wheat (Triticum aestivum and T. durum), namely, glutenin and gliadin, impart viscoelastic properties to bread dough, making wheat well suited for bread-making. Extensive studies on wheat SSPs have been carried out and revealed genetic diversity among wheat cultivars. Here, we review the studies of SSPs from more exotic species in the Triticeae tribe, primarily based on our own recent studies. SSPs of barley (Hordeum vulgare), homologous to those in wheat, exhibit quite different properties to wheat SSPs and do not produce viscoelastic dough. However, SSPs of a wild barley species (H. chilense) possess similar characteristics to the proteins of wheat. SSPs of rye (Secale cereale) substituted for wheat SSPs result in inferior quality. SSPs of Aegilops searsii and Ae. longissima have positive effects on quality, while Ae. umbellulata and Ae. geniculata (Ug genome) SSPs have a negative effect on bread-making quality. SSPs located on chromosome 1M of Ae. geniculata and a chromosome 1E of Thinopyrum elongatum have positive effects in addition lines but not in substitution lines for chromosome 1D of wheat. In contrast, SSPs of Th. intermedium have positive effects, even in cases of substitution for chromosome 1D of wheat, indicating promising potential for improvement of bread-making quality of wheat. Based on these results, we discuss the possibilities for utilizing the genetic variation of exotic Triticeae species for breeding improved quality traits in wheat.

Key Words: Alien chromosome addition lines, homoeologous group, glutenin, gliadin, bread dough.
of the world’s staple foods. However, this characteristic was only recognized because wheat had already been identified as a suitable cereal crop by virtue of its large kernel size and adaptability to various environmental conditions. Had wheat not been suitable for use as a crop plant, the unique nature of its SSPs might not have been discovered.

For this reason, we started to evaluate the SSPs in Triticeae species other than wheat. Since many of the kernels of the wild species are too small to measure the visco-elasticity, we investigated a collection of wheat lines with alien chromosomes in the ‘Tottori Alien Chromosome Bank of Wheat’ (TACBOW) that was established with the support of the National BioResource Project (wheat) in Japan.

There have been numerous efforts to improve resistance to biotic and abiotic stresses, especially by utilizing wild relatives of crop species for breeding. However, progress on quality trait improvement has been slower, primarily due to a reluctance to use alien species in breeding programs because of concerns that wheat grain quality will be reduced. In spite of this, a number of studies have been conducted to investigate improving the end-product quality of wheat using alien species in Triticeae. These studies are the focus of this review.

**Hordeum**

The endosperm of barley (*H. vulgare* subsp. *vulgare*) contains hordein, protein Z, α- and β-hordothionin and α-amylase (reviewed in Brandt *et al.* 1981, Ingverson 1983, Mifflin *et al.* 1984, Shewry and Mifflin 1982). Chromosome regions carrying the hordein genes on chromosome 1H are likely orthologous to the regions on the group 1 chromosome of each of wheat genome. The long arms of group 1 chromosomes in wheat carry genes for HMW-GSs that are homologous to D-hordein genes (Hor-3 locus) present on the long arm of barley chromosome 1H (Fig. 1). The sulfur (S)-rich γ-gliadins, LMW-GSs and S-poor α-gliadins, located on the short arm of group 1 chromosomes in wheat, are the counterparts of the B-(Hor-2 locus), C- and γ-hordeins (Hor-1 locus) on the short arm of chromosome 1H (1HS).

Addition lines of barley chromosomes in wheat were produced by Islam and colleagues (1981); however, the addition line with chromosome 1H, which carries the hordein loci, was found to be sterile and is therefore unavailable (Islam and Shepherd 1981, 1990). Barley only has a single, y-type HMW D-hordein, rather than two, x- and y-type, as in wheat, and it is quite different from its wheat ortholog.

Wild barley (*H. chilense*) has been investigated widely for its potential as a resource for improving wheat bread-making quality traits. In contrast to cultivated barley, *H. chilense* can be hybridized with tetraploid and hexaploid wheat. Tritordeum is a fertile amphidiploid between *H. chilense* and durum wheat (*T. durum*) that possesses quality characteristics similar or comparable to bread wheat (Martín *et al.* 1999). *H. chilense* addition lines containing chromosome 1H, homoeologous to wheat group 1, are

---

**Fig. 1.** Schematic presentation of different homoeologous group-1 chromosomes to indicate the location of major seed storage protein (SSP) genes. Genes for polymeric high molecular weight SSPs (HMW-glutenin subunits in wheat) are located on the long arm and monomeric (Gliadins in wheat) as well as polymeric low molecular weight SSPs (LMW-GSs in wheat) are located on the short arm. These loci are indicated as Gli-1, Gli-3, Gli-1 in genus *Triticum*, *Aegilops* and *Thinopyrum*, as Hor-3, Hor-2, Hor-1 in genus *Hordeum* and Sec-3, Sec-1 in genus *Secale*. In the A-genome of wheat, y-type HMW-glutenin gene is present but not expressed (indicated by unfilled box). This gene is expressed in some wild *Triticum* species like *T. monococcum*, *T. boeoticum*, *T. urartu*, *T. turgidum* subsp. *dicoccoides* and *T. araraticum* (Indicated by 1A*).
also available (Miller et al. 1982). *H. chilense* HMW-GSs (D-hordein) has greater resemblance to wheat HMW-GSs (Pistón et al. 2007) than cultivated barley. Many hordein genes have been sequenced from *H. chilense* (Pistón et al. 2004, Pistón et al. 2005) since the generation of Tritordeum. Our unpublished results from the 1H<sup>8</sup> substitution line for chromosome 1A of wheat indicate no or very limited potential of *H. chilense* proteins, especially HMW-GSs, for improvement of wheat bread-making quality.

**Secale**

Although rye (*S. cereale*) has great potential to increase the genetic variation in wheat, and has been widely used in wheat breeding programs, rye flour does not make soft bread like wheat flour does. Secalins, SSPs of rye, are a polymorphic mixture of polypeptides that are classified into four major groups. The Sec-1 locus encodes both S-poor α-secalins and S-rich 40K γ-secalins and is located on the short arm of chromosome 1R (1RS) (Fig. 1). The Sec-3 locus, encoding HMW-secalins, is located on 1RL, and Sec-2 encoding 40K γ-secalins is on chromosome 2RS. It is expected that introducing Sec-1 and Sec-2 proteins into wheat will create alcohol soluble oligomers and polymers and might decrease the proportion of insoluble glutenins (large aggregates), while Sec-3 should increase glutenin aggregates. However, reconstitution studies in which rye HMW-secalins were added to wheat dough have demonstrated a negative effect of these proteins on dough strength (Kipp et al. 1996). Introducing the rye 1RL chromosome arm (containing Sec-3) into wheat also had a negative effect on dough strength (Graybosch et al. 1999). The negative effect of Sec-3 proteins has been considered to be due to a higher frequency and altered position of cysteine residues in the γ-type HMW-GS gene Glu-Rly (Kipp et al. 1996). Consequently, the translocation chromosome with wheat chromosome arm 1DS and rye chromosome arm 1RL (T1DS.1RL) was preferred for soft wheat products like cookies over others (Kim et al. 2005). The rye chromosome arm 1RS in particular has been widely used in wheat breeding programs worldwide (Lukaszewski 1990, Villareal et al. 1994). Numerous wheat cultivars carrying the 1BL.1RS wheat-rye translocation have been released (Rabinovich 1998). Only four sources of 1RS—two sources from Petkus rye (Germany), one from octoploid Triticale (Japan), and one from Insaye rye (Argentina)—have been the progenitors to the hundreds of commercial wheat cultivars currently grown around the world (Lein et al. 1975, Moonen and Zeven 1984, Tsunewaki 1964, Zeller and Fuchs 1983). The 1RS translocation is the most common wheat-rye translocation, because it confers increased disease resistance (Mettin et al. 1973, Zeller and Hsam 1983, McIntosh et al. 1993), improved yield (Villareal et al. 1991, Carver and Rayburn 1994, Kim et al. 2004) and adaptation to a broad range of abiotic stresses (Rajaram et al. 1983, Villareal at al. 1994).

In contrast to the favorable effects of 1RS on agronomic performance, the effects on bread-making quality have been considered deleterious, and include diminished mixing tolerance, dough stickiness, and reduced loaf volume and crumb grain quality when compared with standard wheat (DhalIWali and MacRitchie 1990, DhalIWali et al. 1987, DhalIWali et al. 1990, Peña et al. 1990, Fenn et al. 1994, Burnett et al. 1995, Lee et al. 1995, See et al. 1995). The extent and range of these deleterious effects are not consistent among 1RS translocation lines. Indeed, some T1BL.1RS sister lines derived from the International Maize and Wheat Improvement Center nursery showed good bread-making quality (Peña et al. 1990). The introduction of the Sec-1 locus on 1RS in the T1BL.1RS translocation lines is accompanied by a concomitant removal of one set of Glu-1/Glu-3 loci on wheat 1BS. It is therefore not clear whether the negative impact on breadmaking quality is due to the presence of Sec-1 or the absence of the wheat loci. Fine translocation lines of 1RS carrying only disease resistance genes without rye secalins have been identified (Yan et al. 2005) and generated artificially (Anugrahwati et al. 2008). In comparison to 1BL.1RS translocations, T1AL.1RS lines have fewer deleterious effects on bread-making quality (Lukaszewski 1993). In terms of dough strength, the translocation lines perform in the order of T1AL.1RS>T1BL.1RS>T1DL.1RS. Assessments have also been made that rank individual group 1 chromosomes in hexaploid Triticale in terms of bread-making quality, as 1B>1R>1A (Amiour et al. 2002).

A chromosome 2BL-2RS wheat-rye translocation line, which contains the Sec-2 locus, has also been shown to have positive effect on bread-making quality (Gupta et al. 1989). This is because of the introduction of additional polymeric proteins that are not ordinarily present in wheat.

**Triticum**

Bread wheat (*T. aestivum*) and durum wheat (*T. durum*) are important cereal crops for human consumption. The primary gene pool of wheat includes the diploid donors of the A genome (*T. monococcum*, *T. boeoticum* and *T. urartu*) and polyplody sharing one or two genomes with wheat. Most of these can be crossed readily with cultivated wheat without the use of specialized methods. Electrophoresis analyses of progenitor wild wheats have demonstrated a high level of allelic variation at the loci encoding gluten proteins; several of these genes have been cloned and sequenced (Lafiandra et al. 1993, Li et al. 2006, Borghi et al. 1996, Ciaffi et al. 1998, Blatter et al. 2004, Vallega and Waines 1987, Levy et al. 1988, Ciaffi et al. 1993, Borghi et al. 1996, An et al. 2006, Jiang et al. 2009). The most interesting feature of this material is that in some lines both x- and γ-type subunits encoded by the Glu-A1 locus are expressed (Fig. 1). In particular, γ-type subunits encoded by the Glu-A1 locus are expressed in *T. monococcum*, *T. boeoticum*, *T. urartu*, *T. turgidum* subsp. dicoccoides and *T. araraticum* (Waines and Payne 1987, Levy et al. 1988, Margiotta et al. 1996, Randhawa et al. 1997). In contrast, the Glu-A1γ locus is silenced in bread
wheat and durum wheat (Harberd et al. 1987, D’ovidio et al. 1996). *Glu-A1x* in bread and durum wheats is characterized by only a few main alleles (1, 2*, 2.1* and null, Payne and Lawrence 1983), and transfer of these subunits from exotic wheats to durum and bread wheat varieties may improve processing quality and protein content. Transfer of *Glu-A1* alleles encoding two subunits from a number of these exotic wheat species into *T. durum* has already been achieved for *T. boeoticum* subsp. *thaoudar* (Rogers et al. 1997), *T. dicoccoides* (Ciaffi et al. 1995) and *T. boeoticum*, *T. urartu*, *T. dicoccoides* and *T. araraticum* (Dhalwal et al. 2002). These lines have improved dough strength, and some have baking performance as good as that of the bread wheat cultivars used as controls.

**Aegilops**

Species in the *Aegilops* genus have played central roles in the evolution of tetra- and hexaploid wheat taxa as donors of the B genome (*Ae. speltoides* or its related species) and D genome (*Ae. tauschii* subsp. *strangulata*). They are also important sources of new genes and alleles for wheat breeding. In this genus SDS-PAGE studies have revealed that many species produce HMW-GSs, LMW-GSs and gliadins. The expression of these subunits may be controlled by loci, similar to *Glu-1*, *Glu-3*, *Gli-1* of wheat on the homoeologous group-1 chromosomes (Fig. 1), but *Gli-2* locus may be on homoeologous group 6 chromosomes as in wheat or other homoeologous group chromosomes from 2 to 7 (Lawrence and Shepherd 1981, Fernández-Calvín and Orellana 1990, Peña et al. 1991, Urbano et al. 1993, William et al. 1993, Mackie et al. 1996a, Xie et al. 2001, Pflüger et al. 2001). The coding sequences for several *Aegilops* HMW-GSs have also been isolated and characterized (Mackie et al. 1996b, Xie et al. 2001, Wan et al. 2000). The results show that the primary structure of *Aegilops* HMW-GSs is similar to the one shared by wheat subunits, (conserved N- and C-terminal regions, a variable central repetitive region, number and arrangement of cysteine and other amino acids) but can also possess novel modifications that are not found in the wheat subunits.

Cultivated wheats have a low level of variation at the *Glu-D1*, *Glu-D3* and *Gli-D1* loci on the D genome. These wheat loci can be easily improved by the introduction of allelic variants of *Ae. tauschii* which has extensive genetic variation at these loci (Lawrence and Shepherd 1981, Gianibelli et al. 2001, Pflüger et al. 2001, Peña et al. 1991, William et al. 1993, Mackie et al. 1996a). *Aegilops* species can be crossed directly to bread wheat or crossed with durum wheat to generate synthetic hexaploid wheat for indirect gene transfer to bread wheat (Mujeeb-Kazi et al. 1998). Another interesting area of research is the improvement of flour quality of durum wheat, which is mainly used for pasta. Substitution of chromosome 1D of bread wheat for chromosome 1A of durum wheat resulted in a large increase in dough strength (Liu et al. 1995, Garg et al. 2007a). As HMW-GSs encoded by the *Glu-D1* locus, especially *Glu-D1d* (5 + 10) and *Gli-D1/Glu-D3*, are the major determinants of breadmaking quality, attempts have been made to transfer chromosome segments of the long arm carrying *Glu-D1d* (5 + 10) on chromosome 1AL and a segment of the short arm carrying *Gli-D1/Glu-D3* to cultivar Cappellini (Ceoloni et al. 1996) and several other wheat cultivars, replacing a null allele of the *Glu-A1* locus (Ammar et al. 1997, Ceoloni et al. 2005). Transfer of the *Gli-D1/Glu-D3* locus to replace *Gli-A1/Glu-A3* (Ponga et al. 1996) resulted in improved bread-making properties, in particular, reduced dough tenacity and improved extensibility. A translocation line, 1AS.1AL-1DL, carrying the *Glu-D1d* (5 + 10) in the durum wheat cultivar Renville background had improved mixing time, but loaf volume was not improved compared with Renville (Klindworth et al. 2005). This further indicates that *Glu-D1* alone is not sufficient for improving bread-making quality and alleles present for LMW-GS and gliadins are equally important. Likewise, Lukaszewski (2006) reported that transfer of the *Glu-D1* locus to chromosome 1R and 1A of Triticale improved its bread-making properties.

Compared with the works on characterization and transfer of *Ae. tauschii* glutenin and gliadin alleles to bread wheat, studies on other *Aegilops* species are limited. However, some efforts have been made to characterize storage proteins from these species. Considerable variation was found in the storage proteins in the Sitopsis section of *Aegilops* (Fernández-Calvín and Orellene 1990, Urbano et al. 1993, Sun et al. 2006). The HMW-GS gene from the S-genome species closely resembles wheat HMW-GSs (Garg et al. 2009a, Sun et al. 2006, Xia et al. 2006, GenBank accession AF513640, AY611728). Numerous gliadins have been sequenced from *Ae. longissima*, *Ae. speltoides*, *Ae. bicorns*, *Ae. searsii* and *Ae. sharonensis* (Van Herpen et al. 2006, Qi et al. 2009). Addition lines of *Ae. searsii* (Pietro et al. 1988) and *Ae. longissima* (Hart and Tullen 1993) are also available. Homoeologous group 1 addition lines of *Ae. searsii* (Garg et al. 2009a) and *Ae. longissima* (Garg et al. 2007b) expressing gliadins and glutenin proteins in the wheat genetic background showed improved dough strength, and thus these lines could be useful resources for improvement of wheat bread-making quality (Fig. 2).

Some studies have also been done on the non-progenitor species of *Aegilops*. *Ae. umbellulata* HMW-GSs have been studied (Brown et al. 1979, Lawrence and Shepherd 1981) and sequenced (Liu et al. 2003). Our studies on *Ae. umbellulata* addition lines have indicated slight negative effects on dough strength (Garg et al. 2009a). Similar negative effects have been found in 1U* addition line of *Ae. geniculata* (Fernández-Calvín and Orellene 1990) growth (Garg et al. unpublished), which may be attributed to the structural features of large HMW-Glu1U subunits that might disturb the normal polymerization of the gluten.

A chromosome 1M* addition line of *Ae. geniculata* showed improved dough strength (Fig. 2), unextractable polymeric protein content (UPP) and mixograph peak time...
Wheat holds an important position in Triticeae. Its unique

strength was reduced in the case of a substitution line for chromosome 1D (Garg et al. 2009b), indicating that chromosome 1D storage proteins are essential for bread-making quality and cannot be replaced by *Th. elongatum* proteins. They may, however, replace proteins coded by chromosome 1A, which is considered to have a negative effect on bread-making quality (Garg et al. 2007a). *Th. elongatum* has been utilized for the generation of a breeding line, Xiaoyan 6, which has improved agronomic and bread-making qualities. A large number of cultivars have been developed and released in China using this germplasm (Li et al. 2008). However, there is no report on introgression of *Th. elongatum* glutenins or gliadins into this germplasm or into other cultivars. A somatic hybrid line between wheat and *Th. elongatum* (Xia et al. 2003) was also shown to have increased dough strength. Derivatives with good bread-making quality from this line showed generation of recombinant HMW-GSs not present in either the wheat or *Th. elongatum* parent (Feng et al. 2004a, Liu et al. 2007).

The *Th. intermedium* addition line TAI-I (He et al. 1988) has been used in China to breed bread wheat cultivars with good bread-making quality. LMW-GS (Xu et al. 2004) and HMW-GS (Cao et al. 2007) genes sequenced from this addition line show similarity in their primary sequence structure to those of wheat, as well as novel modifications that are not found in wheat subunits. Our work on ditelocentric addition lines of *Th. intermedium* (long arm) in a common wheat background (cultivar Vilmorin 27) indicated significant increases in dough strength (Fig. 2), UPP and MPT. This line did not express the wheat *Glu-D1* locus-specific proteins, but still showed improved bread-making quality characteristics (Garg et al. 2008). Thus, *Th. intermedium* HMW-GS can replace those on chromosome 1D of wheat, and it may be possible to breed a line possessing unique flour characteristics. This line even showed straight growth habit and improved grain yield compared with the background cultivar.

The *Th. junceum* HMW-GS sequence also shows basic structural similarity to wheat (DQ073539.1).

**Agropyron, Leymus and other Triticeae genera**

HMW-GSs of *Ag. cristatum* (DQ073531 to DQ073537) and *L. mollis* (DQ073544) have been sequenced, and the basic structure of these sequences is similar to those of wheat. *Dasyphyrum villosum* addition lines have been studied to identify the chromosomal location of seed storage proteins (Montebove et al. 1987). The importance of HMW-GSs is evident from availability of sequences of even more exotic Triticeae species like *Crithopsis delineana* (Guo et al. 2005a, 2005b) and *Taeniatherum caput-medusae* subsp. *crinitum* (Yan et al. 2006) that also show basic sequence similarity with those of wheat.

**Discussion**

Wheat holds an important position in Triticeae. Its unique

---

Fig. 2. Dough strength of selected disomic addition lines of homoeologous group-1 chromosome of wild species of wheat added to cultivated hexaploid wheat genetic background. Addition of 1R and 1U chromosomes expressing SSPs of rye and *Ae. geniculata* resulted in reduction in dough strength. Addition of 1M, 1S, 1Thi, 1S, 1E chromosomes expressing SSPs of *Ae. geniculata*, *Ae. longissima*, *Th. intermedium*, *Ae. searsii*, *Th. elongatum* respectively resulted in improvement of dough strength. Chinese Spring was used for comparison. Specific sedimentation was calculated by dividing SDS sedimentation value with Protein content.

(MPT, Garg et al., unpublished). However, a substitution line of chromosome 1M for chromosome 1D showed reduced dough strength, UPP and MPT, indicating that chromosome 1D storage proteins are essential for bread-making quality and cannot be replaced by *Ae. geniculata* proteins. The *Ae. geniculata* chromosome may be used to replace proteins encoded on chromosome 1A, as this chromosome is considered to exercise negative effects in certain combinations on bread-making quality (Garg et al. 2007a).

HMW-GSs cloned from *Ae. comosa* (AY455789, AY455788) and *Ae. uniaristata* (AY455787, AY455786) were found to be similar to wheat HMW-GSs. Likewise, *Ae. caudata* and *Ae. cylindrica* HMW-GS diversity (Wan et al. 2000, Farkhari et al. 2007) and sequence (Liu et al. 2003, Wan et al. 2002) have been determined and show similarity to wheat. HMW-GSs have also been sequenced from *Ae. ventricosa* (AF226698.1), *Ae. caudata* (AF476959, AF476960), *Ae. kotschyi* (AY303126.1, AY303127.1) and *Ae. crassa* (AF354289).

**Thinopyrum**

The DNA sequence of *Th. elongatum* HMW-GS (Feng et al. 2004a, 2004b, Liu et al. 2008a, 2008b, Wang et al. 2004, 2006) and LMW-GS (Luo et al. 2005) genes possess a basic structure similar to those in wheat. Homoeologous group-1 addition lines of *Th. elongatum* chromosome 1E in wheat showed improved dough strength (Fig. 2), although dough
processing qualities make it suitable for making different products, such as bread, pasta and biscuits, to name a few, each with different quality requirements. Accordingly, studies have been undertaken for improvement of these products, utilizing existing variation in wheat and wheat-related species in Triticeae.

From the Hordeum genus, H. chilense addition lines have been found to be similar to wheat in terms of bread-making quality. Although there are no reports of any additional beneficial effects to wheat quality, a thorough exploration of the genetic diversity in H. chilense is necessary to reveal the genetic resources that may be exploited for wheat improvement projects in the future.

There have been numerous studies investigating rye as a resource for increasing the genetic diversity of wheat, especially for improvement of yield, and resistance to abiotic and biotic stresses. However, the effect of introduced rye chromosomes on wheat bread-making quality has been rather negative. Some alleles of rye storage protein genes have been shown to improve flour quality, as have substitution lines of rye chromosome 1R with chromosome 1A of wheat. However, there has been no practical utilization of these alleles, primarily because there has been greater emphasis on improving agronomic traits of wheat using rye.

The influence of HMW-GS genes on end-product quality is so significant that these genes are some of the most-studied genes in wheat and its related species. Large numbers of genes from wheat and Aegilops species have been sequenced and addition lines of some species, such as Ae. searsii, Ae. longissima and Ae. geniculata (1M+), had better effects on flour quality than others. In particular, Ae. searsii and Ae. longissima are able to compensate well for the function of chromosome 1B and substitution or translocation lines of this chromosome will be a useful breeding resource with superior quality traits. On the other hand, disomic addition lines of chromosome 1U of Ae. umbellulata and chromosome 1U of Ae. geniculata had particularly negative effects on bread-making quality. This indicates that these lines may be better resources for improved cookie-making properties. SSPs located on chromosome 1M of Ae. geniculata have positive effect of bread making quality in addition lines but not in substitution lines for chromosome 1D of wheat. It indicates importance of chromosome 1D specific SSPs for the wheat processing quality.

Maximum improvement to bread-making quality was observed in disomic addition line of chromosome 1E of Th. elongatum. But its substitution lines for chromosome 1D of wheat showed reduced quality. Again indicating that the wild species SSPs are not able to replace chromosome 1D specific proteins. They may be able to replace 1A or 1B specific proteins. But it is not clear. We are preparing substitution lines of wild species for 1A and 1B chromosomes. These substitution lines may reveal usefulness of wild species for improvement of wheat end product quality.

Unique quality characteristics were observed in case of Th. intermedium ditelocentric addition line. The HMW-GS of Th. intermedium improved bread-making quality in addition lines, as well as substitution lines for chromosome 1D. Most of the times alien genetic material is not considered for prebreeding due to the associated negative effects on agronomic performance. But the telocentric addition line of Th. intermedium, expressing HMW-GSs, not only have positive effect on bread making quality, this line also has better plant architecture and yield than background cultivar. Thus Th. intermedium chromosome’s long arm under study has strong potential for improvement of wheat for different aspects and needs extensive study.

The background cultivar for most of the addition lines was Chinese Spring. Which has null, 7+8 and 2+12 HMW-GSs at Glu-A1, Glu-B1 and Glu-D1 loci and has bad bread making quality. So we could easily find the positive effect of five added alien chromosomes from a set of 177 studied. But we do not know if these added alien chromosomes will show their positive effect in the presence of better allele like 1 and 5+10 at Glu-A1 and Glu-D1. We are preparing the translocation lines of these wild species with wheat chromosomes and transferring these added or translocated chromosomes to different wheat genetic backgrounds. But still work is needed to be done to recover the genetic background and see the effect of added proteins in the Glu-A1 (1) or Glu-D1 (5+10) background.

Thus there is abundant variation in the SSPs among Triticeae species. Large-scale exploration of this diversity using the collection of wheat lines available in the Tottori Alien Chromosome Bank or other germplasm banks has the potential to reveal proteins with better bread-making properties than those in wheat, as well as proteins that may confer undiscovered novel flour traits to wheat.

Acknowledgments

This work was partly supported by Grants-in-Aid from the Japan Society for the Promotion of Science (Nos. 19380006 and JSPS08094).

Literature Cited


Seed storage proteins of Triticeae


D’Ovidio, R., S. Masci and E. Porceddu (1996) Sequence analysis of the 5′ non-coding regions of active and inactive 1Ay HMW glutel


Miflin, B.J., B.G. Forde, M. Kreis, S. Rahman, J. Forde and P.R. Shewry


Available from: http://www.biomedcentral.com/1471-2164/10/68


