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Research Information

Natural variation of leaf shape-related traits in wild Einkorn wheat *Triticum urartu* Thum.

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The genus *Triticum* mainly consists of four distinct groups: einkorn (2n=2x=14, nuclear genome constitution AA), emmer (4x, AABB), timopheevi (4x, AAGG) and common wheat (6x, AABBDD). Three species comprising cultivated *T. monococcum* and wild *T. boeoticum* and *T. urartu* belong to the einkorn wheat group. It has been widely accepted that *Triticum monococcum* was domesticated from *T. boeoticum* (Dvorák et al. 1988; Takumi et al. 1993; Heun et al. 1997), and that *Triticum urartu* was the A-genome donor for the polyploid species of *Triticum* (Dvorák 1976; Chapman et al. 1976; Nishikawa 1983; Dvorák et al. 1988; Takumi et al. 1993; Dvorák et al. 1993). *T. urartu* is sporadically distributed in Armenia, southeast Turkey, northeastern Iraq and Lebanon (Tumanjan 1938; Johnson and Dhaliwal 1976). Natural variation in *T. urartu* was previously studied based on nuclear DNA variations (Castagna et al. 1997; Mizumoto et al. 2003) and on morphological traits (Yamagishi 1987). Our previous study showed that both nuclear and chloroplast genomes of *T. urartu* were clearly differentiated from those of *T. monococcum* and *T. boeoticum*, and that the *T. urartu* accessions were classified into two major haplogroups based on their chloroplast DNA variations (Mizumoto et al. 2003; Fig. 1A).

Yamagishi (1987) studied morphological traits of *T. urartu* to distinguish from *T. boeoticum*, in which twelve quantitative traits including flag leaf length and width and some qualitative traits such as auricle pigmentation were examined. The first two principal components from the 12 quantitative traits effectively distinguished the *T. urartu* accessions from the *T. boeoticum* ones. In addition, the awn trait and anther length could be used as useful markers to identify these two species (Tumanjan 1938; Yamagishi 1987). Besides these previous reports, information about morphological characteristics of *T. urartu* is still limited. Leaves of adult plants of *T. urartu* are drooping because of the long auricle (Fig. 1B). For leaf shape, glabrous leaf blade, sheath and auricle were reported as one of diagnostic characters of *T. urartu* (Tumanjan 1938; Yamagishi 1987). Therefore, intraspecific variation of quantitative traits related with leaf shape is needed to be studied in *T. urartu*. Here, we reported natural variation of eight leaf-related traits using 29 accessions of *T. urartu*, and discussed relationship between the leaf shape variation and nuclear and chloroplast DNA variations.

In this empirical study, we analyzed natural variation of leaf shape-related traits using 29 access-

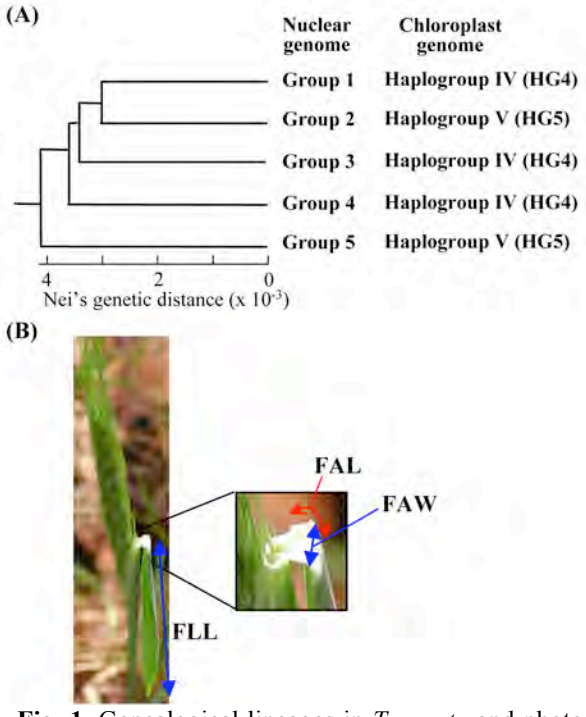

Fig. 1. Genealogical lineages in *T. urartu* and photo of the spike and flag leaf. (A) Summary of the genetic relationship among the *T. urartu* accessions revealed by nuclear AFLP and chloroplast SSRP analyses (Mizumoto et al. 2003). (B) Flag leaf length (FLL), auricle length of flag leaf (FAL) and auricle width of flag leaf (FAW).

Table 1. The strain numbers and sources of plant materials of *Triticum* and *Aegilops* species used in this study

T. monococcum (n=2)	
	KU105, KU3636 (Turkey)
T. boeoticum (n=2)	
	KU101-3 (Iran), KU103 (Iran)
T. urartu (n=29)	
Haplogroup IV (HG4)	
	KU199-11[1] (Turkey), PI428249[4] (Turkey), PI428184[1] (Turkey), PI554598[1] (Turkey), PI428227[3] (Turkey), PI428318[1] (Turkey), PI428225[3] (Turkey), PI428245[1] (Turkey), PI428253[1] (Iraq), PI487268[3] (Syria), PI487272[4] (Syria), PI428316[1] (Iran), PI428317[1] (Iran), PI428257[4] (Armenia)
Haplogroup V (HG5)	
	KU199-1[5] (Armenia), KU199-6[2] (Lebanon), PI428181[2] (Armenia), PI428182[2] (Armenia), PI428183[2] (Armenia), PI428258[2] (Armenia), PI428259[2] (Armenia), PI428264[5] (Lebanon), PI428270[5] (Lebanon), PI538743[5] (Lebanon), PI538747[5] (Lebanon), PI538748[5] (Lebanon), PI538751[5] (Lebanon), PI428254[5] (Turkey), PI487270[5] (Syria)

KU: Plant Germ-Plasm Institute, Faculty of Agriculture, Kyoto University, Japan
PI: National Small Grains Research Facility, USDA-ARS, USA
[1,2,3,4,5]: Group 1, 2, 3, 4 and 5 based on the nuclear genome diversity (Mizumoto et al. 2003)

ions of *T. urartu*, two *T. boeoticum* accessions and two *T. monococcum* accessions (Table 1, Fig. 1A). The sample set of *T. urartu* represented the entire natural habitat range. For each accession, we used seeds propagated from a single plant by selfing. Seeds of the sample accessions were sown in November 2004. Plants were grown in a field of Kobe University, and the accessions were arranged in the field using a randomized design. For each accession, a single healthy plant was chosen for analysis of morphological variation. All morphological traits were measured using the three tillers of each plant that headed earliest, and the trait averages and standard deviations were calculated. In total, eight leaf shape-related traits were studied. For the flag leaf, blade length (FLL), blade width (FLW), auricle length (FAL) and auricle width (FAW) were measured (Fig. 1B). For the first leaf below flag leaf, blade length, blade width, auricle length and auricle width were abbreviated as 1LL, 1LW, 1AL and 1AW, respectively. Trait measurements were done using the first, second, and third columns and spikes, for use as the trait values in subsequent analyses. The morphological trait data were statistically analyzed using JMP software ver. 5.1.2 (SAS Institute).

Large natural variations were found in most examined traits, especially FLL and ILL (Table 2). Leaf blade shape of *T. urartu* was comparatively narrower than those of other einkorn wheat species. Among the examined traits, the highest correlations were significantly observed between FLL and 1LL,

Table 2. Variations in the eight leaf shape-related traits

	T. urartu			*T. boeoticum*	*T. monococcum*	total
	Total (n=30)	HG4 (n=14)	HG5 (n=15)	(n=2)	(n=2)	(n=34)
FLL (cm)	12.03±3.02	14.69±1.53	9.91±1.66	8.27±1.23	11.89±2.86	11.80±3.02
FLW (mm)	7.11±1.15	7.18±0.86	7.18±1.31	7.59±1.18	8.19±2.70	7.20±1.23
FAL (mm)	4.47±0.45	4.40±0.43	4.60±0.39	4.38±0.12	3.68±0.14	4.42±0.47
FAW (mm)	3.54±0.32	3.57±0.27	3.55±0.36	3.49±0.15	4.26±1.15	3.58±0.40
1LL (cm)	20.67±3.74	23.65±2.39	18.39±2.19	15.28±0.91	21.73±0.87	20.40±3.76
1LW (mm)	8.08±2.31	7.50±1.11	8.70±3.01	9.94±1.24	11.13±2.47	8.37±2.37
1AL (mm)	4.19±0.43	3.92±0.42	4.41±0.29	4.23±0.22	4.37±0.01	4.20±0.41
1AW (mm)	4.21±0.58	3.91±0.38	4.48±0.62	5.01±0.02	5.88±0.83	4.35±0.71

Table 3. Correlation among the examined traits in the 29 *T. urartu* accessions

	FLL	FLW	FAL	FAW	1LL	1LW	1AL
FLW	0.118						
FAL	-0.396*	0.267					
FAW	-0.089	0.483**	0.560**				
1LL	0.815***	0.150	-0.039	0.167			
1LW	-0.213	0.746***	0.270	0.294	-0.157		
1AL	-0.603***	0.321	0.676***	0.566**	-0.299	0.382*	
1AW	-0.461*	0.695***	0.556**	0.590***	-0.235	0.672***	0.664***

Pearson's coefficient values (*R*) are represented.
*, **, *** Significant at P = 0.05, P = 0.01, P = 0.001 level of probability, respectively.

Table 4. Eigen vectors for PC1 and PC2 in the *T. urartu* variation

Trait	PC1	PC2
FLL	-0.29	0.57
FLW	0.33	0.43
FAL	0.39	-0.01
FAW	0.35	0.27
1LL	-0.15	0.61
1LW	0.36	0.17
1AL	0.43	-0.15
1AW	0.47	0.06

and between FLW and 1LW (Table 3). To study intraspecific differentiation in *T. urartu*, we conducted PC analysis based on the eight leaf traits. Scatter plots with the first two PC values (PC1 and PC2) of the 29 accessions were well united and continuous (Fig. 2). The first two principal components, PC1 and PC2, captured 72.47% of the total variation (48.03% for PC1, and 24.44% for PC2; Table 4).

The genealogical structure of the leaf shape variations was examined using 29 *T. urartu* accessions. In a graph of the first two axes from the principal component analysis based on eight leaf traits, the plots of the two haplogroups formed separate clusters (Fig. 2A). The cluster with positive PC2 values mainly contained the HG4 accessions, whereas the HG5 accessions belonged to the other cluster with negative PC2 values. The subgroup diversification of *T. urartu* was largely caused by FLL and 1LL (Table 4). The principal component analysis of the eight leaf traits indicated that two haplogroups based on the chloroplast DNA variations were diverged in the *T. urartu* population. Significant difference of the leaf length was observed between the two haplogroups (Table 5). The HG5 accessions with the short leaf length contained accessions mainly collected in Armenia and Lebanon, and the HG4 accessions with the long leaf length included a lot of accessions in Iran and Turkey. Significant difference between the HG4 and HG5 accessions was also found in 1AL and 1AW. The HG5 accessions significantly showed longer and wider auricles of the first leaf below flag leaf than the HG4 ones, indicating the auricle length was not necessarily associated with the leaf length.

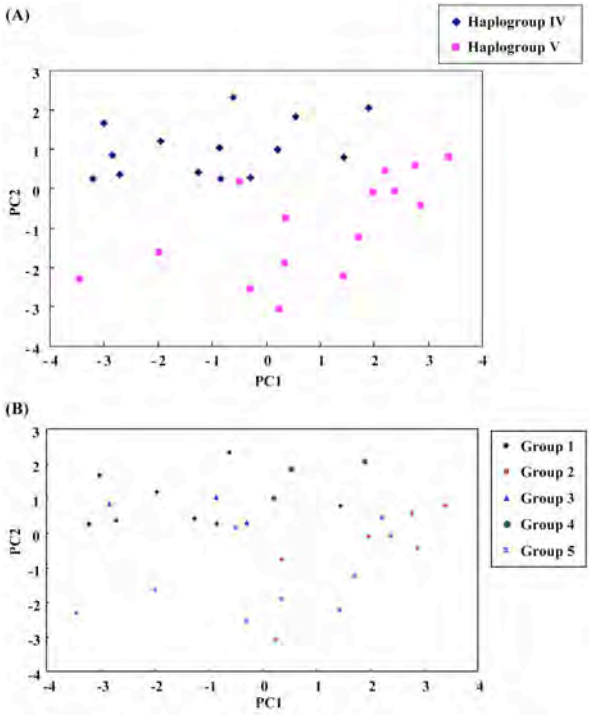

Fig. 2. Graph of the first two axes (PC1 and PC2) from a principal component analysis based on eight leaf-related traits. (A) Relationship between leaf shape variation and chloroplast genome differentiation. (B) Relationship between leaf shape variation and nuclear genome diversification.

Five different clusters could be genealogically divided in the *T. urartu* accessions revealed by the AFLP analysis of total DNA (Mizumoto et al. 2003). In the graph of the first two axes from the principal component analysis, there was no correlation between the plots and the five clusters (Fig. 2B). However, significant differences were found for the six leaf traits, FLL, FAL, 1LL, 1LW, 1AL and 1AW, among the five groups (Table 6). The differences of FLL and 1LL out of the six leaf traits were corresponding to the haplogroup difference.

In conclusion, analysis of natural variation in leaf shape-related traits showed that the *T. urartu* could

Table 5. Comparison of the eight leaf shape-related traits between the two haplogroups of *T. urartu*

	HG4 (n=14)	HG5 (n=15)	*t* statistic	*P*
FLL***	14.69±1.53	9.91±1.66	8.041	<0.0001
FLW	7.18±0.86	7.18±1.31	-0.016	0.9875
FAL	4.40±0.43	4.60±0.39	-1.304	0.2032
FAW	3.57±0.27	3.55±0.36	0.144	0.8865
1LL***	23.65±2.39	18.39±2.19	6.190	<0.0001
1LW	7.50±1.11	8.70±3.01	-1.395	0.1743
1AL***	3.92±0.42	4.41±0.29	-3.679	0.0010
1AW**	3.91±0.38	4.48±0.62	-2.975	0.0061

, * Significant at P = 0.01, P = 0.001 level of probability, respectively.

Table 6. Comparison of the eight leaf shape-related traits among the five groups based on the nuclear genome variations

Trait	Nuclear genome	n	Mean	Standard deviation
FLL	Group 1[a]	8	14.99	1.56
	Group 2[b]	6	9.70	1.69
	Group 3[a]	3	14.30	2.14
	Group 4[a]	3	14.28	1.12
	Group 5[b]	9	10.05	1.73
FLW	Group 1[a]	8	7.05	0.92
	Group 2[a]	6	8.03	1.26
	Group 3[a]	3	6.73	0.09
	Group 4[a]	3	7.98	0.69
	Group 5[a]	9	6.62	1.06
FAL	Group 1[b]	8	4.21	0.28
	Group 2[ab]	6	4.55	0.13
	Group 3[ab]	3	4.36	0.34
	Group 4[a]	3	4.97	0.39
	Group 5[ab]	9	4.64	0.51
FAW	Group 1[a]	8	3.51	0.32
	Group 2[a]	6	3.65	0.31
	Group 3[a]	3	3.51	0.18
	Group 4[a]	3	3.78	0.06
	Group 5[a]	9	3.48	0.39
1LL	Group 1[a]	8	22.90	2.72
	Group 2[b]	6	17.58	1.92
	Group 3[a]	3	23.74	1.25
	Group 4[a]	3	25.55	1.34
	Group 5[b]	9	18.93	2.29
1LW	Group 1[b]	8	7.23	1.07
	Group 2[a]	6	10.75	3.81
	Group 3[ab]	3	7.13	0.82
	Group 4[ab]	3	8.61	0.99
	Group 5[b]	9	7.33	1.25
1AL	Group 1[b]	8	3.80	0.44
	Group 2[a]	6	4.38	0.23
	Group 3[ab]	3	3.86	0.36
	Group 4[ab]	3	4.29	0.31
	Group 5[a]	9	4.43	0.34
1AW	Group 1[b]	8	3.79	0.34
	Group 2[a]	6	4.90	0.53
	Group 3[b]	3	3.91	0.38
	Group 4[ab]	3	4.23	0.44
	Group 5[ab]	9	4.21	0.53

In each trait, mean values followed by the same letters are not significantly different ($P > 0.05$) (Turkey-Kramer's HSD test).

be divided into two major classes; one provided larger leaves and another had smaller leaves. The larger-leaf type accessions belonged to HG4 according to the chloroplast DNA variation analysis in einkorn wheat. Clusters based on the nuclear genome variations, group 1 to 5, also showed significant differences in many leaf shape-related traits. However, the difference patterns did not necessarily reflect the phylogenetic relationship among the five nuclear genome clusters. Because *T. urartu* is an A-genome donor for common wheat, further genetic studies on the intraspecific variations should be important for wheat breeding.

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Research Information

Effect of different water regimes on agronomical traits and irrigation efficiency in bread wheat (*Triticum aestivum* L.) grown in the Nile Delta

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Abstract

Irrigation is the most important factor in determining bread wheat (*Triticum aestivum* L.) yield in Egypt. The effects of different water regimes were investigated during two years on growth and yield components of the cultivar Gemmeiza 9 cultivated under three and four irrigations at 30 days interval, and five and six irrigations at 25 days interval. Grain filling rate and effective grain filling period were also calculated for each treatment. Significant effects of the water regime were found on all measured traits. However, increasing the number of irrigations from five to six, keeping the same interval of time between irrigations, did not significantly increased grain yield, harvest index, number of tillers and spikes per m^2, spike length and fertility, thousand kernel weight and grain weight per spike. The grain production obtained by irrigation (or irrigation efficiency) was similar under three and four irrigations at 30 days interval but drastically decreased under five and six irrigations at 25 days interval. For the number of tillers and spikes per m^2 as well as for grain yield, gains decreased with each additional irrigation, up to three irrigations. Conversely, for the number of grain per spike and to a lesser extent for thousand kernel weight, the highest gains were noted when both the number and frequency of irrigation increased, i.e. when the crop was irrigated five times at 25 days interval, rather than four times at 30 days intervals. The study emphasizes the importance, for irrigated wheat, to define irrigation timing and frequency that allow maximal yield and optimal use of irrigation water.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important crops in Egypt. According to FAO (2009), wheat is cultivated on 1.2 million hectares with a production of 8 million tons. Egypt however still imports 6 million tons of wheat to cover its consumption. An important objective of the Egyptian government is consequently to reduce the dependence on imported wheat by enhancing grain yield and production (Kherallah et al. 2000). As most of the Egyptian wheat is produced under irrigated conditions, it is essential to determine the water regimes leading to highest yield and irrigation efficiency. Irrigated wheat is cultivated in Egypt under low rainfall and late heat stress conditions, especially with late sowing. These conditions correspond to wheat mega-environment 1 (ME1) as defined by Rajaram et al. (1995). Under ME1 conditions, Abd El-Gawad et al. (1994) found that increasing number of irrigation from two to four increased thousand kernel weight. Ibrahim et al. (1996) and Khatun et al. (2007) reported yield increase with the increase of irrigation frequency. Alderfasi et al. (1999) observed a significant increase of plant height, fertile tillering, thousand kernel weight and grain and biological yields with increased amount of irrigation. Dawood and Kheiralla (1994) and

Bankar et al. (2008) observed that five irrigations at crown root initiation, tillering, jointing, flowering and milking stages, led to the highest yield. The present study was carried out to determine the water regime leading to highest yield in the case of the cultivar Gemmeiza 9 in the Nile Delta, and to analyze the differences for yield components and other agronomical traits in the different treatments. Efficiency of irrigation and gains obtained from each additional irrigation were also calculated under for yield and yield components.

Materials and Methods

The experiments were conducted at the Experimental Farm of the Faculty of Agriculture, Minufiya University, Egypt, during the growing seasons 2004-2005 and 2005-2006 (thereafter referred as season 1 and 2) on the bread wheat (*Triticum aestivum* L.) cultivar Gemmeiza 9. The preceding crop was maize in both seasons. The soil texture was a clay loam with a pH of 7.8 and an organic matter concentration of 2.0%. Rainfall was low during the vegetative period (42 and 30 mm during the growing seasons 1 and 2, respectively), and nil during the reproductive period. Average maximal temperature during grain filling was around 32.5°C.

The experiment included four water regimes: 3 irrigations (I3) and 4 irrigations (I4) at 30 days intervals and 5 irrigations (I5) and 6 irrigations (I6) at 25 days intervals. The first irrigation was brought on December 15 for I3 and I4 and December 10 for I5 and I6. As a consequence of differences in the date of the first irrigation as well as in irrigation number and frequency in the different treatments, the last irrigation was done on February 13, March 15, March 20 and April 15 in I3, I4, I5 and I6 treatments, respectively. The four treatments were arranged in a randomized complete block design with four replications. The area of each experimental plot was 12 m^2 (4 × 3 m). Calcium super phosphate (15.5% P_2O_5) was applied during soil preparation at the rate of 15.5 kg P_2O_5 by fed (i.e., 37 kg ha^{-1}). Sowing was done on 15th November in both growing seasons. Seeding density was 350 seeds m^{-2} and row width was 20 cm. Total nitrogen fertilization was applied at a rate of 60 kg N by fed (i.e. around 140 kg ha^{-1}) as urea (46.5%) in two equal doses, before the first and second irrigations.

Days from sowing date to heading and physiological maturity were recorded for each plot. At harvest one square meter was taken randomly from the middle area of each plot to determine plant height (cm), number of tillers and spikes per m^2, spike length (cm), number of spikelets and grains per spike, thousand kernel weight (g) and grain yield per spike (g). Grain, straw and biological yield (t ha^{-1}) were determined from the whole plot area. Harvest index was estimated as the ratio of grain yield to biological yield and was expressed in per cent.

For estimating grain filling rate, five main spikes were collected from each plot at 14, 21, 28, 35 and 42 days after heading. 10 grains from the middle part of each of the 5 spikes were removed, oven dried at 80°C for 24h and weighed. Grain filling rate was calculated as GFR = (wt+1 – wt)/[(t+1) – t] where wt+1 and wt represent grain dry weight per spike at time t+1 and t, respectively, and was expressed in mg $spike^{-1}$ day^{-1}. Effective grain filling period was estimated according to Daynard et al. (1971) as the ratio of the final grain weight per spike to the average grain filling rate.

Data obtained were analyzed using Statistical Package for Social Science, version 10 (SPSS, 1999). Mean of values were compared at 5 % level of probability using Duncan's multiple range test.

Results and Discussion

The different water regimes had a pronounced effect on the duration of the vegetative and reproductive periods, and on the growing cycle duration (Table 1). The shortest vegetative and reproductive periods were noted when plants were

Table 1. Effect of water regime on the duration of the vegetative and reproductive periods of wheatn both growing seasons

Water regime	Days from sowing to heading		Days from heading to maturity		Days from sowing to maturity	
	Season 1	Season 2	Season 1	Season 2	Season 1	Season 2
I_3	86.0^d	86.2^d	66.5^d	66.8^d	152.5^d	153.1^d
I_4	87.5^c	88.3^c	67.0^c	68.5^c	154.5^c	156.8^c
I_5	90.0^b	90.5^b	70.0^b	71.0^b	160.0^b	161.5^b
I_6	92.2^a	92.5^a	72.5^a	73.0^a	164.7^a	165.5^a

For each season, mean values in the same column without a common letter are significantly different ($P<0.05$) according to the Duncan comparison test.

irrigated three times (I3). These results are in agreement with Alderfasi et al. (1999) who found that the number of days from sowing to flowering and maturity was increased by increasing the amount of irrigation from 2000 up to 7500 m^3/ha.

Irrigations number and frequency also showed a significant effect on grain yield (Table 2). In both seasons, the highest grain yield was obtained when plants were irrigated six or five times at 25 days intervals compared with four or three times at 30 days intervals. Grain yield increases from I3 to I4, I3 to I5 and I3 to I6 were 33.0, 42.3 and 46.3%, respectively. Increasing the number and frequency of irrigations was also accompanied by a as already reported by El-Monoufi and Harb (1994) and El-Barbary (1998). Straw and biological yields (averaged over the two seasons) in treatment I6 were 11.8 and 22.3% higher, respectively, than in treatment I3. Irrigating six times at 25 days interval (I6 treatment) allowed an increase of 6.5 and 7.7% of straw and biological yields over the I4 treatment and of 2.0 and 2.3% over the I5 treatment. Increase in grain yield with irrigation number and frequency being higher than increase in straw yield, harvest index increased significantly with water availability, as reported by Moursy (1999). Plant height also significantly increased with the number of irrigations. In treatments I4, I5 and I6, plant height was enhanced by 7.2, 9.9 and 13.3% in the first season and 7.0, 11.4 and 13.0% in the second season, respectively, compared to treatment I3. Plant height was also found to increase with irrigations number up to five times by El- Barbary (1998) and Moursy (1999) or six times by Dawood and Kheiralla (1994), El-Monoufi and Harb (1994) and El-Far and Allam (1995). Yield enhancement due to irrigation was associated to significant increases in number of tillers and spikes per m^2, number of grain per spike and thousand kernel weight. Similar values were found, however, for number of tillers and spikes per m^2 in treatments I5 and I6. The increase in the number of tillers and spikes per m^2 in I6, compared to I3, was 6.0 and 8.1% in the first season and 6.8 and 8.4% in the second season. Number of grains per spike and thousand kernel weight was significantly higher in I5 and I6 treatments, compared to I3 and I4. Similarly, Abd El-All (1991), El-Monoufi and Harb (1994), El-Barbary (1998) and Moursy (1999) reported a significant increase of these components with additional irrigation. The increase in spike fertility was associated with an increase in spike length ($r = 0.995$, $P>0.01$ and $r =0.996$, $P>0.01$) and number of spikelets per spike ($r = 0.994$, $P>0.01$ and $r=0.998$, $P<0.01$). As shown in other ME1 environments (Monneveux et al. 2005), the reduction in thousand kernel weight under limited irrigation is likely to be due to a reduction of photosynthesis associated to stomatal closure, exacerbated by the high temperature and evaporative demand that occur during grain filling (Monneveux et al. 2005). As a consequence of the increase in both number of grains per spike and thousand kernel weight, grain weight per spike was drastically enhanced by irrigation, as reported by Ibrahim et al. (1996) and Moursy (1999).

Mean values of grain filling rate and effective filling period are presented in Table 3. Grain filling rate was significantly lower under water limitation (I3) than under well-watered conditions (I6). However, no significant difference was noted between I5 and I6. Also, plants irrigated five or six times had a higher effective grain filling period compared with those irrigated three or four times.

In summary, both timing and frequency of irrigation increased yield and yield components and affected agronomical traits. However, increasing the number of irrigation from five to six, keeping the same interval of time between irrigations, did not significantly increased grain yield, harvest index, number of tillers and spikes per m^2, spike length and fertility, thousand kernel weight and grain weight per spike. Similar results were obtained by El-Barbary (1998) and Moursy (1999). Moreover, the grain production obtained by irrigation (or irrigation efficiency) was similar in I3 and I4 (1.66 and 1.65 t ha^{-1}), but drastically decreased in I5 (1.41 t ha^{-1}) and I6 (1.21 t ha^{-1}). As shown on Fig. 1, the highest gains obtained for each additional irrigation were noted for the number of grains per spike. Increasing the number of irrigations had more impact on the number of

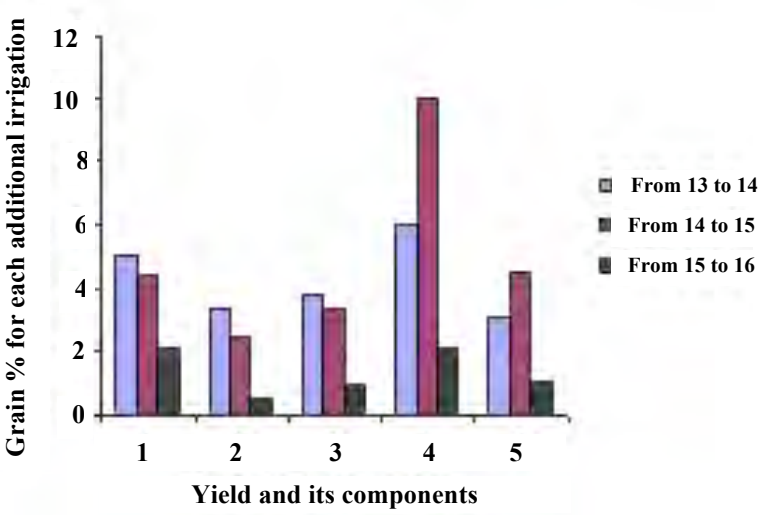

Fig. 1. Relative gain (in per cent) provided by each additional irrigation from three irrigations, for grain yield (1), tillers per m^2 (2), spikes per m^2 (3), number of grain per spike (4) and thousand kernel weight (5).

Table 2. Effect of water regime on yield and its components in both growing seasons

Water regime	Grain yield (t ha^{-1})	Straw yield (t ha^{-1})	Biological yield (t ha^{-1})	Harvest index	Plant height (cm)	Number of tillers m^{-2}	Number of spikes m^{-2}	Number of grains per spike	Spike length (cm)	Number of spikelet per spike	Thousand kernel weight (g)	Grain weight per spike (g)
Season 1												
I_3	4.90^{c}	11.10^{d}	16.00^{d}	0.31^{c}	107.6^{d}	330.7^{c}	298.5^{c}	60.00^{c}	11.73^{c}	21.20^{c}	47.45^{c}	1.80^{c}
I_4	6.55^{b}	11.71^{c}	18.26^{c}	0.36^{b}	115.4^{c}	340.7^{b}	309.5^{b}	63.45^{b}	12.20^{b}	21.80^{b}	49.05^{b}	2.50^{b}
I_5	6.97^{a}	12.12^{b}	19.09^{b}	0.37^{a}	118.3^{b}	348.7^{a}	320.2^{a}	69.20^{a}	13.47^{a}	23.10^{a}	51.20^{a}	2.85^{a}
I_6	7.19^{a}	12.45^{a}	19.64^{a}	0.37^{a}	121.9^{a}	350.5^{a}	322.7^{a}	70.00^{a}	13.60^{a}	23.50^{a}	51.62^{a}	2.90^{a}
Season 2												
I_3	5.05^{c}	11.24^{d}	16.29^{d}	0.31^{c}	108.1^{d}	332.5^{c}	300.5^{c}	61.40^{c}	11.30^{c}	21.30^{c}	47.82^{c}	1.88^{c}
I_4	6.67^{b}	11.74^{c}	18.41^{c}	0.36^{b}	115.7^{c}	344.7^{b}	312.0^{b}	65.20^{b}	11.91^{b}	22.60^{b}	49.11^{b}	2.61^{b}
I_5	7.17^{a}	12.36^{b}	19.53^{b}	0.37^{a}	120.4^{b}	353.5^{a}	322.2^{a}	72.35^{a}	13.20^{a}	24.60^{a}	51.37^{a}	2.87^{a}
I_6	7.33^{a}	12.52^{a}	19.85^{a}	0.37^{a}	122.2^{a}	355.2^{a}	325.7^{a}	74.60^{a}	13.37^{a}	25.50^{a}	51.95^{a}	2.93^{a}

For each season, mean values in the same column without a common letter are significantly different ($P<0.05$) according to the Duncan comparison test.

Table 3. Effect of water regime on grain filling rate for grains and effective grain filling period of main wheat spikes in both growing seasons

Water regime	Grain filling rate (mg/spike/day)										Effective grain filling period (days)	
	Days after 50 % heading.								Average			
	14-21		21-28		28-35		35-42					
	Season 1	Season 2	Season 1	Season 2	Season 1	Season 2	Season 1	Season 2	Season 1	Season 2	Season 1	Season 2
I_1	30.05^{c}	32.39^{c}	42.62^{c}	44.15^{c}	49.77^{c}	52.27^{c}	40.87^{d}	41.83^{d}	40.82^{c}	42.66^{c}	42.87^{b}	44.06^{b}
I_2	38.07^{b}	40.45^{b}	53.75^{b}	54.15^{b}	70.00^{b}	72.90^{b}	54.25^{c}	54.50^{c}	54.01^{b}	55.50^{b}	44.80^{b}	47.02^{b}
I_3	40.40^{a}	43.40^{a}	66.00^{a}	67.25^{a}	90.92^{a}	92.40^{a}	59.90^{b}	60.45^{b}	64.30^{a}	65.87^{a}	48.98^{a}	48.88^{a}
I_4	42.00^{a}	44.42^{a}	69.75^{a}	70.22^{a}	96.00^{a}	96.70^{a}	73.00^{a}	74.01^{a}	70.18^{a}	71.33^{a}	47.02^{a}	46.96^{a}

For each season, mean values in the same column without a common letter are significantly different ($P<0.05$) according to the Duncan comparison test

spikes per m^2 than on the number of tillers per m^2. For these two traits as well as for grain yield, gains decreased with each additional irrigation, up to three irrigations. Conversely, for the number of grain per spike and to a lesser extent for thousand kernel weight, the highest gains were noted when both the number and frequency of irrigation increased, i.e. when the crop was irrigated five times at 25 days interval, rather than four times at 30 days intervals.

These results show the importance of irrigation for wheat crop management in drought and heat prone environments. They also indicate that both irrigation timing and frequency are determining maximal agronomical and economical wheat yield in Egypt, and more generally in ME1 environments. Considering the increasing limitations of water resources, it appears essential to analyze also in details the impact of irrigation timing and frequency on water use efficiency, and more specifically on the efficiency of use of irrigation water. This would help in improving yield and production, while ensuring sustainability of wheat based systems.

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Research Information

Radiation mutants for mapping genes and markers in pericentromeric region of chromosome 3B of Norin 26 wheat

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Bread wheat (*Triticum aestivum* L. 2n=6x=42, AABBDD) has a large genome (17 gigabases (Gb)), of which 80% is composed of repetitive sequences (Smith and Flavell 1975). Such plants with large genomes as wheat, maize (2.5 Gb) and barley (5 Gb) show gradual increase of recombination from the centromeres to telomeres (Lukaszewski and Curtis 1993; Kunzel *et al*. 2000; Anderson *et al*. 2003; Saintenac *et al*. 2009). Mapping studies in other species indicated that recombination suppression in proximal region is general feature in plants and animals (see review by Jones 1987). On chromosome 3B of wheat, for which genome study is most advanced, a detailed survey showed that crossover frequency per physical distance (cM/Mb) within bins C-3BS1-0.33 and C-3BL2-0.22 were only 0.006 and 0.012, respectively, in striking contrast to the highest value of 0.85 in bin 3BS8-0.78-0.87 (Saintenac *et al.* 2009). Thus genes located on recombination-poor region are inaccessible by map-based cloning approaches. One of the methods to achieve the high resolution mapping in the recombination-depleted region of genome is the radiation hybrid (RH) mapping (Goss and Harris 1975; Riera-Lizarazu *et al.* 2007). RH method was recently applied to construct the high-resolution RH map of chromosome 1D of wheat (Kalavacharla *et al.* 2006) and also used in physical mapping of chromosome 3B (Paux *et al.* 2008). This RH mapping approach allows ordering molecular markers previously unordered within a chromosomal bin and does not need allelic polymorphism. In addition, RH maps with the required resolution can be produced by altering the dosage of radiation. The objective of this study is to develop chromosome structural mutants induced by irradiation for mapping the *Igc1* gene in pericentromeric region of chromosome 3B of Norin 26 wheat (Yamano *et al.*, in preparation). *Igc1* is known as the suppressor to *Gc3-C1*, one of the gametocidal (Gc) genes in wheat (Tsujimoto and Tsunewaki 1985). We here report development of chromosome structural mutants of chromosome 3B of Norin 26 wheat induced by irradiation for mapping genes in centromeric region (Fig. 1). The parental plants, *Tritucum aestivum* cv. 'Norin 26' (N26) and *T. aestivum* cv. 'Chinese Spring' 3B-3C substitution line (CS-3C"(3B")), which has a pair of the 3C chromosomes derived from *Aegilops triuncialis* substituting for chromosome 3B, were grown in the

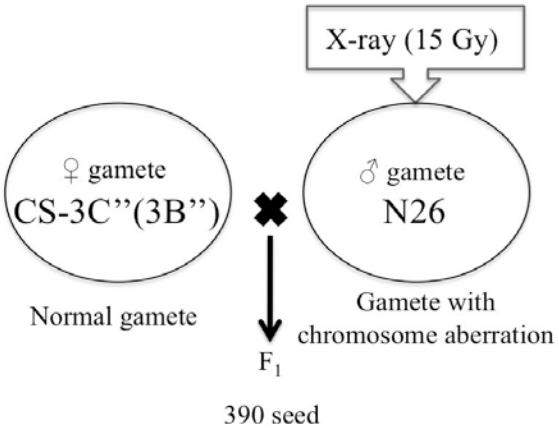

Fig. 1. A crossing scheme to produce radiation mutants for chromosome 3B of N26 wheat. CS-3C"(3B") was used as female parent with normal chromosomes. Pollen of N26 was irradiated with 15 Gy of X-ray to induce chromosome aberrations, which was used as male parent.

Table 1. Germination and growth of the F_1 plants derived from the cross between CS-3C"(3B") and irradiated N26.

	Survived	Dead			Total
		Not germinated	Germinated		
			with shoot	with root	
Number (%)	199 (51.0)	160 (41.0)	5 (1.28)	15 (3.85)	390 (100.0)

Table 2. Number of lines with deletions in pericentromeric region of chromosome 3B.

	With deletion				Without deletion	Total
	3BS	3BL	Both	Subtotal		
Number (%)	45 (22.8)	42 (21.3)	35 (17.8)	122 (61.9)	77 (39.1)	199 (100.0)

The lines were classified into 'With deletion' when at least one ISBP marker was absent and 'Without deletion' when all ISBP markers tested was present. Lines with deletions were further divided to '3BS', '3BL', and 'Both' based on the location of missing ISBP markers. Note that proportion of lines was based on the survived lines (see also Table 1.).

field located at the Department of Agriculture, Kyoto University, Kyoto, Japan in the year 2009. Each line was planted in a pot. The whole spike of N26 at efflorescence was irradiated with 15 Gy of X-rays at the radiation facility in Tottori University, Japan. Then, the irradiated pollen of N26 ($N26^{IR}$) was used as male parent to cross to CS-3C"(3B"). The progeny of the cross was expected to have the 3B chromosome from $N26^{IR}$ monosomically and no 3B from CS. In total, 390 F_1 seed was obtained. All 390 seed was sawn on a filter paper soaked in water, and germinated plants were cultivated in a plant incubator. We could finally recover 199 F_1 progeny, which accounted for 51.0% out of total progeny (Table 1). A large portion of seed (160 seed) could not germinate, six plants were dead during early stages of development, and 15 were dead after rhizogenesis without shoot.

Total genomic DNA was extracted from frozen leaves harvested four weeks after seeding, using the DNeasy Plant Mini Kit (QIAGEN), according to the manufacturer's protocol. A total of 102 insertion site-based polymorphism markers (ISBP, Paux *et. al* 2006) were selected from each contig assigned to bins C-3BS1-0.33 (51 ISBP markers) and C-3BL2-0.22 (51 ISBP markers) of chromosome 3B for physical mapping (The complete list of the markers will be provided elsewhere (Yamano *et al.*, in preparation). PCR reactions were carried out in 15 µl of 0.5 units of *Taq* polymerase, 0.5 pmol for primer, 25 mmol for $MgCl_2$, 2.5 mmol for each dNTP and 25 ng for template DNA. ISBP markers were amplified under the following touchdown method; 95 °C for 5 min, 10 cycles of 95 °C for 30 sec, 65 °C for 30 sec decreasing by 0.5 °C per cycle and 72 °C for 30 sec, and 30 cycles of 95 °C for 30 sec, 60 °C for 30 sec and 72 °C for 30 sec, and 72 °C for 7 min. PCR products of ISBP markers were visualized on the 1.5% agarose gel stained by ethidium bromide. As positive and negative controls, total genomic DNA of N26 and CS-3C"(3B"), respectively, were used as templates in PCR. Scoring presence and absence of the ISBP markers, we found that 122 F_1 progeny (61.9% of the recovered and 31.3% of total F_1 progeny) had at least one breakpoint along the chromosome 3B of N26 (Table 2). Out of the 122 chromosome 3B deletion lines, 45, 42 and 35 plants had breakpoints in short arm of 3B, long arm of 3B and both arms, respectively. In total, 592 breakpoints were found in bin C-3BS1-0.33 or C-3BL2-0.22 through the analysis of 122 chromosome deletion lines with 102 markers. The number of markers deleted in individual plant ranged from 0 to 64. Ninety-six of 102 tested ISBP markers were absent at least one deletion line. The average marker retention frequency in total 199 F_1 progeny was 95.75%. This value is higher than that reported in previous report (74%) in the RH panel of chromosome 1D of wheat (Kalavacharla *et al.* 2006). These differences may reflect the marker locations; while we selected markers from pericentromeric region of 3B, which occupies a quarter of total 3B and where includes an inevitable part to inherit 3B to next generation, Kalavacharla *et al.* (2006) evenly picked up markers along chromosome 1D.

The radiation mutants produced in this study inherited chromosome 3C monosomically, which induces the gametocidal (Gc) effect in gametogenesis (Endo 1978). Depending on the presence or absence of the *Igc1* gene, the suppressor of the Gc action of chromosome 3C (Tsujimoto and Tsunewaki 1985), the radiation mutants will differ in seed-fertility; fertile in the presence of *Igc1* and semi-sterile in the absence of *Igc1*. In future we will analyze the location of the *Igc1* gene by the RH mapping approach.

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Meeting Reports

The Forth Triticeae Meeting of Japan, 2009

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The Forth Triticeae Meeting of Japan was held at Awara Hot Spring, Fukui on November 27 and 28, 2009. Eighty-three researchers including students from universities and institutes participated in the meeting. We had one special lecture, one panel discussion with plenary lecture, six oral presentations, and forty-seven poster presentations. The abstracts of oral presentations and poster titles are listed below. Young researchers and students as well as elder researchers had a good opportunity to know a wide field of Triticeae research, and all participants enjoyed local foods and hot spring in Fukui (Fig. 1). Next meeting will be held in Hokkaido area next year. I thank all participants for joining the meeting.

Special Lecture

Problems and perspectives of wheat and barley production in japan - based on changes in agricultural and food policies and a case of Fukui Prefecture -

Taichi Kitagawa
Department of Economic Science, Fukui Prefectural University

Panel Discussion

Keynote lecture

Wheat research in Japan: how can it contribute to the world community?

Masa Iwanaga
Director General, National Institute of Crop Science

The author argued that: (1) wheat research in Japan had made major contribution to scientific advancement for polyploidy genetics and crop evolution during 1920's to 1990's, (2) wheat's relative importance for genetics as model species, however, has declined since then, (3) wheat breeding and genetics contributed to crop improvement as exemplified by successful use of Japanese genetic resources for the development of high-yielding semi-dwarf wheats with wide adaptation that triggered "Green Revolution", (4) wheat research in Japan should and can contribute to global environmental and food problems by focusing its objectives to such global problems. Wheat is unique in the sense that a vast amount of genetic diversity is available for crop breeding. Moreover, recent technological progress for effective use of exotic germplasm for variety development now makes it possible for tapping such a diverse germplasm for practical variety development. This will present a new opportunity for wheat research to be regarded as a model for science application for social causes.

Oral Presentation

O01. Current status of the polymorphism survey project by NBRP-wheat: perspective for adopting SSR markers in map-based cloning of agronomically important genes

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The National Bioresource Project-Wheat (NBRP-Wheat), launched by the Japanese government in 2002, is aimed to maintain and distribute seed stocks and DNA clones of wheat. Additionally to its primary roles in handling seed stocks and DNA clones, the second-term NBRP-Wheat, started in 2007, features the collection and characterization of DNA markers. The objectives of the project are; (1) to make the resources of the NBRP-Wheat more valuable for molecular studies by addition of genotype information, and (2) to find a set of DNA markers that is suitable

for detecting polymorphisms among wheat samples. In this presentation, I reported current status of our effort to demonstrate PCR-amplification profiles and discussed possible use of the markers in map-based cloning projects. The 48 plant lines (NBRP polymorphism panel) subjected to survey includes; eight *Aegilops* species with representative diploid genomes, *Triticum monococcum*, *T. boeoticum*, *T. urartu*, *T. durum*, *T. spelta* and 31 hexaploid wheat accessions. We also took samples of *Hordeum vulgare*, *H. spontaneum*, and *Secale cereale* as outgroup species. One of the characteristics of our polymorphism panel is that we have many Japanese cultivars being used in ongoing wheat breeding programs. We started our survey with those SSR markers mapped by Somers et al. (2004). So far, we obtained amplification profiles of more than 1100 SSR primers for the 48 lines. The electrophoretic patterns and the associated information are provided to researcher upon request through the NBRP-wheat web site (http://www.shigen.nig.ac.jp/wheat/komugi/strains/aboutNbrpMarker.jsp). Collaborating with Dr. Y. Yamazaki at National Institute of Genetics, Japan, we are developing an interactive database of SSR markers, where the researchers are able to access to electrophoretic patterns, primer sequences and conditions for PCR. People can also find possible polymorphic markers between given two lines in the NBRP panel. The database is to open to public in December 2009. We will also propose a set of 210 SSR markers that would be useful for polymorphism survey in hexaploid wheat.

The working scheme for map-based cloning could be divided into four steps; (1) rough mapping, (2) fine mapping, (3) construction of BAC contigs, and (4) identification of candidate genes. Our data on SSR markers will help researchers roughly map their gene-of-interest. For fine mapping, however, our SSR markers are not sufficient to find markers tightly linked to the target gene. Our effort should be oriented towards using advanced genome information of related species, i.e., barley, rice, and maize. Equally important would be use of tetraploid and diploid progenitors in fine mapping projects so that we can overcome the limited diversity intrinsic to hexaploid wheat genomes.

O02. Studies on Cleistogamous barley

Ning Wang
National Institute of Agrobiological Sciences

Natural variants of barley have been described in which the palea and lemma remain tightly closed throughout the period of pollen release. Such closed flowering is known as cleistogamy. The size of the lodicule in the cleistogamous flower is typically smaller than that in the noncleistogamous type. Cleistogamy also provides a means of escape from cereal head blight infection and minimizes pollen-mediated gene flow. We have isolated *cleistogamy1* (*Cly1*) by positional cloning and show that it encodes an *AP2* transcription factor, which is an ortholog of Arabidopsis thaliana *AP2*. The expression of *Cly1* was concentrated within the lodicule primordia. We established a perfect association between a synonymous nucleotide substitution at the miR172 targeting site and cleistogamy. Cleavage of mRNA directed by miR172 was detectable only in a noncleistogamous background. We conclude that the miR172-derived down-regulation of *Cly1* promotes the development of the lodicules, thereby ensuring noncleistogamy, although the single nucleotide change at the miR172 targeting site results in the failure of the lodicules to develop properly, producing the cleistogamous phenotype.

O03. Diversity and wide adaptability of heading time-related genes in wheat and barley

Hidetaka Nishida
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Heading time of wheat and barley is a complex character comprised of vernalization requirement, photoperiodic response, and earliness *per se*. Each character is controlled by multiple genes. Many of them are shared by wheat and barley. Allelic variations in these genes enable wheat and barley to adapt to the different climate conditions in the world. In Japan, early-heading has been a desirable character that enables double-cropping with summer crops and avoids maturing at rainy season, intermittent rain of which causes pre-harvest sprouting. However, new problem is arising by the frequent occurrence of warm winter caused by global climate change. Warm winter makes ears develop extremely earlier than usual winter. They suffer from transient chilling temperature in early spring and result in death and yield decrease. To avoid such problems, understanding of genetic control of heading time is increasing its importance. Vernalization genes, *Vrn-1*, *Vrn-2*, and *Vrn-3*, and photoperiodic response genes, *Ppd-1* and *Ppd-2* have already cloned. Recent progress in molecular studies on these genes facilitated the detection of allelic variations and genotyping of many landraces by using DNA markers. We analyzed the geographical distribution of alleles for some of these genes in wheat and discussed their roles on adaptability. We also compared the results of genotyping by molecular markers and conventional test cross and discussed the application of the markers for marker assisted selection.

O04. Association Breeding Strategies: From Theory to Practice

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Association breeding strategies utilize phenotypic and genotypic information to increase gain from selection and reduce selection cycle time. Three approaches will be elaborated that utilize molecular marker information for crop improvement: 1) association breeding which uses association mapping in a breeding program, 2) marker-assisted recurrent selection (MARS), and 3) genomic selection (GS). Plant breeders frequently introduce new germplasm into their breeding programs and discard undesirable materials resulting in new marker/QTL associations that must be evaluated frequently. Association breeding and MARS are are based on the selection of statistically significant, marker-trait associations. Association breeding facilitates the discovery of novel alleles whose relative allelic value can be assessed as often as necessary. In contrast, genomic selection incorporates genome-wide marker information in a breeding value prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small effect QTL. In genomic selection, a training population representative of the breeding germplasm is genotyped with genome-wide markers and phenotyped in a target set of environments. That data is used to train a prediction model. The prediction model is used to estimate the breeding values of lines in a population using only the marker scores. Prediction models can incorporate performance over multiple environments, G x E effects, specific screening techniques, and novel expertise. Because of reduced generation time, annual genetic gain for GS is predicted to be two to three fold greater than for a conventional marker-assisted selection program, even with only a modest prediction accuracy of 0.50.

O05. Variation of wheat, barley, rye and their related species in the countries formerly belonging to the Soviet Union

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Wheat and barley were born in the western Asia and transmitted to the eastern Asia across barriers of high mountains, desert and/or cold weather. To reveal the routes of their transmission we have been investigating the genetic variation of cultivated and wild species of Triticeae in the remote areas of China and its outside regions. In this context we were interested in the plants in the regions formerly belonging to the Soviet Union. Dr. K. Sato (RIB, Okayama Univ.) and I first visited N. I. Vavilov Research Institute of Plant Industry (VIR), Russia, in 2006 to look for the collaborators in the regions. After detailed planning with the researchers in VIR, we practiced explorations in Armenia and Azerbaijan in 2008, and Tajikistan and Uzbekistan in 2009. The Japanese members in the explorations were Drs. K. Sato, K. Kato, and H. Nishida (Okayama University), H. Tsujimoto and H. Tanaka (Tottori University), and H. Tsuyuzaki (Akita Prefectural University). We observed great variation of wheat, barley, rye and their wild species. Especially, the adaptive strategy of rye from wild to cultivated fields that was investigated in Armenia, and restoration from the modern cultivars to the traditional landraces that was observed in Tajikistan were reported. These studies were supported by Grant-in-Aid, MEX, Japan (Dr. Takeda, 19255009).

O06. Wheat breeding in the northern part of India using *Imperata cylindrica*-mediated system

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Compared to other systems using maize and finger millet for haploid production, *Imperata cylindrica*-mediated system has many advantages such as coincidence with wheat flowering and abundant pollen availability throughout the day. *Imperata* plants grow in wild around whet fields and do not require cultivation in polyhouse as it is a wild weedy species, resulting in energy saving. These advantages suggest that haploid production using *Imperata* system has potential to be the most useful methods in exercising doubled haploid breeding in wheat for accelerating the genetic upgraded programs with enhanced precision and efficiency (Chaudhary et al, 2005). Although *Imperata cylindrica* is known as one of the ten world's worst weeds, it is the most useful plant for haploid production in wheat breeding. The productivity of the wheat in the northern part of Indian subcontinent is adversely affected on account of damages inflicted by abiotic and biotic stress to the bread wheat varieties that are currently under cultivation. Therefore, under the sponsorship of international collaboration program of JSPS (Japan Society of Promotion of Science) and DST (Department of Science and Technology, India) we are aiming to breed a new variety of bread wheat that has a part of chromatin from rye to confer resistance to various abiotic and biotic stresses. The research is currently underway as follows; 1) molecular cytogenetic analysis of the newly developed wheat recombinants for the desired rye chromatin, 2) development of doubled haploid (DH) populations from the triticale x wheat, following chromosome elimination technique, and 3) cytological and genetic mechanism of haploid production using *Imperata cylindrica* pollen.

Poster Presentation

P01.
Heading traits and flowering time-gene expression patterns in the alloplasmic wheat lines showing late-heading compared with the euplasmic lines
Shimada, S. and K. Murai (Fukui Prefectural University)

P02.
Expression patterns of wheat *FLOWERING LOCUS T* (*WFT*) derived from *Aegilops tauschii* in synthetic hexaploid wheats
Fujiwara, Y. and K. Murai (Fukui Prefectural University)

P03.
Microarray analysis of genes for pistillody, homeotic transformation of stamens into pistil-like structures in alloplasmic wheat line
Yamamoto, M. and K. Murai (Fukui Prefectural University)

P04.
Analysis of chasmogamy and cleistogamy in *Hordeum*
Ishihara, N., N. Wang, T. Komatsuda and K. Kakeda (Mie University)

P05.
Molecular analysis of the self-incompatibility (*S*) locus in *Hordeum bulbosum*
Matsuda, T. and K. Kakeda (Mie University)

P06.
Characterization of Japanese old wheat grown in Edo period
Kobayashi, F. (NIAS, JSPS Research Fellow)

P07.
Analysis of *MRP* gene located on homoeologous group 2 chromosomes in common wheat
Kikuchi, R. and H. Handa (NIAS)

P08.
Genotyping of Japanese wheat cultivars by DNA markers associated with wheat yellow mosaic virus resistant gene, *YmIb*
Kojima H.[1], Z. Nishio[2], M. Seki[1], H. Matsunaka[1,3], C. Otobe[1] and S. Oda[1] (1. NICS, NARO, 2. NARCH, NARO, 3. KONARC, NARO)

P09.
Allelic variation on the crossability of common wheat
Mishina, K.[1], A. Manickavelu[2], H. Sato[1], M. Katsumata[1], H. Sassa[1] and T. Koba[1] (1. Laboratory of Genetics and Plant Breeding, Graduate School of Horticulture, Chiba University, 2. Laboratory of Plant Genome Science, Kihara Institute for Biological Research, Yokohama City University)

P10.
Identification of barley chromosomes in the addition lines of common wheat by molecular markers and GISH
Kawaguchi, T., Y. Gunji, S. Kikuchi and T. Koba (Laboratory of Genetics and Plant Breeding, Graduate School of Horticulture, Chiba University)

P11.
Chromosome pairing in the amphidiploid between *T. durum* cv. Langdon and *Ae. uniaristata*
Nagataki, K., S. Kikuchi and T. Koba (Laboratory of Genetics and Plant Breeding, Graduate Shool of Horticulture, Chiba University)

P12.
Genetic study on spike morphology of bread wheat (*Triticum aestivum*)
Abdollahi, P., A. Manickavelu, K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P13.
Analysis of global expression patterns in wheat during the allopolyploidization course
Kouyama, S., K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P14.
Molecular characterization of wheat *NAC* genes in response to salt-stress
Tetus, Y., A. Hoshikawa, M. Saito, K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P15.
Genetic diversity and global analysis of gene expression patterns in Chinese wheat cultivars for salt response
Naruse, T., A. Hoshikawa, K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P16.
Promoter analysis of *APETALA2*-like genes in common wheat
Umehara, T., M. Yasumoro, M. Takaku, K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P17.
Production of transgenic wheat suppressing α/β-gliadins by the RNAi method and their protein profiles revealed by the 2D-PAGE
Nakamura, M., M. Saito, Y. Tetsu, K. Kawaura, Y. Ogihara (KIBR, Yokohama City U.)

P18.
Comparative gene expression analysis of susceptible and resistance line in common wheat infected by *Puccinia triticina*
Manickavelu, A.[1], K. Kawaura[1], N. Yahiaoui[2], B. Keller[2], A. Suzuki[3], K. Yano[3], Y. Ogihara[1] ([1]KIBR,

Yokohama City U., [2]Inst. Plant Biology, U. Zurich, [3]Fac. Agr., Meiji U.)

P19.
Structure of multigene encoding α/β-gliadin in wheat genome
Kawaura, K.[1], J. Wu[2], T. Matsumoto[2], H. Kanamori[3], S. Katagiri[3], Y. Ogihara[1] ([1]KIBR, Yokohama City U., [2]NIAS, [3]STAFF Inst.)

P20.
Relationship between amylose content and soft flour baking quality
Nishio, Z. (NARC Hokkaido)

P21.
Analysis of the floral homeotic genes in barley
Shitsukawa, N. (Res. Inst. Bioresour., Okayama U.)

P22.
Transcriptome analysis of hexaploid wheat synthetic lines showing type 2 hybrid necrosis
Mizuno, N. and S. Takumi (Kobe U.)

P23.
Transcriptome analysis of aborted growth phenotype in triploid hybrids between tetraploid wheat and *Ae. tauschii*
Hatano, H., N. Mizuno and S. Takumi (Kobe U.)

P24.
Expression patterns of senescence-associated genes during wheat development
Kajimura, T. and S. Takumi (Kobe U.)

P25.
Alternative splicing of the *WDREB2* transcripts in ABA-sensitivity mutants of common wheat
Kurahashi, Y., F. Kobayashi and S. Takumi (Kobe U.)

P26.
Comparison of three homoeologous cDNAs encoding aminolevulinic acid dehydratase in common wheat
Takenouchi, U. and S. Takumi (Kobe U.)

P27.
Preliminary analysis of QTL identification for cold-responsive gene expression using recombinant inbred lines of common wheat
Motomura, Y., F. Kobayashi and S. Takumi (Kobe U.)

P28.
Variation of ABA sensitivity at the seedling stage of hexaploid synthetic wheat lines
Iehisa, M. O. J., Y. Kurahashi and S. Takumi (Kobe U.)

P29.
Association analysis of heading time and nucleotide sequence of a *TaHd1* ortholog in *Aegilops tauschii*
Okamoto, E., Y. Okumura and S. Takumi (Kobe U.)

P30.
Natural variation of vernalization requirement for heading in *Aegilops tauschii*
Koyama, K., J. Nakamura and S. Takumi (Kobe U.)

P31.
Transcriptome analysis of hexaploid wheat synthetic lines showing hybrid chlorosis
Nakano, H., N. Mizuno and S. Takumi (Kobe U.)

P32.
Development of barley NILs for various functional polysaccharides content and their quality characteristics
Tonooka, T. (NICS)

P33.
Preliminary report for the use of Cot filtration in barley whole genome shot-gun analysis
Nankaku, N., Y. Motoi and K. Sato (RIB, Okayama University)

P34.
Estimation of whaterlogging tolerance in common wheat landraces in Yunnann province of China
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P35.
cancelled

P36.
Deletion lines of chromosome 3B of Norin 26 wheat for deletion mapping of *Igc1*
Yamano, S. (Kyoto U.)

P37.
Identification of SSR markers associated with cleistogamy in hexaploid wheat
Sagara, Y. (Kyoto U.)

P38.
Super-wide hybridization in Triticeae/Avenae: possibility of involvement of cohesin in chromosome elimination
Ishii, T., T. Ueda, H. Tanaka, and H. Tsujimoto (Grad. Sch. Agric., Tottori Univ.)

P39.
Genetic variation in *Aegilops tauschii* accessions by using SSR marker
Tanaka, K., Y. Fujii, H. Tanaka and H. Tsujimoto (Grad. Sch. Agric., Tottori Univ.)

P40.
Effects of alien glutenin subunits expressed in common wheat endosperm on the protein profile

Arakawa, T., H. Tanaka and H. Tsujimoto (Grad. Sch. Agric., Tottori Univ.)

P41.
Identification of repetitive sequences in pearl millet wild relative, *Pennisetum orientale*
Matsumoto, N., T. Ishii, H. Tanaka and H. Tsujimoto (Grad. Sch. Agric., Tottori Univ.)

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Mapping of *MRP* as the candidate gene for QTL to reduce mycotoxin accumulation in wheat grains
Niwa, S. (Kihara Insti.Biol. Res., Yokohama City U.)

P43.
Search for bulb formation factors in *Hordeum bulbosum*
Yoshikawa, M. (Kihara Insti.Biol. Res., Yokohama City U.)

P44.
Genetic diversity and geographical differentiation of organellar genomes in *Aegilops nelecta* and *Ae. columnaris*
Yasugi, Y. (Kobe U.)

P45.
Genetic diversity of Indian wheat landraces revealed by chloroplast SSRLP analysis
Takagi, T. (Kobe U.)

P46.
Genetic diversity of dough physicality related to making noodle quality in cultivated tetraploid wheat
Taguchi, J. (Kihara Insti.Biol. Res., Yokohama City U.)

P47.
Multiplex quantitative analysis for trichothecene genes expression of *Fusarium graminearum* in different genotypes of wheat spikes
Miyazaki, T. (Kihara Insti.Biol. Res., Yokohama City U.)

Fig. 1. The Forth Triticeae Meeting of Japan, 2009 - Participant Group Photo

(Editorial comment)
Dr. K. Murai summarized the meeting report of "The Forth Triticeae Meeting of Japan, 2009" held on November 27 and 28 in Awara Hot Spring, Fukui, Japan. We circulate the abstracts of oral presentations and the titles of poster presentations as edited by Dr. Murai.

Wheat Inf. Serv. 109: 21-22, 2010. www.shigen.nig.ac.jp/ewis

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Journal articles:

Payne PI, Holt LM, Law CN (1981) Structural and genetical studies on the high molecular weight subunits of wheat glutenin. Theor Appl Genet 60:229-236.

Book chapters:

Peacock WJ, Dennis ES, Gerlach WJ (1981) Molecular aspects of wheat evolution: repeated DNA sequences. In: Evans LT and Peacock WJ (eds.) Wheat Science - Today and Tomorrow. Cambridge Univ. Press, Cambridge, UK, pp. 41-60.

Books:

Knott DR (1989) The Wheat Rusts - Breeding for Rust Resistance. Springer-Verlag, New York, USA.

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Abbreviations should be explained at first occurrence.

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Gene names and protein names must carefully be discriminated. Gene names and loci should be italicized; protein should be upright. The SI units (http:// physics.nist.gov/Pubs/SP330/contents.html) should be used throughout.

Nomenclature
Nomenclature of genes and chromosomes should follow the 'Catalogue of gene symbols for wheat' (McIntosh *et al*.: 10th Int. Wheat Genet. Symp. 2003).

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The DDBJ/EMBL/GenBank accession numbers must be provided for newly reported nucleotide sequences.

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