Homoeologous Recombination: A Novel and Efficient System for Broadening the Genetic Variability in Wheat

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Abstract: Gene transfer from wild wheat relatives to bread wheat is restricted to homologous recombination. The presence of the Pairing homoeologous 1 (Ph1) gene in the long arm of wheat chromosome 5B allows only homologous chromosomes to pair and recombine, resulting in diploid inheritance of polyploid wheat. Previously, we identified a potent homoeologous pairing promotor gene(s) (Hpp-5Mg); its carrier chromosome 5Mg derived from Aegilops geniculata and its wheat homoeologous chromosome 5D freely recombined in the presence of the Ph1 gene. In this study, we investigated the efficacy of Hpp-5Mg on homoeologous recombination in the absence of Ph1. In Hpp-5Mg/ph1bph1b plants, we observed a vast genome-wide increase in homoeologous recombination and multiple crossovers (CO), including CO breakpoints in proximal regions of the chromosomes where recombination is known to be suppressed. We tested the efficacy of Hpp-5Mg/ph1bph1b-induced homoeologous recombination by producing new recombinants for the wheat streak mosaic virus resistance gene, Wsm3, present in the wheat-Thinopyrum intermedium Robertsonian translocation (RobT T7BS.7S#3L). A recombination frequency of 6.5% was detected by screening the progenies double monosomic for T7BS.7S#3L and 7B by genomic in situ hybridization. This recombination frequency was about 100-fold higher compared with the recombinant frequency of 0.06% observed by using ph1b-induced homoeologous recombination alone. Our results indicate that chromosome 5Mg promotes homoeologous recombination between wheat and wild wheat relative chromosomes, which helps in the generation of pre-breeding materials thereby accelerating wheat crop improvement.

Keywords: bread wheat; pairing homoeologous 1 (Ph1); homoeologous pairing promotor; homoeologous recombination; genomic in situ hybridization

1. Introduction

Bread wheat, Triticum aestivum L., is an allohexaploid species (2n = 6x = 42, genomes AABBDD) and its 16 Gb genome is one of the largest among crop plants. In perspective, a single wheat chromosome is twice the size of the entire rice genome. Wheat is the most important staple food worldwide providing more than 20% of the protein and calorie requirement of humans, occupying more acreage than any other food crop in the world. Bread wheat originated less than 10,000 years ago from the hybridization events between tetraploid emmer wheat (T. turgidum subsp. dicoccum, (Schrank ex Schüb) Thell., 2n = 4x = 28, genomes AABB) and Aegilops tauschii Coss. (2n = 14, genome DD) in a farmer’s field (reviewed in Huang et al. [1]). This recent origin and sparse sampling of gametes during its origin could be attributed to the narrow genetic base that limits the genetic variability in wheat.

The success of gene transfer from wheat’s wild relatives to bread wheat largely depends on the evolutionary distance of the species involved. Species belonging to the primary gene pool of wheat...
share completely homologous genomes. This group includes landraces of T. aestivum, landraces and wild strains of T. turgidum and the D-genome wild ancestor Ae. tauschii. Gene transfers from these species are achieved easily by direct hybridization and homologous recombination. The A-genome species T. monococcum L. and T. urartu Tumanian ex Gandilyan share homology for six of the seven A-genome chromosomes except 4A of polyploid wheats, which is highly rearranged and does not pair with any chromosome of diploid wheats (for review, see [2]).

The secondary gene pool of wheat includes polyploid Triticum/Aegilops species that have at least one homologous genome in common with common bread wheat. If the target gene(s) is located on homologous chromosomes, it also can be transferred easily by homologous recombination. Species belonging to the tertiary gene pool are more distantly related and represent a large reservoir of agronomically useful genes that can be exploited in wheat improvement, including genes conferring resistance to biotic and abiotic stress tolerance (reviewed in Jiang et al. [3]; Friebe et al. [4]). However, their chromosomes are not homologous to wheat chromosomes but more distantly related homoeologous chromosomes. Therefore, the gene transfer from these species to wheat cannot be achieved by homologous recombination. Meiotic pairing analysis of wide hybrids showed that wild relative and wheat homoeologous chromosomes failed to pair and recombine because of stringent homoeologous pairing recombination barriers [3,5].

Wheat aneuploid analysis [6] provided the first major breakthrough in mapping genes that control homologous and homoeologous chromosome pairing and recombination in wheat (reviewed in Sears [7]). This led to the identification of a major pairing homoeologous gene (Ph1) in the long arm of chromosome 5B [8,9] that suppresses homoeologous pairing and ensures strict homologous chromosome pairing and diploid inheritance in hexaploid wheat. A second suppressor of homoeologous recombination in wheat, Ph2, also has been identified, which is less effective than Ph1 [10]. The Ph2 gene locus has many co-segregating genes, among them the DNA mismatch repair gene TaMSH7 is considered as a promising candidate for Ph2 [11]. Deletion of the Ph1 gene in the mutant stock ph1b [12] allows homoeologous pairing to occur, leading to recombination among chromosomes of wheat and distantly related species permitting limited gene transfer and has been widely used for manipulation of homoeologous recombination and crop improvement [2,4,13–15]. However, the frequency of ph1b-induced homoeologous recombination is low and is usually restricted to distal chromosome regions because recombination is suppressed in proximal regions of chromosomes [2].

Earlier, we reported that chromosome 5Mg of Ae. geniculata Roth. (2n = 4x = 28, U8U8MgMgMg) escapes the diploid pairing control and freely recombines with homoeologous chromosomes of wheat in the presence of Ph1, even in proximal chromosome regions where recombination is usually suppressed [16,17]. We further showed that 5Mg harbors homoeologous pairing promotor gene(s) (Hpp-5Mg) in proximal regions of the short or long arm spanning the centromere [17]. In the present study, we investigated the effect of Hpp-5Mg on homoeologous recombination in the absence of Ph1. In Hpp-5Mg/ph1bph1b plants we observed a vast genome-wide increase in homoeologous recombination and multiple crossing-over (CO) breakpoints including those in the proximal regions, where COs are known to be suppressed. We tested the efficacy of Hpp-5Mg/ph1bph1b-induced homoeologous recombination by producing new recombinants for wheat streak mosaic virus resistance gene, Wsm3 present in the wheat-Thinopyrum intermedium (Host) Barkworth and D.R. Dewey Robertsonian translocation, RobT T7BS.7S#3L [18]. Genomic in situ hybridization (GISH)-based progeny screening of Hpp-5Mg/ph1bph1b genotypes double monosomic for T7BS.7S#3L/7B identifies 6.5% wheat-Th. intermedium recombinants. This is a 100-fold increase in induced homoeologous recombinant frequency compared to 0.06% observed by using ph1b alone [18]. Our results indicate that chromosome 5Mg promotes homoeologous recombination between wheat and wild wheat relative chromosomes, which can greatly accelerate gene transfers from distantly related species to wheat.
2. Materials and Methods

2.1. Plant Material and Chromosome Preparations

The cytogenetic stocks and hybrid plants used in this study are listed in Table 1. Chromosome 5M\textsubscript{g} was transferred to wheat from two different Ae. geniculata accessions and, thus, have been designated as 5M\textsubscript{g}#1 and 5M\textsubscript{g}#2. 5M\textsubscript{g}#1 is a complete Ae. geniculata chromosome whereas 5M\textsubscript{g}#2 has a tiny segment of 5D of wheat at the telomeric region of the long arm [17]. In the present study, all experiments were performed with 5M\textsubscript{g}#1.

Table 1. Cytogenetic stocks used for studying homoeologous recombination in wheat.

| Accession | Chromosome Number | Chromosome Constitution | Description |
|-----------|-------------------|--------------------------|-------------|
| TA6708    | 42                | DS5M\textsubscript{g}#1(5D) | One pair of 5D of wheat substituted by a pair of 5M\textsubscript{g}#1 from Ae. geniculata, TA1800 |
| TA3809    | 42                | Ph1 mutation             | Deletion mutant of Ph1 locus induced by X-ray irradiation |
| TA5624    | 42                | T7BS-7S\textsubscript{g}#3L | One pair of wheat-Th. intermedium translocation chromosome, involving 7BS of wheat and 7S\textsubscript{g}#3L of Th. intermedium substituting for chromosome 7B of wheat |

For chromosome preparations, the seeds were germinated in petri dishes on moist filter paper. Root tips (1–2 cm long) were incubated overnight in ice water. The root tips were fixed overnight in an ethanol:glacial acetic acid (3:1) and the fixed root tips were squashed in a drop of 45% acetic acid [19]. All slides were stored at −70 °C until use.

2.2. Genomic In Situ Hybridization (GISH)

Genomic DNAs of parental genomes were used as probes (Table S1). Total genomic DNAs from T. urartu (A genome), Ae. tauschii (D genome) and Ae. comosa Sm. in Sibth. and Sm. (M genome) were isolated using a Qiagen DNeasy Plant Mini Kit (Qiagen Inc., Valencia, CA, USA) following manufacturer’s instructions. The DNA concentration of each sample was quantified using a NanoDrop\textsuperscript{®} 1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). Approximately 1 µg of genomic DNA of each species was labeled with either digoxigenin-11-dUTP or biotin-16-dUTP according to the manufacturer’s instructions (Roche, Indianapolis, IN, USA). Probes were purified with the QIAquick nucleotide removal kit (Qiagen Inc., Valencia, CA, USA). The GISH hybridization solution contains 50% formamide, 10% dextran sulfate, 2× SSC, 2 µg/mL of each of 2 labeled genomic DNA probes, and unlabeled total genomic DNA of wheat as a blocker. The probe:blocker ratio was about 1:50. After post-hybridization washes, the probes were detected with Alexafluor 488 streptavidin (Invitrogen, Grand Island, NY, USA) for biotin-labeled probes, and rhodamine-conjugated anti-digoxigenin (Roche) for dig-labeled probes. Chromosomes were counterstained with 4′,6-diamidino-2-phenylindole (DAPI) in Vectashield antifade solution (Vector Laboratories, Burlingame, CA, USA). The images were captured with a Zeiss Axioplan 2 microscope using a cooled CCD camera CoolSNAP HQ2 (Photometrics, Tucson, AZ, USA) and AxioVision 4.8 software (Carl Zeiss Microscopy LLC, Thornwood, NY, USA). The final contrast of the images was processed using Adobe Photoshop CS5 software (Adobe, San Jose, CA, USA).

3. Results

3.1. Homoeologous Recombination in the Presence of 5M\textsubscript{g} and Absence of Ph1

Previously, we identified chromosome 5M\textsubscript{g} from Ae. geniculata, which escapes the diploid pairing control and freely recombines with 5D of wheat in the presence of Ph1, even in proximal chromosome regions where recombination is usually suppressed [17]. In this study, we investigated homoeologous
recombination of wheat in the presence of 5Mg and absence of Phi. We crossed the phi1b mutant stock with the DS5Mg#1(5D) substitution line and then selected plants homozygous for phi1b and double monosomic for 5Mg#1 and 5D (Table 1). The recombination frequency was determined in the 57 self-progeny plants by GISH. Surprisingly, we observed 63 recombinant chromosomes between 5Mg#1 and 5D, or between 5Mg#1 and 5A or 5B. In the 57 plants analyzed, the observed homoeologous recombination frequency was higher than 100% (Figure 1), including plants that contained more than one recombinant chromosome. The recombinant frequency of the same cross in the presence of Phi was 10% (11 recombinants out of 110 progenies screened) [17].

The GISH patterns of the 5Mg#1/5D recombinants revealed that 46 recombinants had more than two CO breakpoints per chromosome arm. Up to five CO sites were detected in two recombinant chromosomes (Figure 1b). In addition, we also observed recombinant chromosomes between D-genome and A- or B-genome chromosomes (Figure 1a and Figure S1). Recombinants with multiple COs and COs in the proximal regions were also detected (Figure 1a and Figure S1). In phi1b mutants, homoeologous CO breakpoints were restricted to distal region in few chromosomes with 2.0 ± 0.82 (n = 10) frequency of intergenomic exchanges per plant, and recombinants with multiple COs and CO in proximal region were not detected (Figure 2). Overall, these results support our previous hypothesis that chromosome 5Mg harbors homoeologous pairing promotor gene(s) (Hpp-5Mg) [17] that affect homoeologous recombination and CO interference, and this effect is more pronounced in the absence of the Phi gene.

Figure 1. Genomic in situ hybridization (GISH)-based identification of recombinant chromosomes derived from plants with 5Mg#1 and without Phi (Hpp-5Mg/phi1bphi1b). (a) A partial mitotic metaphase cell having 4 recombinant chromosomes derived from homoeologous recombination between 5Mg#1 and 5D (white arrows), and between the wheat subgenomes (yellow arrows). (b–f) Recombinants with five (b), four (c), three (d), two (e), and one CO sites (f); (g) recombinants with COs in both the short and long arm; (h) recombinants derived from multiple homoeologous recombination events between 5Mg#1 and 5D, 5A, and 5B of wheat. A total of 63 recombinant chromosomes involving 5Mg#1 were identified, out of 57 plants screened. COs sites are indicated by arrows. 5Mg#1 is visualized in green, 5D in red, and 5A or 5B in blue fluorescence. Bar = 10 µm.
Figure 2. GISH patterns of mitotic metaphase chromosomes in the absence of 5M\#1 and Ph1 (ph1bph1b). (a) No recombinant chromosomes; (b) one recombinant chromosome; (c) three recombinant chromosomes. White arrows indicate the recombinant chromosomes; A-, D-, and B-genome chromosomes were visualized by green, red, and blue fluorescence, respectively. Recombinants with multiple COs and COs in the proximal region were not detected in 10 ph1b mutant plants analyzed. Yellow arrows point to the rearranged chromosome 4A. Bars = 10 µm.

3.2. Potential Use of Chromosome 5M\# in Wheat Improvement

We have studied ph1b-induced homoeologous recombination for producing recombinants for the wheat streak mosaic virus resistance gene, Wsm3, present in the wheat-Thinopyrum intermedium (RobT T7BS.7S\#3L). Only one plant out of 1690 plants screened contained a wheat-Th. intermedium recombinant chromosome amounting to a recombinant frequency of 0.06% [18]. We tested the efficacy of Hpp-5M\#ph1bph1b-induced homoeologous recombination by producing new recombinants for Wsm3 present in RobT T7BS.7S\#3L. The RobT line was crossed with the ph1b stock and the ph1b stock was also crossed with the disomic substitution line DS5M\#1(5D). The F1s were intercrossed and plants homozygous for ph1b and heterozygous for 5M\# were selected along with T7BS.7S\#3L. The recombinant frequency was determined in the self-progenies by GISH. Two hundreds plants were screened out of which homoeologous recombination event between the RobT T7BS.7S\#3L and chromosome 7B of wheat was detected in 13 plants amounting to a homoeologous recombination frequency of 6.5% (Figure 3). The homoeologous recombination frequency of 6.5% in the 5M\#/ph1b, ph1b stock was ~100-times greater compared to ph1b alone. Importantly, recombinants were recovered that had CO breakpoints in the proximal regions where COs are rarely observed in ph1b-induced recombination. Also, recombinants with double COs in interstitial regions were recovered (Figure 3c,f).
Figure 3. \textit{Hpp-5M}\textsuperscript{g} \textit{ph1bph1b}-induced homoeologous wheat-	extit{Th. intermedium} recombinants. (a) RobT T7BS-7S\#3L; (b) chromosome 7B; (c–f) recombinant chromosomes derived from \textit{Hpp-5M}\textsuperscript{g} \textit{ph1bph1b}-induced homoeologous recombination between (T7BS-7S\#3L) and (7B); (c) COs in proximal region; (d) COs in interstitial and distal regions; (e,f) recombinants having more than two CO sites. Four recombinants involving translocation at distal region are not shown in the figure. Total genomic DNA of \textit{Th. Intermedium} was used as a probe to detect the \textit{Th. Intermedium} chromatin (red fluorescence). GAA repeats (green fluorescence) were used to identify chromosome 7B of wheat. Bar = 10 μm.

4. Discussion

Gene transfer from distantly related species of the tertiary gene pool to wheat cannot be achieved by homologous recombination because the \textit{Ph1} gene on chromosome arm 5B suppresses homoeologous recombination \cite{8,9}. Previously, we had identified a potent homoeologous pairing promotor gene(s) (\textit{Hpp-5M}\textsuperscript{g}) and showed that its carrier chromosome 5M\textsuperscript{g} of \textit{Ae. geniculata} and its wheat homoeologous chromosome 5D freely recombined in the presence of \textit{Ph1} \cite{17}. Similarly, a few studies have shown that homoeologous recombination can occur in the presence of \textit{Ph1} particularly in hybrids between wheat and \textit{Ae. speltoides} Tausch or \textit{Amblyopyrum muticum} (Boiss.) Eig \cite{20–22}. Chromosome 5U in \textit{Ae. umbellulata} Zhuk. \cite{23} and chromosome 5E in \textit{Elytrigia elongata} (Host) Nevski have also been shown to promote recombination between homoeologous chromosomes \cite{24}, implying that the activity of \textit{Ph1} in wheat can be suppressed by the genes of wild wheat relatives.

Distal localization of COs/chiasmata is a very common feature of wheat chromosomes and those of its close relatives \textit{Aegilops}, barley, rye, and oat \cite{25}. In wheat and barley, the distal halves of the arms represent nearly the entire length of the genetic maps \cite{26–28}. Molecular cytological analysis using immunofluorescence of MLH3 (barley MutL homologue, a marker for class-I interfering COs) on pachytene chromosomes of barley also revealed that the distribution of CO events is strongly biased towards the distal chromosomal regions \cite{29}. This bias limits the genetic variability and reduces the efficiency of map-based cloning and breeding approaches in these crops. Hence, identification of a potential route to manipulate COs distribution toward the proximal region would be highly valuable for generating pre-breeding materials for plant breeders and would accelerate crop improvement. In \textit{Hpp-5M}\textsuperscript{g} \textit{ph1bph1b} plants, we found a massive increase in homoeologous recombination and multiple COs per chromosome arm (Figure 1 and Figure S1) including in proximal regions in the chromosomes where COs are never observed even in homoeologous recombination. Thus,
manipulation of recombination between wheat and its wild relatives can be achieved by using Hpp-5M*5 in wide crosses.

We tested the efficacy of the Hpp-5M*5 mechanism by producing new recombinants for the wheat streak mosaic virus resistance gene Wsm3 present in the wheat-Th. intermedium (RobT) T7BS.7S#3L (Figure 3). Progeny screening revealed that 6.5% were wheat-Th. intermedium recombinants with CO breakpoints covering the entire length of the Th. intermedium chromosome arm (Figure 3c–f), which is about 100-times higher compared to that observed by using the ph1b mutant alone. The frequency of ph1b-induced recombination is genome and chromosome specific. Friebe et al. [14] reported a frequency of ph1b-induced recombinants for the short arm of the Th. intermedium chromosome 4J* of 2% (5 recombinants out of 245 progenies screened), whereas Danilova et al. [18] reported a much lower frequency of ph1b-induced recombinants for the wheat-Th. intermedium (RobT) 7S#3 (1 recombinant out of 1690 progenies screened, 0.06%). The difference in recombination frequencies observed for the 4J*S and 7SL arms may indicate that the J* genome has a greater genomic affinity to the B and D genomes of wheat compared to that of the S genome of Th. intermedium. However, observations in the cultivated rye, Secale cereale L. showed that even different arms of the same chromosome can have drastic differences in ph1b-induced recombinants frequencies. Lukaszewski et al. [30] observed recombinant frequency of 0.6% for the short arm and 16.3% for the long arm of rye chromosome 2R. In addition, a higher frequency of 6.7% was also reported for the short arm of rye chromosome 1R [31].

The COs and the process of recombination generate novel combination of parental alleles at each generation and this genetic variability plays a central role in evolution, speciation and selection of improved cultivars in plant breeding [32–36]. Recent studies in Arabidopsis meiosis showed that natural variation in CO frequency between different ecotypes was controlled by a procrossover E3 ligase gene HEI10 [37]. Genotypes with extra copies of HEI10 had higher CO frequencies in euchromatin but not in pericentromeric heterochromatic regions. It would be interesting to detect the similar pattern of increased copy numbers of HEI10 gene corresponding to increased CO frequencies in wheat. The quantitative trait loci affecting the recombination frequency in wheat was detected in 6A and 6B at 50.2 and 47.8 cM respectively. HEI10 is the candidate gene in these regions, which favors the increase in recombination frequencies in wheat [38]. Therefore, it might be intriguing to know that CO frequency in wheat nullisomic-6D-tetrasomic-6A or 6B which will reveal the effect of HEI10 in increasing in CO frequency of wheat.

The RECQ4A and RECQ4B proteins in Arabidopsis are reported to have anticrossover activity [39,40]. Serra et al. [41] generated Arabidopsis recq4a recq4b double mutants and combined them with duplicated HEI10 gene and observed a massive increase in CO frequency in euchromatic chromosome regions, providing a genetic framework for engineering meiotic recombination landscapes in plant genomes [41]. However, recombination remained suppressed in the pericentromeric regions similar to wild-type genotypes. Underwood et al. [42] noticed increased recombination in pericentromeric regions in H3K9me2 and non-CG DNA methylation pathway mutants in Arabidopsis. Similar procrossover and anticrossover genes and epigenetic mutants remain to be identified in wheat.

Generally, the presence of one CO in a chromosomal region suppresses the formation of another CO in the nearby regions and this phenomenon is termed as class I CO interference [32]. However, in Hpp-5M*5/ph1bph1b plants the phenomenon of class I CO interference is absent resulting in the clustering of several CO events at a close proximity (Figure 1 and Figure S1). In 5M*5/ph1bph1b-induced homoeologous recombination of the wheat-Th. intermedium (RobT) T7BS.7S#3L, we also observed recombinants with double COs in interstitial and proximal regions (Figure 3e–f). This opens the possibility of transferring small desired alien segments from wild species to wheat with reduced linkage drag. Further studies on the molecular cloning of Hpp-5M*5 gene(s) and its interaction with Ph1 gene will revolutionize the transfer of desired genes from species of tertiary gene pool to wheat, making it more efficient and also allow the transfer of target genes that are located in interstitial and proximal regions of the chromosomes. We do not know if Hpp-5M*5 also effects homologous recombination, which is presently under investigation.
**Supplementary Materials:** The following are available online at http://www.mdpi.com/2073-4395/10/8/1059/s1.

Figure S1: Genomic in situ hybridization (GISH)-based identification of recombinant chromosomes derived from plants with 5M#1 and without Ph1 (Hpp-5M//ph1ph1b). Table S1: Plant materials used in preparing the chromosome painting probes.

**Author Contributions:** D.-H.K. performed most of the experiments; D.-H.K., B.F. and B.S.G. wrote the manuscript; D.-H.K., B.F. and B.S.G. designed the experiments and analyzed the data. All authors have read and agreed to the published version of the manuscript.

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**References**

1. Huang, S.; Sirikhachornkit, A.; Su, X.; Faris, J.D.; Gill, B.S.; Haselkorn, R.P.; Gornicki, P. Phylogenetic analysis of the acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the Triticum/Aegilops complex and the evolutionary history of polyploid wheat. *Proc. Natl. Acad. Sci. USA* 2002, 12, 8133–8138. [CrossRef] [PubMed]

2. Qi, L.L.; Friebe, B.; Gill, B.S. Homoeologous recombination, chromosome engineering and crop improvement. *Chromosome Res.* 2007, 15, 3–19. [CrossRef]

3. Jiang, J.; Friebe, B.; Gill, B.S. Recent advances in alien gene transfer in wheat. *Euphytica* 1994, 73, 199–212. [CrossRef]

4. Friebe, B.; Jiang, J.; Raupp, W.J.; McIntosh, R.A.; Gill, B.S. Characterization of wheat-alien translocations conferring resistance to diseases and pests: Current status. *Euphytica* 1996, 91, 59–87. [CrossRef]

5. Molnár-Lang, M.; Linc, G.; Szakács, É. Wheat–barley hybridization: The last 40 years. *Euphytica* 2014, 195, 315–329. [CrossRef]

6. Sears, E.R. *Aneuploids of Common Wheat*; Research Bulletin; Missouri Agricultural Experiment Station: Columbia, MO, USA, 1954; Volume 572, p. 59.

7. Sears, E.R. Genetic control of chromosome pairing in wheat. *Annu. Rev. Genet.* 1976, 10, 31–51. [CrossRef]

8. Riley, R.; Chapman, V. Genetic control of the cytologically diploid behavior of hexaploid wheat. *Nature* 1958, 182, 713–715. [CrossRef]

9. Sears, E.R.; Okamoto, M. Intergenomic chromosome relationship in hexaploid wheat. In Proceeding of the 10th International Congress of Genetics, Montreal, QC, Canada, 20–27 August 1958; pp. 258–259.

10. Mello-Sampayo, T. Genetic regulation of meiotic chromosome pairing by chromosome 3D of *Triticum aestivum*. *Nat. New Biol.* 1971, 230, 23–24. [CrossRef]

11. Sutton, T.; Whitford, R.; Baumann, U.; Dong, C.; Able, J.A.; Langridge, P. The Ph2 pairing homoeologous locus of wheat (*Triticum aestivum*): Identification of candidate meiotic genes using a comparative genetics approach. *Plant J.* 2003, 36, 443–456. [CrossRef]

12. Sears, E.R. An induced mutant with homoeologous pairing in common wheat. *Can. J. Genet. Cytol.* 1977, 19, 585–593. [CrossRef]

13. Gill, B.S.; Friebe, B.; Raupp, W.J.; Wilson, D.L.; Cox, T.S.; Brown-Guedira, G.L.; Sears, R.S.; Fritz, A.K. Wheat Genetics Resource Center: The first 25 years. *Adv. Agron.* 2006, 85, 73–135.

14. Friebe, B.; Qi, L.L.; Wilson, D.L.; Chang, Z.L.; Seifers, D.L.; Martin, T.J.; Fritz, A.K.; Gill, B.S. Wheat–Thinopyrum intermedium recombinants resistant to wheat streak mosaic virus and *Triticum* mosaic virus. *Crop Sci.* 2009, 49, 1221–1226. [CrossRef]

15. Lukaszewski, A.J. Manipulation of homologous and homoeologous chromosome recombination in wheat. *Methods Mol. Biol.* 2016, 1429, 77–89. [PubMed]

16. Liu, W.; Rouse, M.; Friebe, B.; Jin, Y.; Gill, B.S.; Pumphrey, M.O. Discovery and molecular mapping of a new gene conferring resistance to stem rust, Sr53, derived from *Aegilops geniculata* and characterization of spontaneous translocation stocks with reduced alien chromatin. *Chromosome Res.* 2011, 19, 669–682. [CrossRef]

17. Koo, D.-H.; Liu, W.; Friebe, B.; Gill, B.S. Homoeologous recombination in the presence of Ph1 gene in wheat. *Chromosoma* 2017, 126, 531–540. [CrossRef]
18. Danilova, T.V.; Zhang, G.; Liu, W.; Friebe, B.; Gill, B.S. Homoeologous recombination-based transfer and molecular cytogenetic mapping of a wheat streak mosaic virus and *Triticum* mosaic virus resistance gene *Ws3* from *Thinopyrum intermedium* to wheat. *Theor. Appl. Genet.* 2017, 130, 549–556. [CrossRef]

19. Koo, D.-H.; Sehgal, S.K.; Friebe, B.; Gill, B.S. Structure and stability of telocentric chromosomes in wheat. *PLoS ONE* 2015, 10, e0137747. [CrossRef]

20. Riley, R. The diploidization of polyploid wheat. *Heredity* 1960, 15, 407–429. [CrossRef]

21. Dover, G.A.; Riley, R. Prevention of pairing of homoeologous meiotic chromosomes of wheat by an activity of supernumerary chromosomes of *Aegilops*. *Nature* 1972, 240, 159–161. [CrossRef]

22. Dvorak, J.; Deal, K.R.; Luo, M.-C. Discovery and mapping of wheat *Ph1* suppressors. *Genetics* 2006, 174, 17–27. [CrossRef]

23. Riley, R.; Chapman, V.; Miller, T.E. The determination of meiotic chromosome pairing. In Proceedings of the 4th International Wheat Genetics Symposium, Columbia, MO, USA, 6–11 August 1973; pp. 713–738.

24. Dvorak, J. Chromosomal distribution of genes in diploid *Elytrigia elongata* that promote or suppress pairing of wheat homoeologous chromosomes. *Genome* 1987, 29, 34–40. [CrossRef]

25. Lukaszewski, A.J. Unexpected behavior of an inverted rye chromosome arm in wheat. *Chromosoma* 2008, 117, 569–578. [CrossRef] [PubMed]

26. Gill, K.S.; Gill, B.S.; Endo, T.R.; Boyko, E.V. Identification and high density mapping of gene-rich regions in chromosome group-1 of wheat. *Genetics* 1996, 143, 1001–1012. [PubMed]

27. Künzel, G.; Korzun, L.; Meister, A. Cytologically integrated physical restriction fragment length polymorphism maps for the barley genome based on translocation breakpoints. *Genetics* 2000, 154, 397–412. [PubMed]

28. Saintenac, C.; Falque, M.; Martin, O.C.; Paux, E.; Feuillet, C.; Sourdille, P. Detailed recombination studies along chromosome 3B provide new insights on crossover distribution in wheat (*Triticum aestivum* L.). *Genetics* 2009, 181, 393–403. [CrossRef]

29. Phillips, D.; Wnetrzak, J.; Nibau, C.; Barakate, A.; Ramsay, L.; Wright, F.; Higgins, J.D.; Perry, R.M.; Jenkins, G. Quantitative high resolution mapping of *HvMLH3* foci in barley pachytene nuclei reveals a strong distal bias and weak interference. *J. Exp. Bot.* 2013, 64, 2139–2154. [CrossRef]

30. Lukaszewski, A.J.; Rybka, K.; Korzun, V.; Malychev, S.V.; Lapinski, B.; Whitkus, R. Genetic and physical mapping of homoeologous recombination points involving wheat chromosome 2B and rye chromosome 2R. *Genome* 2004, 47, 36–45. [CrossRef]

31. Mercier, R.; Mézard, C.; Jenczewski, E.; Macaisne, N.; Grelon, M. The molecular biology of meiosis in plants. *Annu. Rev. Plant Biol.* 2015, 66, 297–327. [CrossRef] [PubMed]

32. Dvorak, J. Chromosomal distribution of genes in diploid *Elytrigia elongata* that promote or suppress pairing of wheat homoeologous chromosomes. *Genome* 1987, 29, 34–40. [CrossRef]

33. Phillips, D.; Wnetrzak, J.; Nibau, C.; Barakate, A.; Ramsay, L.; Wright, F.; Higgins, J.D.; Perry, R.M.; Jenkins, G. Quantitative high resolution mapping of *HvMLH3* foci in barley pachytene nuclei reveals a strong distal bias and weak interference. *J. Exp. Bot.* 2013, 64, 2139–2154. [CrossRef]

34. Wang, Y.; Copenhaver, G.P. Meiotic recombination: Mixing it up in plants. *Annu. Rev. Plant Biol.* 2018, 69, 640–646. [CrossRef] [PubMed]

35. Lamberg, C.; Franklin, F.C.H.; Wang, C.-J.R. Understanding and manipulating meiotic recombination in plants. *Plant Physiol.* 2017, 173, 1530–1542. [CrossRef] [PubMed]

36. Lamberg, C.; Heckmann, S. Tackling plant meiosis: From model research to crop improvement. *Front. Plant Sci.* 2018, 9, 1–15. [CrossRef]

37. Jordan, K.W.; Wang, S.; He, F.; Chao, S.; Lun, Y.; Paux, E.; Sourdille, P.; Sherman, J.; Akhunova, A.; Blake, N.K.; et al. The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. *Plant J.* 2018, 95, 1039–1054. [CrossRef]

38. Seguela-Arnaud, M.; Crismani, W.; Larcheveque, C.; Mazel, J.; Froger, N.; Choinard, S.; Lemhemdi, A.; Macaisne, N.; van Leene, J.; Gevaert, K.; et al. Multiple mechanisms limit meiotic crossovers: TOPO3α and two BLM homologs antagonize crossovers in parallel to FANCM. *Proc. Natl. Acad. Sci. USA* 2015, 112, 4713–4718. [CrossRef]
40. Seguela-Arnaud, M.; Choinard, S.; Larcheveque, C.; Girard, C.; Froger, N.; Crismani, W.; Mercier, R. RMI1 and TOP3α limit meiotic CO formation through their C-terminal domains. *Nucleic Acids Res.* **2017**, *45*, 1860–1871. [CrossRef]

41. Serra, H.; Lambing, C.; Griffin, C.H.; Topp, S.D.; Nageswaran, D.C.; Underwood, C.J.; Ziolkowski, P.A.; Sequela-Arnaud, M.; Fernandes, J.B.; Mercier, R.; et al. Massive crossover elevation via combination of HEI10 and recq4a recq4b during Arabidopsis meiosis. *Proc. Natl. Acad. Sci. USA* **2018**, *115*, 2437–2442. [CrossRef]

42. Underwood, C.J.; Choi, K.; Lambing, C.; Zhao, X.; Serra, H.; Borges, F.; Simorowski, J.; Ernst, E.; Jacob, R.; Henderson, I.R.; et al. Epigenetic activation of meiotic recombination near *Arabidopsis thaliana* centromeres via loss of H3K9me2 and non-CG DNA methylation. *Genome Res.* **2018**, *28*, 1–13. [CrossRef]

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