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High crossability of wild barley (*Hordeum spontaneum* C. Koch) with bread wheat and the differential elimination of barley chromosomes in the hybrids

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Abstract Four bread wheat (*Triticum aestivum* L.) cultivars, 'Aobakomugi', 'Chinese Spring', 'Norin 61' and 'Shinchunaga', were pollinated with five barley lines/cultivars consisting of three cultivated barley (*Hordeum vulgare* L.) lines, 'Betzes', 'Kinai 5' and OHL089, and two wild barley (*Hordeum spontaneum* C. Koch) lines, OUH602 and OUH324. Crossability, expressed as the percentage of embryo formation, varied from 0 to 55.4% among the cross combinations. The two wild barley lines generally had a higher crossability than the previously reported best pollinator, 'Betzes', and some Japanese wheat cultivars were better as the female parent than 'Chinese Spring'. Ninety four hybrid plants were obtained from 250 embryos cultured, and their somatic chromosome numbers ranged from 21 to 36. Eighteen plants were mosaic in chromosome number. Twenty one-chromosome plants appeared most frequently (45.7%) followed by 28-chromosome plants (14.9%). C-banding analysis revealed that elimination of barley chromosomes was mainly responsible for the occurrence of aneuploid plants. In hypoploids derived from 'Betzes'-crosses, chromosome 5 was preferentially eliminated as previously reported, while in hypoploids derived from OUH602-crosses, chromosome 4 was preferentially eliminated. The wild barley line OUH602 may be a useful parent for producing a new wheat-barley addition set because of its high crossability with wheat and a different pattern of chromosome elimination.

Key words *Hordeum spontaneum* · *Triticum aestivum* Crossability · Chromosome elimination · C-banding

Introduction

Six of the seven possible wheat-barley addition lines were developed from the cross between bread wheat (*Triticum aestivum* L.) cv 'Chinese Spring' and cultivated barley (*Hordeum vulgare* L.) cv 'Betzes' (Islam et al. 1981) and they have been widely used for assigning biochemical and molecular markers to particular barley chromosomes (Shepherd and Islam 1992). However, the addition line for barley chromosome 5 (wheat homoeologous group 1) has not yet been obtained. According to Islam and Shepherd (1990) this is because the long arm of Betzes chromosome 5 carries a genetic factor(s) which causes meiotic abnormalities and, consequently, wheat lines carrying this chromosome arm are sterile. The lack of wheat-barley addition 5 sometimes causes a problem in the mapping of barley genes using the wheat-barley addition lines. For example, several genes were assigned to barley chromosome 5 simply because they were not localized to any of the six addition lines developed. Although part of this problem may be solved with the recent recovery of a ditelosomic addition line for the short arm of chromosome 5 (Islam and Shepherd 1990; Shepherd and Islam 1992), efforts to produce addition lines of wheat carrying a whole chromosome 5, or its long arm, should be continued to complete the series and so provide a system for the unequivocal localization of barley genes. Such lines are also essential to transfer genes on this chromosome arm into the wheat genome.

As mentioned by Shepherd and Islam (1992), wheat-barley addition 5 might be produced by using chromosome 5 from barley cultivars other than 'Betzes'. Alternatively, some wheat cultivars may not suffer from the adverse effect of 'Betzes' chromosome 5. However, such experiments have not been extensively conducted. This is mainly because crossing wheat as a female with cultivated barley is very difficult when barley cultivars other than 'Betzes' are employed (Fedak 1980; Islam et al. 1981; Sethi et al. 1986; Koba et al. 1991; Molnár-Láng and Sutka 1994). The reciprocal cross is inadequate for producing fertile wheat-barley addition lines because the barley cytoplasm causes pistillody in combination with the wheat nucleus (Islam and Shepherd 1990). Recently, Koba and Shimada (1992) showed that some Japanese wheat cultivars had high crossabilities with 'Betzes'. However, the search for a barley parent better than 'Betzes' has not been widely conducted.

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Another problem in making wheat×barley hybrids is that, instead of the expected 28-chromosome hybrids, aneuploids as well as wheat haploids were predominantly obtained mostly due to the elimination of barley chromosomes (Islam et al. 1981; Finch and Bennett 1982). Aneuploid hybrids, especially hypoploids, should produce a narrower range of addition lines in their progeny. Koba et al. (1991) conducted isozyme analysis of 13 aneuploid hybrids, 12 of which had 'Betzes' as the barley parent, and showed that chromosomes 1 and 5 were preferentially eliminated. Linde-Laursen and von Bothmer (1988) also found that these two chromosomes, along with chromosomes 6 and 7, were preferentially eliminated in aneuploid hybrids derived from the cross between wild hexaploid barley, *Hordeum lechleri*, and cultivated barley. Xu and Snape (1988) suggested that chromosome 6 of *H. bulbosum* was the first to be eliminated in barley×*H. bulbosum* hybrids. However, because of the limited information so far available, it is uncertain whether barley chromosomes are eliminated in a specific order in crosses with wheat.

Wild barley (*Hordeum spontaneum* C. Koch), the closely related species of cultivated barley, is highly polymorphic (Nevo 1992; Zhang et al. 1993) and carries useful genes for the improvement of cultivated barley (Brown et al. 1988). However, this species has been rarely used in crosses with wheat. Islam (unpublished, cited in Islam and Shepherd 1990) crossed a wild barley line with 'Chinese Spring' wheat and obtained a low percentage of seed set. Therefore, more lines should be tested to evaluate its crossability with wheat. Wheat-wild barley addition lines would enable the precise analysis of the wild barley genome. Such information may be useful not only for breeding but also for phylogenetic study.

In order to produce a new wheat-barley addition set including the currently missing addition 5, and to examine the cytological behavior of the hybrids, we pollinated wheat cultivars with cultivated and wild barley lines/cultivars. This paper reports the results of the crosses and a C-banding analysis of the hybrids obtained.

Materials and methods

The wheat and barley lines/cultivars used in this study are shown in Table 1. All wheat cultivars are reported to be crossable with cultivated barley in previous studies (Islam et al. 1981; Koba et al. 1991; Koba and Shimada 1992), and wheat cultivars other than 'Chinese Spring' are Japanese cultivars. Of the five barley lines/cultivars used, OUH602 and OUH324 are wild barley (*H. spontaneum*) and the others are cultivated barley (*H. vulgare*). Two lines, OUH602 and OUL089, have a black lemma, which is controlled by a dominant gene (*B*) located in the long arm of barley chromosome 5 (Tsuchiya 1983). We included these lines in the hope that the black lemma would be a selection marker for chromosome 5.

Wheat plants were grown in 21-cm diameter pots and barley plants were mainly grown in the field. Crossings were conducted in the greenhouse from late April to early May, 1994 and the crossing method of Koba and Shimada (1992) was used. Generally 6–8 spikes were pollinated in each cross combination.

At 15–20 days after pollination, caryopses were aseptically dissected with a surgical knife under a binocular microscope and the number of embryos formed was examined. The excised embryos were cultured in test tubes on half-strength Murashige and Skoog basal medium (Murashige and Skoog 1962) supplemented with 30 g/l sucrose, 7 g/l agarose and 1 g/l malt extract and maintained at 20°C in the dark until germination. Seedlings were grown at 15°C in the light for about 2 weeks and then vernalized at 5°C for at least 1 month. After the vernalization treatment, seedlings were planted in vermiculite, then transplanted into soil.

Table 1 The wheat and barley lines/cultivars used. Abbreviations for wheat cultivars are shown in brackets

Lines/cultivars	Source
Wheat (*T. aestivum*)	
Aobakomugi [Aoba]	[a]
Chinese Spring [CS]	[b]
Norin 61 [N61]	[a]
Shinchunaga [Scn]	[a]
Wild barley (*H. spontaneum*)	
OUH602 (var. *transcaspicum* Vav., 2-rowed, black lemma)	[a]
OUH324 (collected in Syria, 2-rowed)	[a]
Cultivated barley (*H. vulgare*)	
Betzes (2-rowed)	[c]
Kinai 5 (2-rowed)	[a]
OUL089 (a linkage tester, 6-rowed, black lemma)	[a]

[a] The Barley Germplasm Center, Okayama University
[b] Dr. Y. Furuta, Gifu University
[c] Dr. K.W Shepherd, University of Adelaide

Root tips were collected from seedlings growing in vermiculite or soil and pretreated in ice water for 22–24 h and then fixed in ethanol: acetic acid (3:1) for 3 days at room temperature. The fixed root tips were stored in a freezer until used. The somatic chromosome number of each seedling was determined by the acetocarmine squash technique from at least two root tips. The preparations were subsequently C-banded using the method of Giraldez et al. (1979). Barley chromosomes were identified according to the C-banding patterns reported by Linde-Laursen (1981) and Kakeda et al. (1991), and wheat chromosomes using the patterns obtained by Endo (1986). Barley chromosomes were numbered according to the standard barley nomenclature. Chromosome constitutions were determined from at least three C-banded cells of each plant, or sector in the case of mosaic plants.

At heading time, upper leaves of each hybrid plant were sampled and analyzed for phosphoglucomutase, an isozyme marker for barley chromosome 4 (Benito et al. 1985), according to the method of Haishima et al. (1993).

Results

Wheat×barley crosses

In the present study, crossabilities were defined as the percentages of pollinated florets that formed embryos (Koba et al. 1991). Crossabilities of 17 cross combinations ranged from 0 to 55.4% (Table 2). The crossability of each cross combination was compared with the value of the 'Shinchunaga'×'Betzes' cross by a chi-square test. This cross was used as a standard because it had the highest crossability among the cross combinations involving 'Betzes', which was the best crossable barley in previous studies (Islam et al. 1981; Koba et al. 1991). Two cross combinations, 'Shinchunaga'×OUH602 (55.4%) and

Table 2 Numbers and percentages of embryos and seedlings obtained in wheat×barley crosses and numbers of 21-chromosome plants included

Cross combination	No. of pollinated florets	Embryos		Plants			No. of 21-chromosome plants
		No.	floret (%)	No.	embryo (%)	floret (%)	
Aoba× OUH602	121	35	28.9 +	10	28.6	8.3 ns	8
CS × do	204	19[a]	9.3 ns	10	55.5	5.8 ns	8
N61 × do	154	11	7.1 –	8	72.7	5.2 ns	2
Scn × do	240	133[b]	55.4 +	26	27.7	17.6 +	5
Aoba× Betzes	108	4	3.7 –	4	100	3.7 ns	4
CS × do	93	2	2.2 –	2	100	2.2 ns	1
N61 × do	228	23	10.1 ns	12	52.2	5.3 ns	9
Scn × do	**134**	**22**	**16.4**	**6**	**27.3**	**4.5**	**1**
Aoba× Kinai 5	154	1	0.6 –	0			
CS × do	162	0	0 –				
N61 × do	304	3	1.0 –	2	66.7	0.7 –	0
Scn × do	177	10	5.6 –	4	40.0	2.3 ns	0
N61 × OUH324	23	6	26.1 ns	3	50.0	13.0 ns	0
Scn × do	19	4	21.1 ns	2	50.0	10.5 ns	1
CS × OUL089	22	1	4.5 ns	0			
N61 × do	60	1	1.7 –	1	100	1.7 ns	1
Scn × do	88	15	17.0 ns	4	26.7	4.5 ns	3

ns, + and -: not significant, significantly higher and lower than the value of the Scn×Betzes cross at the 5% level, respectively (χ^2 test)
[a] Of 19, 18 embryos derived from 172 florets were cultured
[b] Of 133, 94 embryos derived from 148 florets were cultured

'Aobakomugi'×OUH602 (28.9%), gave significantly higher crossabilities than the 'Shinchunaga'×'Betzes' cross (16.4%).

Barley lines/cultivars showed greatly different crossabilities depending upon the wheat parent and vice versa. This indicates that crossability between wheat and barley is controlled by both parental genotypes. Therefore, it is difficult to evaluate the general crossabilities of respective wheat and barley parents. Among the barley lines/cultivars, both wild barley lines OUH602 and OUH324 generally showed higher crossabilities than 'Betzes' and OUL089, while 'Kinai 5' was the least crossable. Among the wheat cultivars, 'Shinchunaga' generally showed the highest levels of crossabilities with any of the barley lines/cultivars crossed. On the other hand, 'Aobakomugi' and 'Norin 61' had high crossabilities only with selected barley lines/cultivars. 'Chinese Spring' wheat generally had a low level of crossability.

Embryo culture

The frequencies of embryos that developed viable plants differed greatly among cross combinations (Table 2). Sometimes, more than one shoot was formed from a single embryo indicating the occurrence of polyembryony.

The frequencies of pollinated florets that developed viable plants varied from 0 to 17.6% (Table 2). The 'Shinchunaga'×OUH602 cross again showed the highest value, owing largely to its extremely high frequency of embryo formation (55.4%). In total, 94 plants were obtained from the 250 embryos cultured and 54 of these plants were derived from cross combinations involving the wild barley line OUH602.

Cytology and isozyme analysis

Of the 94 plants, 76 had a stable chromosome number, whereas 18 were mosaic with different chromosome numbers among root tips.

Representative somatic chromosome numbers ranged from 21 to 36. Non-mosaic plants that had the expected 28 chromosomes were infrequent (14.9%) and were obtained only from 6 of the 14 cross combinations. Instead, 21-chromosome plants occurred most frequently (45.7%). Hypoploids, as well as hyperploids, were also obtained, with the former being predominant. Among the hyperploids, three plants had the unexpectedly high chromosome number of 36.

Twenty one-chromosome plants were assumed to be wheat haploids. This was confirmed in 36 plants (83.7%) by C-banding. The frequencies of wheat haploids varied greatly among cross combinations. In six cross combinations, 75% or more of the plants were wheat haploids (Table 2).

The chromosome constitutions of 33 somatically stable plants with barley chromosome(s) are shown in Table 3. C-banded somatic metaphases of some representative plants are illustrated in Fig. 1. All but one of the 28-chromosome plants had a haploid chromosome complement from both the wheat and barley parents, as expected (Fig. 1a); one exceptional plant from the 'Shinchunaga'× OUH602 cross had two representatives of barley chromo-

Table 3 Chromosome constitutions of wheat×barley hybrids with stable chromosome numbers

Cross combination	No. of plants	2n	Barley chromosome constitution						
			1	2	3	4	5	6	7
N61 × OUH602	1	23	0	0	1	0	0	0	1
	2[a]	28	1	1	1	1	1	1	1
Scn × do	1	22	0	0	1	0	0	0	0
	1	23	0	0	1	0	0	1	0
	1	24	1	0	0	0	0	1	1
	1	25	0	1	1	0	0	1	1
	1	26	1	1	1	0	0	1	1
	4	27	1	1	1	0	1	1	1
	1	28	1	0	1	1	2	1	1
	4	28	1	1	1	1	1	1	1
N61 × Betzes	1	23	1	0	1	0	0	0	0
	1[b]	25	1	1	1	1	0	0	0
Scn × do	1	25	1	1	0	1	0	0	1
	1	27	1	1	1	1	0	1	1
	3	28	1	1	1	1	1	1	1
N61 × Kinai5	1	25	1	1	1	0	0	0	1
	1	28	1	1	1	1	1	1	1
Scn × do	1	23	1	0	0	0	0	0	1
	1	27	1	0	1	1	1	1	1
	2	28	1	1	1	1	1	1	1
N61 × OUH324	1	27	1	0	1	1	1	1	1
	1	28	1	1	1	1	1	1	1
Scn × do	1	27	1	0	1	1	1	1	1
Total	33								

[a] In one root of one plant, wheat chromosome 6B was present as two telocentrics (6BS+6BL)
[b] Wheat chromosome 6B was present as two telocentrics (6BS+6BL)

Table 4 Chromosome constitutions of wheat×barley hybrids with mosaic chromosome numbers

Cross combination	No. of plants	2n	Barley chromosome constitution						
			1	2	3	4	5	6	7
Aoba × OUH602	1	25	1	0	1	0	1	0	1
		27	1	1	1	0	1	1	1
	1[a]	29–31	1	1	1	1	2	1	1
CS × do	1	22	0	0	1	0	0	0	0
		24	1	0	1	0	1	0	0
	1	24	1	0	1	0	0	1	0
		25	1	0	1	0	0	1	1
N61 × do	1	23	1	0	1	0	0	0	0
		24	1	0	1	0	0	0	1
	2[a]	34–36	2	2	2	2	2	2	2
Scn × do	1	21	0	0	0	0	0	0	0
		22	0	0	1	0	0	0	0
	1	22	0	0	1	0	0	0	0
		23	0	0	1	0	0	1	0
	1	24	1	0	1	0	0	1	0
		25	1	1	1	0	0	1	0
	1	26	1	1	1	0	0	1	1
		28	1	1	1	1	1	1	1
	1[b]	26	1	1	1	0	0	1	1
		27–28	1	1	1	0	1	1	1
	1	27	1	1	1	0	1	1	1
		28	1	1	1	1	1	1	1
	1	28	1	1	1	1	1	1	1
		29	1	1	1	1	1	2	1
CS × Betzes	1	21	0	0	0	0	0	0	0
		22	0	0	0	0	0	0	1
N61 × do	1[a]	34–36	2	2	2	2	2	2	2
N61 × OUH324	1	26	1	1	0	1	0	1	1
		27	1	1	0	1	1	1	1
Scn × OUL089	1	21	0	0	0	0	0	0	0
		22	0	0	0	0	0	1	0
Total	18								

[a] Aneuploidy for wheat and/or barley chromosomes was observed
[b] In the 28-chromosome sector, an unidentified wheat chromosome was duplicated

some 5, but lacked chromosome 2. In hypoploids, elimination of one to six barley chromosomes was observed, but wheat chromosomes were not eliminated (Fig. 1b-d). Aberrations of wheat chromosomes were found in two plants, where wheat chromosome 6B was present as two telocentrics (6BS+6BL) (Fig. 1e).

Table 4 shows the chromosome constitutions of mosaic plants carrying a barley chromosome(s). Mosaic sectors within a plant had similar chromosome constitutions to each other and differed by the loss or duplication of only one or two barley chromosomes. Three plants with 36 chromosomes had all seven barley chromosomes in duplicate in addition to a wheat haploid complement (Fig. 1 f). In these plants, aneuploidy not only of barley chromosomes but also of wheat chromosomes was observed in some cells.

Table 5 summarizes the barley chromosomes eliminated in 30 hypoploids with stable or mosaic chromosome numbers which are shown in Tables 3 and 4. In this table, eliminated chromosomes in mosaic hybrids were counted from chromosome constitutions with a maximum number of barley chromosomes. The data were grouped by the barley parent because hypoploids with the same barley parent generally showed a similar pattern of chromosome elimination.

In 18 hypoploids having OUH602 as the barley parent, chromosome 4 was always eliminated while chromosome 3 was eliminated in only one plant. It should be noted that all four 27-chromosome plants from the 'Shinchunaga'× OUH602 cross lacked chromosome 4 (Table 3). Thus, in OUH602-crosses chromosome 4 is first and most frequently eliminated. On the other hand, in five hypoploids having 'Betzes' as the barley parent, chromosome 5 was always eliminated. In other hypoploids, the tendency for chromosome elimination was not clear because of the limited number of plants obtained.

Hybrids having more than 21 chromosomes were analyzed for the presence or absence of phosphoglucomutase, an isozyme marker for barley chromosome 4 (Benito et al. 1985). Except for one plant, the results of isozyme analysis coincided with the results of C-banding analysis indicating that roots and shoots have the same chromosome constitutions as far as barley chromosome 4 is concerned.

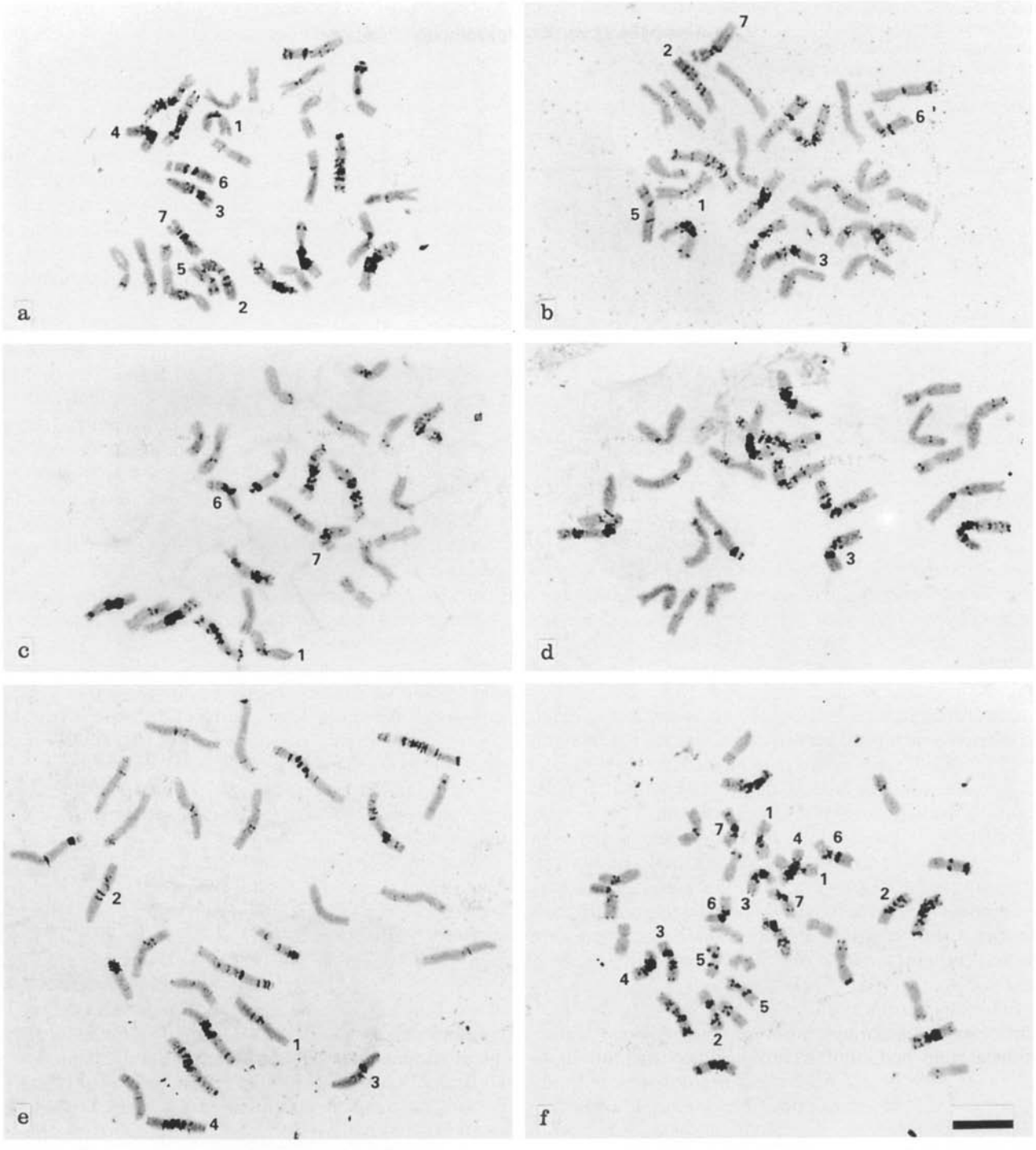

Fig. 1a–e C-banded somatic chromosomes of wheat×barley hybrids. **a** 'Shinchunaga'×OUH602 2n=28; **b** 'Shinchunaga'×OUH602 2n=27; **c** 'Shinchunaga'×OUH602 2n=24; **d** 'Shinchunaga'×OUH602 2n=22; **e** "Norin 61'×'Betzes' 2n=24+2t; f,'Norin 61'×OUH602, 35-chromosome cell of a 2n=34–36 plant. Barley chromosomes are numbered according to the standard barley nomenclature. The bar represents 10 μm

In the exceptional plant (the 29–31 chromosome plant from the 'Aobakomugi'×OUH602 cross, Table 4), the isozyme marker could not be observed, probably implying that barley chromosome 4 was eliminated, or could be deleted, in the shoots where the isozyme was sampled.

Morphology of the hybrids

In hybrid plants, the morphological characteristics of the wheat parent predominated. As the number of barley chro-

Table 5 Barley chromosomes eliminated in wheat×barley hypoploid hybrids classified according to barley parents. In mosaic hybrids, counts were based on chromosome constitutions with a maximum number of barley chromosomes

Barley parent	Stable or mosaic hybrid	No. of plants	Barley chromosome eliminated						
			1	2	3	4	5	6	7
OUH602	Stable	10	4	4	1	10	6	2	2
	Mosaic	8	2	5		8	5	3	4
	Subtotal	18	6	9	1	18	11	5	6
Betzes	Stable	4		1	1	1	4	3	2
	Mosaic	1	1	1	1	1	1	1	
	Subtotal	5	1	2	2	2	5	4	2
Kinai 5	Stable	3		2	1	2	2	2	
OUH324	Stable	2		2					
	Mosaic	1		1					
	Subtotal	3		2	1				
OUL089	Mosaic	1	1	1	1	1	1		1
Total		30	8	16	6	23	19	11	9

mosomes in hybrids decreased, the spikes became shorter and more similar to those of wheat haploids. The 36-chromosome hyperploids most clearly showed some barley characteristics, such as well developed auricles, anthocyanin pigmentation in the leaf sheath, and occasional triplet spikelet structure within a spike. The 27- or 28-chromosome hybrids lacking barley chromosome 2 had wide leaves and compact spikes. A *B* gene carrier, OUL089, did not develop hybrids having chromosome 5. However, in the hybrids carrying the barley chromosome 5 from OUH602, the spikes had black pigmentation of the glumes and rachis indicating that the *B* gene was expressed even in the presence of the wheat chromosome complement. Furthermore, the degree of coloration was dependent on the numbers of chromosome 5; hybrids with a pair of chromosome 5 showed stronger coloration than those with a single chromosome 5.

Discussion

In the present study, the two wild barley lines, especially OUH602, were highly crossable as the male parent with wheat, exceeding the previously reported best pollinator, 'Betzes' (Islam et al. 1981; Koba et al. 1991). The best crossability (55.4%), observed in the 'Shinchunaga'× OHU602 cross (Table 2), exceeds the previous highest value (27.1%) reported in the 'Aobakomugi'×'Betzes' cross (Koba and Shimada 1992). Since we employed essentially the same crossing technique as reported by Koba and Shimada (1992), the present high crossabilities can probably be ascribed to the genotypes of the wheat and barley parents employed. The wild barley line OUH602 may carry a crossable genetic factor(s) similar to the *kr* alleles in wheat (Snape et al. 1979). In the reciprocal cross, i.e. barley×wheat, Fedak and Jui (1981) showed that wheat chromosomes of homoeologous group 5, carrier chromosomes of the *kr* genes, affect crossability.

Despite efficient embryo recovery, the frequency of embryos that produced viable plants was rather low compared with the report by Koba et al. (1991). Differences in embryo-culture medium may be responsible for this. Since most embryos at least started shooting and/or rooting, use of a more refined embryo-culture medium may increase the recovery of viable plants. However, in terms of the frequency of pollinated florets that developed viable plants, the present best value obtained in the 'Shinchunaga'× OUH602 cross (17.6%) is still twice as high as the previously reported best value given by Koba et al. (1991).

Hybrid plants obtained in the present study showed variable chromosome numbers ranging from 21 to 36. This range is similar to that observed in previous studies (Islam et al. 1981; Koba et al. 1991). C-banding analysis clearly revealed that the variation in somatic chromosome numbers was mainly caused by the elimination of barley chromosomes and that duplication of wheat and barley chromosomes occurred to a limited extent. Elimination or duplication of chromosomes seems to have occurred mostly during an early stage of embryogenesis because most plants had a stable chromosome number, and even mosaic plants showed rather similar chromosome constitutions between sectors (Tables 3 and 4). Islam et al. (1981) inferred that spindle abnormalities at the early zygotic divisions are responsible for the occurrence of elimination or duplication of chromosomes. Duplication of the barley genome in 36-chromosome hyperploids (Fig. 1e) may be due to fertilization of the wheat egg by an unreduced barley gamete. Pickering and Morgan (1985) also reported the duplication of a particular parental genome in interspecific crosses within *Hordeum*.

We confirmed that there is wide variation in the frequencies of euploid hybrids, aneuploids, and wheat haploids among cross combinations (Tables 2 and 3), as previously reported (Fedak 1980; Islam et al. 1981; Finch and Bennett 1982; Sethi et al. 1986; Koba et al. 1991). For example, the 'Aobakomugi'×'Betzes' cross produced only wheat haploids, as Finch and Bennett (1982) observed in the TH 3929 wheat×2x P-4 barley cross. On the other hand, a half of the hybrids from three cross combinations were euploid, although Koba et al. (1991) obtained only euploid hybrids from the cross combinations involving the barley cultivar 'Haruna Nijyo'. These observations suggest that the degree of barley chromosome elimination differs among cross combinations.

In the present study, barley chromosome 4 was preferentially eliminated in hypoploids derived from OUH602-crosses, while chromosome 5 was predominantly eliminated in hypoploids derived from 'Betzes'-crosses (Table 5). Preferential elimination of 'Betzes' chromosome 5 was also reported by Koba et al (1991), and in that report chromosome 4 was the last chromosome to be eliminated. These observations indicate that the homoeologous group of preferentially eliminated chromosomes differs according to the barley genotype. It appears that the wheat genotype does

not alter the homoeologous group of preferentially eliminated barley chromosomes (Tables 3 and 4) but does affect the degree of barley chromosome elimination.

The cause of preferential elimination of OUH602 chromosome 4 is not clear. In this line (OUH602), a complete series of primary trisomics has been established and have been used for associating linkage groups to a particular chromosome (Tsuchiya 1960) and for determining interchanged chromosomes in reciprocal translocation lines (Konishi and Linde-Laursen 1988). The C-banding patterns of this line (Fig. 1a) did not show any conspicuous differences from those of cultivated barley (Kakeda et al. 1991) except that the short arm of chromosome 5 carries additional interstitial bands, which were also found in other *H. spontaneum* lines (Linde-Laursen 1981). From these facts, it is impossible to assume a translocation between chromosomes 4 and 5 to explain preferential elimination of chromosome 4 from OUH602.

In conclusion, the wild barley line OUH602 is a useful parent for producing a new wheat-barley addition set because of its high crossability with wheat and a different pattern of chromosome elimination. For producing addition 5, the black-lemma character controlled by the *B* gene on the long arm of chromosome 5 would be a good selection marker. A wheat-wild barley addition set and the existing 'Chinese Spring'-'Betzes' addition set may complementarily contribute to the genetics and breeding of barley and wheat.

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