X Chromosome Control of Meiotic Chromosome Synapsis in Mouse Inter-Subspecific Hybrids

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Abstract

Hybrid sterility (HS) belongs to reproductive isolation barriers that safeguard the integrity of species in statu nascendi. Although hybrid sterility occurs almost universally among animal and plant species, most of our current knowledge comes from the classical genetic studies on Drosophila interspecific crosses or introgressions. With the house mouse subspecies Mus m. musculus and Mus m. domesticus as a model, new research tools have become available for studies of the molecular mechanisms and genetic networks underlying HS. Here we used QTL analysis and intersubspecific chromosome substitution strains to identify a 4.7 Mb critical region on Chromosome X (Chr X) harboring the Hstx2 HS locus, which causes asymmetrical spermatogenic arrest in reciprocal intersubspecific F1 hybrids. Subsequently, we mapped autosomal loci on Chrs 3, 9 and 13 that can abolish this asymmetry. Combination of immunofluorescent visualization of the proteins of synaptonemal complexes with whole-chromosome DNA FISH on pachytene spreads revealed that heterosubspecific, unlike consubspecific, homologous chromosomes are predisposed to asynapsis in F1 hybrid male and female meiosis. The asynapsis is under the trans-control of Hstx2 and Hst1/Prdm9 hybrid sterility genes in pachynemas of male but not female hybrids. The finding concurred with the fertility of intersubspecific F1 hybrid females homozygous for the Hstx2Mmm allele and resolved the apparent conflict with the dominance theory of Haldane’s rule. We propose that meiotic asynapsis in intersubspecific hybrids is a consequence of cis-acting mismatch between homologous chromosomes modulated by the trans-acting Hstx2 and Prdm9 hybrid male sterility genes.


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Introduction

Hybrid sterility (HS) is a postzygotic reproductive isolation barrier restricting gene flow between the related taxa during speciation. It is defined as a condition where two parental forms inter se produce a hybrid that is sterile [1]. One of the most interesting findings coming from previous studies is a disproportionately large effect of Chr X on reproductive isolation, particularly on hybrid sterility and inviability. The large X-effect was described in diverse organisms, and evolutionary biologists designated it as one of the speciation rules [2–5]. Another speciation principle, called Haldane’s rule [6], points to the empirical findings that hybrid inviability and sterility predominantly afflict the heterogametic (XY or ZW) sex. The dominance theory originally proposed by Muller [7] explained the sex-dependent effect on hybrid fitness by the manifestation of recessive X-linked alleles in hemizygous XY males but not in XX females [8–10]. We have chosen M. m. musculus and M. m. domesticus subspecies (hereafter, Mmm and Mmd) as model organisms to study mammalian HS [for review see [11–13]]. Both subspecies diverged from a common ancestor approximately 0.3 to 0.5 million years ago [14] and formed a hybrid zone across Europe after their secondary contact [15]. The repeated introgressions of Mmm genes into Mmd genome and vice versa across their hybrid zone indicate incomplete reproductive isolation between both young subspecies [16,17]. Such early-stage model is superior in that it reduces the risk of analyzing HS genes that evolved as a consequence and not as the cause of speciation after full reproductive isolation of the related taxa [5,18]. Numerous genetic and genomic tools are available for the mouse model, including the full genomic sequence of inbred strains representing both subspecies and additional 17 laboratory inbred strains [19] and a panel of 28 mouse intersubspecific chromosome substitution (consomic) strains carrying individual Mmm chromosomes or their parts on Mmd
Background [20]. A variety of commercially available antibodies detecting meiosis-specific proteins and histone modifications permit immunodetection of subnuclear structures important for meiotic chromosome synopsis and segregation [21,22].

We identified the first hybrid sterility gene in mice, hybrid sterility 1 – Hst1 – as a polymorphic variant on Chr 17 between two laboratory strains, C57BL10/Sn and C3H/Di, both predominantly of Mmm origin (at that time still linkage group IX). When mated with Mmm wild mice trapped in Central Bohemia near Prague, these crosses produced sterile or fertile male hybrids, depending on their Hst1 alleles [23]. Recently, Hst1 was identified by the forward genetics approach as PR domain containing 9 (Prdm9) [24] and later was shown to control meiotic recombination hotspots [25,26].

In a study of genetic architecture of F1 hybrid male sterility, the results of Mmm×Mnd backcross predicted a minimum of four independently segregating HS loci. However, QTL analysis of the data revealed only two strong HS loci, Hst1/Prdm9 and a locus on Chr X [27]. This paradox could be explained either by the action of multiple minor HS loci undetected by relatively low-power QTL analysis or by different behavior of two major HS loci on the hybrid background. The latter alternative was supported in an experiment showing that these two HS loci are not sufficient to recapitulate the F1 HS phenotype on B6 (Mnd) genetic background [22]. Moreover, for the first time a compelling evidence was provided for the mechanism of HS, showing that aberrant meiotic pairing of heterospecific homologous chromosomes and meiotic arrest are the consequence of intersubspecific hybrid genetic background [22].

Here we report on the role of Chr X in male and female meiosis in mouse intersubspecific hybrids. We localized the Hstx2 locus controlling the asymmetry of HS in reciprocal intersubspecific F1 hybrid males to a 4.7 Mb interval on Chr X and mapped three autosomal loci that can abolish this asymmetry. We observed the predisposition of heterospecific homologs to asynapsis in male and female meiosis as the initial step of intrameiotic breakdown of the sterile hybrids. The effects of Hstx2 or Hst1/Prdm9 on the degree of asynapsis in pachynema of male but not female intersubspecific hybrids concurred with the fertility of Mmm×Mnd F1 hybrid females homozygous for the Hstx2\textsuperscript{Mmm} allele and resolved the apparent conflict with the dominance theory of Haldane’s rule. Based on detailed meiotic analysis of the mouse model of intersubspecific F1 hybrids we propose that HS genes operate on “sensitized” genetic background resulting from the difficulties of proper meiotic synopsis of heterosubspecific autosomal homologs and consequent epigenetic dysregulation of X-Y chromosomes [22]. Accordingly, classical HS genes Prdm9 [24,28] and Hstx2 [27] realize their HS-specific phenotypes by interacting, directly or indirectly, with the process of meiotic pairing and synopsis of heterospecific homologs.

Results

Fine mapping of Hstx2 and its role in HS asymmetry of reciprocal F1 hybrids

Dobzhansky-Muller incompatibilities (DMIs) between the nascent species often result in asymmetry of HS or inviability of reciprocal F1 hybrids [27,29–31] although relatively little is known about their genetic control or mechanistic basis. Previously we have shown that asymmetry in male sterility of reciprocal hybrids between Mmm mouse subspecies represented by the PWD/Ph (hereafter PWD) inbred strain [32] and Mnd represented by the C57BL/6j inbred strain (hereafter B6) is controlled by the central region of Chr X (64.9 Mb–98.1 Mb, GRCh38). To localize the locus responsible for HS asymmetry we crossed consomic F1 females (B6.PWD-Chr X×B6) with PWD males. All 124 male offspring carried B6/PWD heterosubspecific autosomal pairs while Chr X loci were either PWD or B6, depending on the recombination breakpoints. Testes weight (TW, range 56–186 mg) and sperm count (SC, 0–13.5 million) were used as surrogate for QTL analysis of male fertility phenotypes. Their segregation localized a hybrid sterility locus to the 34.6–35.7 cM (1.5-LOD support interval) interval with the maximum LOD score 30 and 23 at 34.8 cM for TW and SC. As shown in Fig. 1A-D all males that received the PWD allele at the DXMit87 locus had small testes bellow 100 mg and little (below 10\textsuperscript{6}) sperm in duc tus epididymis. This hybrid sterility locus causes complete sterility on F1 hybrid intersubspecific background, and we designate it hybrid sterility chromosome X 2, Hstx2. Earlier, we reported localization of the locus at lower resolution in the (PWD×B6)×B6 backcross (Dzur-Gejdsoova 2012).

To further refine the position of Hstx2, a new partial consomic strain B6.PWD-Chr X.1s was created with extended proximal interval of the Chr X\textsubscript{PWD} sequence compared to B6.PWD-Chr X.1 [for strain description see ref [29]].

The borders of the PWD sequence of the introgressed Chr X\textsubscript{PWD} were compared to those of the existing proximal, central and distal partial consomic strains B6.PWD-Chr X.1, B6.PWD-Chr X.2 and B6.PWD-Chr X.3 [20] using high-resolution Mouse Universal Genotyping Array (MegaMUGA) (Table S1). To localize the region carrying Hstx2 on Chr X\textsubscript{PWD}, females of all four Chr X partial consomic strains were crossed with PWD males and the fertility of male offspring was examined (Fig. 2). The (B6.PWD-Chr X.1×PWD)F1 and (B6.PWD-Chr X.3×PWD)F1 hybrid males were semiferile with testes weight comparable to (B6×PWD)F1 males, while (B6.PWD-Chr X.1s×PWD)F1 and (B6.PWD-Chr X.2×PWD)F1 were fully sterile with small testes (p<0.0001, t-test) and no sperm in duc tus epididymis (Fig. 2). Thus (B6.PWD-Chr X.1s×PWD)F1 hybrids carried the Hstx2\textsuperscript{PWD} allele and fully reconstructed the HS phenotype of (PWD×B6) males, showing meiotic arrest at epithelial stage IV and to lesser degree at late pachyten e/diplotene stage (Table S2). The position of Hstx2 was localized to the 4.7 Mb interval delineated by UNC39094273
for the distal end of B6.PWD-Chr X.1 PWD sequence and UNC30934795 for the distal end of B6.PWD-Chr X.1s (X: 64,880,641–69,581,094, GRCm38).

**Introgressed Hstx1PWD causes teratozoospermia in Mmd genome and maps to the same genomic region as Hstx2**

The Hstx1 locus in the proximal part of Chr XPWD causes male sterility when introgressed onto the B6 background [33]. Contrary to the F1 hybrid meiotic arrest at late pachytene/diplotene stage controlled by Hstx2 [22], Hstx1PWD in the B6 genome causes postmeiotic breakdown and abnormal morphology of a fraction of non-functional sperm. Here we genotyped the male progeny of females heterozygous for PWD and B6 form of Chr X from the backcross generations 4–9 to B6 background and selected 71 Chr X single-recombinants with PWD centromeric end for fertility testing. The Hstx1 locus mapped within the interval spanned by DXMit76 and DXMit143 (Fig. S1).

To further localize Hstx1, we phenotyped all four B6.PWD-Chr X partial consomics and found a high percentage of abnormal sperm cells in B6.PWD-Chr X.1s compared to other three partial consomics and B6 males (p < 0.05 t-test, Fig. 2). The analysis of partial consomic strains independently confirmed the Hstx1 localization to the same 4.7 Mb interval of Chr X that carries Hstx2. However, because B6.PWD-Chr X.2 males did not show high frequency of abnormal sperm in spite of their Hstx1PWD allele, we assumed that Hstx1 needs to interact with another genetic factor from the proximal region of Chr X^PWD to manifest the abnormal sperm phenotype (Fig. 2, see also [33]).

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**Figure 1. Single QTL mapping of Hstx2 on Chr X.** (A) QTL analysis of testes weight in the (B6.PWD-Chr X × B6)F1 × PWD cross showed a 1.5-LOD support interval between 34.6 cM to 35.3 cM on Chr X. (B) Distribution of testes weight of males carrying PWD or B6 allele of DXMit87 marker with LOD score 30. (C) QTL analysis of sperm count in ductus epididymis shows the same 1.5 LOD support interval as for testes weight. (D) Distribution of sperm count of males carrying PWD or B6 allele of DXMit87 marker (Chr X: 66.65 Mb, GRCm38) with LOD score above 20.

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**Hstx1 and Hstx2 candidate genes**

The 4.7 Mb Chr X candidate region of *Hstx1* and *Hstx2* loci carries 11 known protein-coding genes and 20 miRNA genes (Fig. S2). Of these, seven protein-coding genes, namely cancer/testis antigen 2 (*Ctag2*), RIKEN cDNA 4930447F04 gene (*4930447F04Rik*), SLIT and NTRK-like family, member 2 (*Slitrk2*), RIKEN cDNA 4933436I01 gene (*4933436I01Rik*), fragile X mental retardation syndrome 1 homolog (*Fmr1*), fragile X mental retardation 1 neighbor (*Fmr1nb*), and AF4/FMR2 family member 2 (*Aff2*) show high expression in adult tests. Of them, *Aff2* is expressed pre-meiotically in spermatogonia, *Fmr1* and *Fmr1nb* show expression in early prophase I, and *Ctag2*, *4930447F04Rik* and *Slitrk2* are expressed in meiotic and postmeiotic cells. Finally, *4933436I01Rik* is expressed in haploid cells. Sorted populations of testicular cells from PWD and B6 strains and immature 14.5 dpp tests of their reciprocal hybrids did not show significant differences in relative mRNA expression levels of six meiotic and/or postmeiotic genes (Fig. S3). All 20 miRNAs in the candidate region are expressed in male germ cells but do not undergo meiotic sex chromosome inactivation (MSCI) [34]. Only the *Mir465* cluster displayed a significant increase of expression in the first meiotic prophase of PWD and B6 sorted testicular cells (Figure 3A, B). The miRNA expression profiling of sterile (PWD×B6)F1 and fertile (B6×PWD)F1 14.5dpp tests showed 1.5- to 2-fold upregulation of *Mir880-5p*, *Mir465a/b-3p* and *Mir465b-5p* in sterile males, while *Mir743a*, *Mir743-5p*, *Mir880* and *Mir465c-3p* showed 1.2- to 4-fold down-regulation (Figure 3C, D).

Re-sequencing candidate genes from PWD genomic DNA and BAC clones [35] and inspection of the PWD exome sequence revealed seven non-synonymous substitutions of the 4933436I01Rik PWD allele compared to B6 (see also [36]). Of the remaining genes, *Aff2* carries five, *Fmr1nb* and *Slitrk2* carry two, *4930447F04Rik* and *Ctag2* carry one, and *Fmr1* does not carry any non-synonymous substitution. Inspection of Sanger Institute Mouse Genome Project (http://www.sanger.ac.uk/resources/mouse/genomes/) confirmed the same SNPs for PWK, a closely related *Mmm* inbred strain. Search of miRNA sequences revealed one SNP in the seed sequence of *Mir743a*, changing AAAGACA in B6 to AAAGAGC in PWD (Table 1).

Reproductive isolation genes in *Drosophila* and in mouse have been shown to evolve rapidly and to undergo positive selection [37–39]. Three of the candidates for the *Hstx1* locus, *Ctag2*, 4933436I01Rik and *Fmr1nb*, displayed an elevated rate of protein evolution (Table 1). In particular, 4933436I01Rik is among the most rapidly evolving genes on Chr X [40,41], showing weak but significant expression in primary spermatocytes and strong postmeiotic expression [42], https://www.genevestigator.com/gv/). *Fmr1nb*, another possible candidate, shows high expression in pre-pachytene spermatocytes [43].

**Intrasubspecific autosomal polymorphisms suppress asymmetry of HS**

The ability of *Hstx2<sup>B6</sup>* to rescue the meiotic arrest of *Mmm×Mmd* F1 hybrids is subject to intrasubspecific *Mmm* polymorphisms. While asymmetric male sterility of (PWD×B6)F1 hybrids depends on the presence of the *Hstx2<sup>PWD</sup>* allele, another inbred strain derived from *Mmm*, known as STUS produces fully sterile F1 hybrid males with B6 mice regardless of the direction of the cross [44]. To map the STUS/PWD autosomal allele variants that ensure full intrameiotic arrest in males carrying *Mmm* Chr X<sup>B6</sup>, we genotyped 84 test-cross males from crosses of B6 females with (PWD×STUS)F1 or (STUS×PWD)F1 males. QTL analysis of the sperm count (binomial, sperm cells present or absent) revealed QTLs on Chr

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**Figure 2. Fine mapping of Hstx1 and Hstx2 HS loci on Chr X using partial consomic strains.** The partial consomic B6.PWD-Chr X.# x B6 and B6.PWD-Chr X.# x PWD strains were crossed with B6 or PWD males for mapping in a test and hybrid, respectively. Tests weight and sperm count were used as fertility phenotypes. The borders of introgressed PWD sequence (black) were determined by MegaMUGA genotyping for B6.PWD-Chr X.1 (abbreviated here X.1), B6.PWD-Chr X.1s (X.1s) and B6.PWD-Chr X.2 (X.2). For B6.PWD-Chr X.3 (X.3) mapping see (20). The map positions correspond to genome assembly GRCm38, megabase scale, for details see Table S1. doi:10.1371/journal.pgen.1004088.g002
3, Chr 9 and Chr 13, while QTL for the testes weight mapped on Chr 3 and Chr 13 (Fig. 4). The reciprocal cross of (STUS x PWD) females with B6 males yielded only sterile male offspring without sperm in ductus epididymis (Table S3), strongly indicating that these autosomal QTLs interact with Mmm Chr XB6. Several interesting candidate genes with meiotic functions have been found in these QTL regions, including Hormad1, Sycp1, H2afx or Msh3 (Table S4). Admittedly, 1.5-LOD support intervals of the QTLs proved quite large and none of the selected candidates displayed a dN/dS ratio indicative of their rapid evolution. 

Hstx2 affects meiotic pairing and spermatogenic differentiation

The meiotic arrest of (PWD x B6)F1 hybrid males is associated with failure of proper synopsis of homologous heterosubspecific autosomes, delay of DNA double-strand break (DSB) repair on unsynapsed autosomes and dysregulation of meiotic sex chromosome inactivation (MSCI) at the first meiotic prophase. However, full fertility and complete autosomal synapsis is restored when Chr 17 is PWD/PWD consubspecific on otherwise PWD/B6 F1 background [22]. Here we focused on the fertility parameters and

Figure 3. Expression profiling of a cluster of MiRNA genes within the Hstx1/Hstx2 critical region. (A) Log fold-change of expression ratio of PWD versus B6 MiRNA genes in flow-sorted testicular cells. Significant overexpression of Mir465 cluster in PWD germ cells is shown in red. (B) Validation of Mir465 overexpression in PWD primary spermatocytes by qRT PCR. Data normalized to U6 non-coding RNA (C) Log fold-change of expression ratio of MiRNA genes in (PWD x B6)F1 versus (B6 x PWD)F1 (abbreviated PB6F1 and B6PF1) 14.5 d old testes. Significant upregulation in red (P < 0.05). (D) qRT PCR validation of differences in Mir465 expression. Data normalized to Mir152. doi:10.1371/journal.pgen.1004088.g003
pachytene chromosome synapsis in F1 hybrid males differing at the \(Hstx2\) locus (Fig. S4A–E). The \(Hstx2^{PWD}\) allele in (B6.PWD-Chr X.1s×PWD) hybrid males ensured full sterility, meiotic arrest at mid-late pachynemas, almost absent diplotype spermatocytes and a lack of sperm. Immunostaining of SYCP3 and SYCP1, components of lateral and central elements of synaptonemal complexes or HORMAD2 protein revealed unsynapsed autosomes in 90% of pachynemas of both, (PWD×B6) and (B6.PWD-Chr X.1s×PWD) F1 hybrid males. The super-resolution structured illumination microscopy documented irregular spots of SYCP1 on some univalents and nonhomologous synapsis and/or translocations (Fig. 5), resembling “tangles” observed in pachynemas with reduced frequency of DSBs \([45]\). In contrast, (B6.PWD-Chr X.1×PWD) males carrying \(Hstx2^{B6}\) were semifertile, with partial meiotic arrest at late pachytene stage. Only 34% of pachynemas showed asynapsis of one or two pairs of autosomes (Fig. S4A–E). It can be concluded that in F1 hybrid males the \(Hstx2^{B6}\) allele partially restores fertility and significantly reduces the frequency of pachynemas with asynapsis and the number of unsynapsed autosomes per cell.

To test whether the occurrence of meiotic asynapsis is not limited to the (PWD×B6) strain combination, we checked chromosome synapsis in pachytene spermatocytes of (STUS×B6)F1 and (PWD×SCHEST)F1 hybrids. SCHEST is a wild-derived strain of \(Mmd\) (J.P., unpublished). Both F1 hybrids were sterile, showing no sperm (STUS×B6) or few sperm (PWD×SCHEST, \(<0.9\) mil.) in ductus epididymis. In both cases >90% of pachytene spermatocytes revealed multiple pairs of unsynapsed autosomes (Fig. S4A, B). Thus, asynapsis in \(Mmm×Mmd\) intersubspecific hybrids is a more general phenomenon, not confined to the incompatibilities between B6 and PWD genome.

### Table 1. Missense SNPs of candidate genes in the \(Hstx1/Hstx2\) critical region on Chr X.

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<th>Gene Symbol</th>
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- SNPs for protein coding genes were extracted from the PWD exome sequence compared to B6 reference genome (GRCm38) and confirmed by classical re-sequencing.
- PWK SNPs were obtained from Sanger Institute Mouse Genome Project.
- Rate of protein evolution is based on one to one comparison with rat orthologs. (GRCm37).

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**Hybrid Sterility X2 Controls Meiotic Synapsis**

**Hstx2 and Hst1/Prdm9 regulate male but not female asynapsis of heterosubspecific homologs**

Asynapsis preferentially affects autosomal pairs with heterosubspecific homologs, and their pairing failure is strongly influenced by the \(Prdm9\) and \(Hstx2\) genes in sterile hybrid males (\([22]\) and above). We asked whether the genetic control of meiotic asynapsis differs between male and female gametogenesis of intersubspecific hybrids. The pachytene chromosome asynapsis was not observed in PWD and B6 spermatocytes, but occurred in 14% and 29% of pachytene oocytes of the same genotype. In (PWD×B6)F1 hybrid females, 47.5% of pachynemas showed asynapsis, but contrary to the F1 hybrid males the frequency of asynaptic oocytes was not dependent on the \(Prdm9\) and \(Hstx2\) genotypes (\([22]\) and above). The conclusion was reached from the comparison of male and female meiosis in hybrids between particular consomics and PWD. Thus, 46% of (PWD×B6)F1 pachytene oocytes displayed asynapsis that was completely absent in spermatocytes of the same genotype. Moreover, 46.5% and 44% of oocytes of (B6.PWD-Chr X.1×PWD)F1 and (B6.PWD-Chr X.1s×PWD)F1 hybrids showed asynaptic autosomes (Fig. 6B), compared to 34.1% and 96.4% of pachynemas of the corresponding male genotypes. It can be concluded that contrary to male meiosis, Chr 17 and \(Hstx2\) do not change the overall frequency of asynaptic pachynemas in female meiosis of intersubspecific hybrids. However, detailed analysis of female hybrids consubspecific for Chr 17\(^{PWD}\) showed a lower frequency of asynapsis.
number of unsynapsed autosomes per cell ($p<0.01$) when compared with the other intersubspecific F1 hybrid genotypes (Fig. 6C). Thus, *Prdm9/Hst1* and/or some other genes on Chr 17 exert a limited effect on asynapsis in female hybrids as well. The elevated incidence of asynaptic oocytes predetermined to elimination in intersubspecific ovaries was reflected by a reduced ratio of diplotene/pachytene oocytes in ovarian cell spreads (Fig. 6D).

**Heterosubspecific but not consubspecific homologs are sensitized to asynapsis in female intersubspecific hybrids as well**

We have shown that consubspecific (PWD/PWD) homologous autosomes evade asynapsis in otherwise heterosubspecific (PWD/B6) genomic background of hybrid males. The finding indicated a *cis*-type of asynapsis control based on some kind of mismatch between orthologous chromosomes of *Mmm* and *Mmd* origin [22]. Considering the difference between male and female hybrids in the overall frequency of asynapsis and the male-limited effect of HS genes we asked whether the mismatch of heterosubspecific homologs lowering their synapsis efficiency also operates in female meiosis.

For this purpose we analyzed primary oocytes of female hybrids between PWD and chromosome substitution strains carrying Chr 17$^{PWD}$, Chr X$^{PWD}$ or Chr X.1$^{sPWD}$, respectively. We compared the efficacy of meiotic synapsis of consubspecific (PWD/PWD) Chr 17 and Chr X homologs with matching heterosubspecific pairs in (PWD$\times$B6)F1 pachytene oocytes and oocytes from the parental controls. Using the whole-chromosome DNA FISH we also visualized Chrs 2, 16, 18, 19 and X. In (PWD$\times$B6)F1 pachynemas Chr 2 showed the lowest incidence of asynapsis. The frequency of univalents of small autosomes 16, 17, 18 and 19 varied between 18% and 49% in asynaptic pachytene oocytes. Strikingly, Chr X displayed the highest frequency (64%) of asynapsis (Table 2).

The asynapsis of consubspecific Chr 17$^{PWD/PWD}$ homologs dropped to zero in (PWD$\times$B6)$^{PWD}$F1 oocytes, although the total frequency of pachynemata with asynapsis was the same as in (PWD$\times$B6) hybrids. In (PWD$\times$B6)$^{PWD}$-Chr X.1sF1 oocytes, 69.9 Mb of the centromeric part of Chr X was consubspecific for the PWD sequence, while the end of the chromosome, 101.4 Mb in length, was PWD/B6 heterosubspecific. Nevertheless, the partial PWD homozygosity was sufficient to reduce Chr X asynapsis from 64% down to 5.6% of pachytene oocytes (Table 2). It can be concluded that asynapsis in intersubspecific female and male hybrids follows the same rule, depending on yet unspecified sequence incompatibility between individual homologs of *Mmm* and *Mmd* origin.

**Pursuing the dominance theory of Haldane’s rule**

To explain Haldane’s rule of hybrid sterility, the dominance theory posits the recessive nature of X-linked variants that disrupt
Gametogenesis in hemizygous (XY) but not in homozygous (XX) sex [9]. In its most straightforward interpretation the F1 hybrid females should be sterile in the same way as their hemizygous male sibs if their genotype were made homozygous for an incompatible Chr X variant. We constructed such genotype by crossing consomic females B6.PWD-Chr.X.1s with PWD males. The resulting female hybrids were PWD/B6 heterosubspecific for the whole autosomal genome but consubspecific for proximal 69.9 Mb of Chr XPWD, encompassing the \textit{Hstx1/2} hybrid sterility locus. Contradicting the simple interpretation of Muller’s dominance hypothesis the (B6.PWD-Chr.X.1s×PWD)F1 hybrid females were fully fertile, as were the parental controls (Table S5). However, the results were concordant with the testis-specific function of \textit{Hstx2} \textsuperscript{PWD}. Thus, to follow the dominance theory, the

Figure 5. Super-resolution microscopy of synaptonemal complexes on spreads of (B6.PWD-Chr X.1s×PWD) pachytene spermatocytes. (A) Detail of a pachytene spermatocyte of a sterile male immunostained by SYCP3 (red) and SYCP1 (green) antibodies. Properly synapsed bivalents (arrows) show two parallel threads of transverse filaments decorated by SYCP1 antibody which form the central region embedded in SYCP3 lateral elements. Unsynapsed chromosomes lack transverse filaments but display some irregular SYCP1 spots (arrowheads). (B) Example of a nonhomologous pairing and/or translocations, and asynapsis in pachynema of (B6.Chr X.1s×PWD)F1 sterile male. Bar 2000 nM.
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preponderance of male-limited HS in species with heterogametic sex could be explained by a predominance of recessive, compared to dominant, mutations of HS genes and their male-limited expression. Admittedly, the latter premise is in conflict with HS obeying the Haldane’s rule in birds and Lepidoptera.

Discussion

The role of Hstx2 in F1 hybrid sterility

Disproportionate involvement of Chr X in HS has been well documented in classical studies of Drosophila hybrids (for review see [46,47]) and repeatedly reported in hybrids of the house mouse subspecies [27,33,36,48]. The introgression of Chr X PWD of M. m. molossinus into M. m. domesticus genetic background resulted in abnormal sperm morphology and inability to fertilize eggs. This phenotype is controlled mainly by the Hstx1 locus supported by additional loci on Chr X [33]. With the aim to positionally clone the Hstx2 gene we narrowed down the critical region to a 4.7 Mb interval (Chr X: 64.88 Mb–69.58 Mb) and showed that it also carries the Hstx1 locus. In contrast to Hstx1 phenotype, the intrameiotic arrest is controlled from a single Hstx2 locus on Chr X. The Hstx2/Hstx1 critical interval is overlapped by and may be identical with the 8.4 Mb QTL responsible for the sterilizing effect of M. m. molossinus Chr X PWD introgressed into the genetic background of M. m. domesticus inbred strain [30]. Using the position on Chr X, spermatogenic expression, and dN:dS ratio Good and coworkers [41] predicted nine candidate genes for X-linked hybrid sterility, three of which (Ctag2, 4933436I01Rik and Fmr1nb) also occur in the present list of Hstx1/2 candidates. Moreover, the Sha2 locus of the Japanese house mouse Mus m. molossinus [49], potentially identical with Hstx1, maps to the same interval. Sha2 is responsible for spermiogenic arrest in B6 males carrying Chr X M. m. molossinus.

Figure 6. Meiotic asynapsis in female hybrids. Abbreviations of consomic strains and their hybrids: DX.1 – B6.PWD-Chr X.1; DX.1PF1 – (B6.PWD-Chr X.1×PWD)F1; DX.1sPF1 – (B6.PWD-Chr X.1s×PWD)F1; DX.1B6F1 – (B6.PWD-Chr X.1×B6)F1; DX.1sB6F1 – (B6.PWD-Chr X.1s×B6)F1; DX.1sD17F1 – (B6.PWD-Chr X.1s×B6.PWD-Chr 17)F1; D17B6F1 – (B6.PWD-Chr 17×B6)F1; B6PF1 – (B6×PWD)F1; PB6F1 – (PWD×B6)F1; PD17F1 – (PWD×B6.PWD-Chr 17)F1. (A) Chromosome synapsis in pachytene oocytes of B6 and (B6.PWD-Chr X.1s×PWD)F1 18.5–19.5 dpc female fetuses was analyzed by combination of SYCP1, SYCP3 and CREST (centromeric heterochromatin) immunostaining or by HORMAD2 and SYCP3 to detect unsynapsed chromosomes. Bar, 10 μm. (B) The frequency of oocytes showing one or more asynaptic chromosomes is similar (>40%) irrespective of Hstx2 and Prdm9/Hst1 genotype. (C) Although the (PWD×B6), (B6.PWD-Chr X.1×PWD), (B6.PWD-Chr X.1×PWD) and (B6.PWD-Chr 17×PWD)F1 hybrid females do not differ in percentage of pachytene oocytes with asynapsis, the (B6.PWD-Chr 17×PWD)F1 females, conspecific for Chr 17 PWD, carry significantly less asynapsed chromosomes per cell. (D) The frequency of diplonemas in spread oocyte preparations was significantly lower (p<0.01, χ2 test) in intersubspecific hybrids than in parental inbred strains.
introduction [49]. Among the candidate genes in the region, 
*Fmr1* and 4933436I01Rik are expressed in the appropriate cell
type during germ cell differentiation and display two and seven
non-synonymous substitutions, respectively. The critical region
also contains the *Mir465* cluster of miRNA genes, which show a
significant difference in expression between reciprocal F1 hybrids.
Moreover, *Mir743a* carries a single SNP in its seed sequence.
Admittedly, the *Hst1/Hst2* candidate region is still too large to
finalize the list of *Hst2*/Hst1 candidate genes. Recently, many
ampliconic genes on the mouse and human Chr X were shown to
be unique for a given species and expressed predominantly in
testicular germ cells [50]. These features make them potential
candidates for reproductive isolation genes. The *Hst1/Hst2*
critical region is flanked by amplicons 4930527E24Rik and *Xlr*
(amplicons 7 and 9 in [51]). However, none of the candidate
protein-coding genes or *Mir* genes is located within a known
amplicon and all protein-coding candidates have an ortholog in
other mammalian species.

The incompatible alleles of major HS loci are not fixed to homozygosity within *Mmd* and *Mmm* subspecies, in agreement with the idea of the early stage of their speciation. *Hst1/Prdm9* is polymorphic for “sterility” and “fertility” alleles in natural populations and in inbred strains [23,44,52] and the same is true for the X-linked HS QTLs [44,53]. The asymmetric contribution of *Mmm* and *Mmd* genomes to HS of reciprocal hybrids reveals polymorphic control as well. Chr X<sup>39</sup> causes meiotic arrest depending on PWD/STUS polymorphic modifiers on Chrs 3, 9 and 13.

The proximal part of Chr X carries loci for major incompati-
labilities also outside the *Mus musculus* group of mouse subspecies. Introgression of Chr X of *Mus spretus* into B6 inbred strain reduced tests weight and fertility [54], with the largest LOD score mapping approximately 10 Mb proximal to the *Hst1/Hst2* region. The males were semi-fertile, with many tubules containing normally developing spermatozoa but some tubules completely devoid of germ cells. The testes of (*Mus domesticus*×B6) F1 hybrid males displayed premeiotic block with Sertoli cells and dividing spermatogonia. The QTL analysis of a backcross population revealed two major loci, again on Chr 17 and Chr X, but with positions distal to *Prdm9* and to *Hst1/Hst2* loci, respectively [55]. These crosses confirmed the large X-effect in mice but did not reveal common HS genes beyond the group of mouse subspecies.

Laboratory crosses of wild-derived inbred strains continue to reveal new details about the genetic control and mechanistic basis of hybrid sterility, but their direct role in speciation is less clear. In an alternative approach, evolutionary biologists collect wild mice from the house mouse hybrid zone to analyze the introgression of (sub)species-specific DNA markers. Because this approach can reflect all kinds of incompatibilities restricting the gene flow, the results are usually complex, uncovering multiple regions on autosomes and Chr X. Nonetheless, at least two common themes have emerged from the field data and laboratory crosses, namely the large X-effect and a specific role of 60 Mb–80 Mb interval of Chr X in reproductive isolation of *Mmm*/*M. m. molossinus* and *Mmd* [16,17,56,57].

### The role of meiotic chromosome asymmetry in intersubspecific reproduction barrier

More than 90% of primary spermatocytes of sterile *Mmm×Mmd* F1 hybrids fail to synapse properly their chromosomes at the pachytene stage of meiosis. Unsynapsed autosomes carry DMC1/ RAD51 foci on unrepaired DSBs and are decorated by the phosphorylated form of histone H2A.FX. The sex body containing X and Y chromosomes is often malformed or disappears, and transcriptional inactivation of sex chromosomes (MSCI) is disrupted [22,58]. Such failure of chromosomes to synapse can be under <i>trans</i>- or <i>cis</i>-control. Mutations of various meiotic genes involved directly or indirectly in meiotic chromosome pairing and synapsis cause asymmetry of multiple autosomes in <i>trans</i> [59]. A null allele of the *Prdm9* gene on *Mmd* background causes male and female sterility associated with synapsis and failure to form the sex body [60], the phenotype similar to sterile *Mmm×Mmd* hybrids [22,24]. Null mutations of *Syf1*, *Hormad1* or *Mrd4*, the candidate genes regulating the *Hst2*-controlled asymmetry of HS, also cause asymmetry. Contrary to genes acting in <i>trans</i>, certain structural mutations of chromosomes such as translocations or inversions can cause local, <i>cis</i>-acting asymmetry, followed by meiotic arrest and sterility [43,61–63]. To distinguish between the <i>trans</i>- and <i>cis</i>-control of asymmetry in sterile *Mmm×Mmd* males, we modified the F1 hybrids using the intersubspecific chromosome substitution strains B6.PWD-Chr17F1 [20]. In (B6.PWD-Chr17F1×PWD)F1 hybrids we compared the ability of consubspecific and heterosub-
specific (PWD/PWD vs PWD/B6) chromosomes to synapse on otherwise F1 hybrid background. These experiments clearly showed that asymmetry is regulated primarily in <i>cis</i>, because heterosubspecific chromosome pairs in male as well as in female meiosis were more prone to failure to synapse. The sensitivity of heterosubspecific chromosome pairs to asymmetry was strongly modified in <i>trans</i> by the *Prdm9* and *Hst2* HS genes because only
**Haldane’s rule and male-specific effect of Hstx2<sup>PWD</sup> in mouse hybrids**

Hybrid sterility affects preferentially heterogametic sex, males in *Drosophila* or mammals, and females in birds and *Lepidoptera*. Several hypotheses have been proposed to explain Haldane’s rule, including the dominance theory, the faster-male theory, the faster X theory and meiotic drive [47]. According to Muller’s dominance theory, Haldane’s rule can be explained by hemizygosity of the X (Z) chromosome in the heterogametic sex. Both, recessive and dominant X (Z)-linked HS genes could control HS in heterogametic sex, but only dominant HS genes could stabilize the homogametic sex. Using attached-X chromosome, Coyne and others tested the prediction by making *Drosophila* hybrid females homozygous for the recessive-acting X chromosome. In *D. simulans* <i>x</i> <i>D. mauritiana</i> or <i>D. sechellia</i> hybrids the female hybrids carrying two <i>D. simulans</i> Chr X were fertile, contrary to the prediction for review see [47] and references therein). The authors argued that because HS genes are male specific, suggesting extra development sensitivity of spermatoogenesis relative to oogenesis, their recessive forms manifest DMI in male but not in female gametogenesis. Indeed, the mouse *Hst1*/*Pdm9* and *Hstx2* are also male-specific HS loci, therefore not contradicting the fertility of female *MmmxMnd* F1 hybrids homozygous for the *Hstx2<sup>Mmm</sup>*(allele. To accommodate the dominance theory with X-linked, male-specific HS genes, their recessive nature could be tested by a dominant transgene from the *Mmm* subspecies.

**A mechanistic model of F1 hybrid sterility**

We propose a mechanistic model of HS based on the assumption that cis-controlled pachytene asynapsis is the primary cause of apoptosis of primary spermatocytes and sterility in intersubspecific hybrids of the house mouse (Fig. 7). We have found that the number of unsynapsed autosomes per cell varies, indicating that the same type of cis-acting mechanism operates on individual autosomes. Although the molecular mechanism of homologous chromosome recognition during meiotic pairing and asynapsis is unknown in mammals, one possibility is that fast evolving noncoding DNA and/or RNA sequences interfere with homology search of single-strand 3’ends on heterosubspecific homologs during DSB repair, thus interfering with their synapsis during the first meiotic prophase (see also [45]). Alternatively, the process of homolog recognition can be affected earlier, before meiotic recombination begins.

The male-specific action of the *Hstx2* or *Pdm9*/*Hst1* HS genes could explain why the same perturbation of sequence homology acts differently in male and female meiosis. While in female pachynemases the percentage of meiocytes with asynaptic homologs are still unknown, our assay of meiotic synapsis, comparing the consubspecific versus heterosubspecific pairing homologs, offers a genetic approach to solving the problem. Such experiments are in progress.

**Materials and Methods**

**Animals and ethics statement**

The animals were maintained at the Institute of Molecular Genetics in Prague and Institute of Vertebrate Biology in Studenec (Academy of Sciences), Czech Republic. The project was approved by the Institutional Animal Care and Use Committee of the Institute of Molecular Genetics, AS CR, protocol No. 141/2012. The principles of laboratory animal care (NIH Publication No. 85-23, revised 1985) as well as specific Czech Law No. 246/1992 Sb. compatible with the corresponding EU regulations and standards, namely Council Directive 86/609/EEC and Appendix A of the Council of Europe Convention ETS123, were observed.

C57BL/6J [B6, mostly *M. m. domesticus*) originated from The Jackson Laboratory (Bar Harbor, ME). The PWD/Ph (PWD) and STUS strains were derived from wild *M. m. musculus* [32,53]. The chromosome substitution (conosomic) strains C57BL/6J-*Chr #6*<sup>PWD</sup> [20], abbreviated here B6-PWD-Chr #, were maintained in a pathogen-free barrier facility with a 12 h light/12 h dark cycle. The mice had ad libitum access to a standard rodent diet (VELAZ, ST-1, 3.4% fat) and acidified water. All males were sacrificed at the age of 60 to 70 days.

**Genotyping, phenotyping and histology**

All 124 male mice from (B6-PWD-Chr X*B6*F1×PWD cross and 71 male progeny from (B6-PWD-Chr X*B6*F1x B6 cross were genotyped using SSLP Chr X markers listed in Table S6. Genomic DNA from mouse tails and spleens was prepared by the HotSHOT method [64] followed by phenol-chloroform cleaning [65]. For genotyping B6-PWD-Chr X*#* partial conosomics and 84 males of B6×(PWD×STUS) test-cross we used MegaMUGA high-density genotyping array carrying 77,000 markers on Illumina Infinium Platform (http://csbio.unc.edu/CCstatus/index.php).

Eight weeks old male progeny of the crosses were phenotyped for testes weight (TW), sperm count (SC) and percentage of abnormal spermatozoas as described [33]. The B6×(PWD×STUS) males were phenotyped at 60 days of age as described [44]. For histological analysis the paraffin-embedded testicular sections were stained with periodic acid Schiff and hematoxylin-eosin and observed using a Nikon Eclipse 200 microscope. The Penguin 150CL CCD color camera (Pixera) was used to capture photographs, which were processed using Adobe Photoshop (Adobe Systems).

**QTL analysis**

QTL mapping of recombinant males from (B6-PWD-Chr X*B6*F1×PWD and B6×(PWD×STUS) crosses was performed using the R 12.1 and its R/qtl package [66] Marker positions were taken from MGI mouse genetic map [67]. Standard interval mapping was implemented using *scancme* function. TW and logSC were modeled as continuous variables, fertility/sterility as a binary variable. Genotype probabilities between markers were calculated at a grid size of 5 cM and with genotyping error rate of 0.01%. Genome-wide significance was calculated by 1000 permutations and compared to a 5% threshold.
Fluorescence-activated cell sorting of spermatogenic populations

Three spermatogenic populations (leptotene+zygotene+early pachytene, mid-late pachytene+diplotene, and spermatids) were isolated using fluorescence-activated cell sorting (FACS) as described earlier [43,68] from PWD and B6 testes. The cells were directly sorted into QIAzol lysis reagent of the miRNeasy Mini isolation kit (QIAGEN). Small aliquots of cells were sorted in Krebs-Ringer bicarbonate medium for indirect immunofluorescence analysis. The population composition was estimated by staining with anti-SYCP3, anti-SYCP1, anti-γH2AFX antibodies (details below) and DAPI (Vectashield). All sorted populations showed 85–90% purity of the desired cell type.

Microarray miRNA and protein-coding gene transcription analysis and qRT-PCR validation

Total RNA was isolated from sorted cells and 14.5 dpc testis using the miRNeasy Mini isolation kit (QIAGEN) as recommended. RNA concentration was determined by NanoDrop (NanoDrop Technologies) and its integrity checked in Agilent 2100 bioanalyzer, RNA Lab-On-a-Chip (Agilent Technologies). The total RNA (20–30 ng for gene expression and 120 ng for miRNA expression) was converted to cRNA using the Affymetrix Two-Cycle Target Labeling kit according to the manufacturer’s instructions or using the Affymetrix 3’ IVT Express Kit. Affymetrix GeneChip Mouse Genome 430.2.0 array, and Affymetrix GeneChip miRNA 1.0 Array was hybridized with...
cRNA. The data obtained from the experiments were analyzed using Bioconductor [69] (http://www.bioconductor.org/) and the R project for statistical computing (version 2.12; http://www.r-project.org/). The probes were annotated to Ensembl gene identifiers using the custom chip description file, which was based on NCBI build 37. The data were normalized using RMA (Affymetrix GeneChip Mouse Gene 1.0ST Array) and quantile normalization (Affymetrix GeneChip miRNA 1.0). We used Linear Models for Microarray Data Package, limma version 3.6 [70] for statistical evaluations of expression differences as described [22]. The microarray dataset is deposited in the NCBI Gene Expression Omnibus (GEO) with series accession number GSE41707 [22] GSE49442 and GSE49443. Expression of different X-linked protein-coding genes on spermatogenic populations were derived from NCBI GEO profiles or NCBI GEO database GSE7306 [43] and GSE49444.

For qRT-PCR of protein-coding genes, reverse transcription of isolated RNA samples was carried out using Applied Biosystems (ABI) high-capacity cDNA reverse transcription kit. The quantification of miRNAs was performed using FastStart DNA Master SYBR Green I kit (Roche) and amplified in LightCycler 2000 (Roche). Reactions without reverse transcriptase were utilized as negative control. The assays were done in biological and technical triplicates. The data were analyzed using LightCycler Software version 3.5.3 (Roche). For validation of miRNA expression we used ABI TaqMan MicroRNA assays and followed the manufacturer's instructions. The reactions were cycled in Applied Biosystems 7300 Real-time PCR system, and associated software was used for data analysis. The reactions were also carried out using biological and technical triplicates and proper negative controls. The highest and stably expressed miRNAs, U6 non-coding RNA for sorted cells and Mir152 for 14.5 dpc testis, were used as the reference for data normalization. The primers were designed using Primer 3 software (http://frodo.wi.mit.edu/). Sequences of primers are given in Table S6.

**Sequencing, SNP and PWD exome analysis**

Exome sequence analysis was carried out for PWD/Ph mice at BGI Europe using Illumina HiSeq 2000 sequencers. The PWD exome sequence was aligned to NCBI build 37. The data were normalized using RMA (Affymetrix GeneChip Mouse Gene 1.0ST Array) and quantile normalization (Affymetrix GeneChip miRNA 1.0). We used Linear Models for Microarray Data Package, limma version 3.6 [70] for statistical evaluations of expression differences as described [22]. The microarray dataset is deposited in the NCBI Gene Expression Omnibus (GEO) with series accession number GSE41707 [22] GSE49442 and GSE49443. Expression of different X-linked protein-coding genes on spermatogenic populations were derived from NCBI GEO profiles or NCBI GEO database GSE7306 [43] and GSE49444.

**Immunostaining and DNA FISH of spread meiocytes**

The meiocyte spreads were prepared by using the hypotonic protocol as described earlier [21,71]. The nuclei were immunostained using following primary antibodies; rat polyclonal anti-SYCP3 (Abcam, #15092), mouse monoclonal anti-SYCP1 (Abcam, #15087), guinea pig anti-histone linker H1t [72], human autoimmune anti-centromere (AB-Incorporated, #15-235), mouse monoclonal anti-hH2AFX (Upstate, #05-636), mouse monoclonal antibody anti-SYCP3(3-D1) (Santa Cruz #74569), rabbit polyclonal antibody HORMAD2(C-18) (Santa Cruz #82192) and the secondary antibodies: goat anti-Rabbit IgG-AlexaFluor488 (Molecular Probes, A-11034), goat anti-Mouse IgG-Alexa Fluor 568 (Molecular Probes, A-11031), goat anti-Rabbit IgG-Alexa Fluor 568 (Molecular Probes, A-11036), goat anti-Mouse IgG-Alexa Fluor 350 (Molecular Probes, A-21049), goat anti-Mouse IgG-Alexa Fluor 647 (Molecular Probes, A-21236), goat anti-Rabbit IgG-Alexa Fluor 647 (Molecular Probes, A-21245) and goat anti-Guinea pig IgG-Cy3 (Chemicon, #AP108C). The immunolabeled meiocytes were subjected to DNA FISH using Metasystems XMP XCYting Mouse Chromosome N Whole Painting Probes for Chr 2, 16, 17, 18, 19 and X as described [73]. The images were acquired using a Nikon Eclipse 400 (Tokyo, Japan) microscope with motorized stage control using a Plan Fluor objective, 60× (Nikon, MRH00601) and captured using a DS-QiMc monochrome CCD camera (Nikon) and NIS elements program. The fluorescent intensity of images was adjusted using Adobe Photoshop CS software (Adobe Systems). For super-resolution microscopy the meiotic spreads were examined with the Zeiss Axioimager Z.1 platform equipped with the Elyra PS.1 super-resolution system for SR SIM and the LSM780 module for CLSM, using Alpha Ph Azo 63×/1.40 oil Zeiss objective (total magnification 1008×) with appropriate oil (Immorsol 518F, by Zeiss). SR-SIM setup was rotation and 5 phases for each image layer. Up to 7 (usually 3) 110 nm Z-stacks were acquired per image. Staging of meiotic prophase I in males and females were done as described earlier [22].

**Statistics**

Multiple biological replicates of each genotype were analyzed for cellular phenotypes and RNA expression. The significance of body weight, testes weight, sperm morphology and breeding phenotypes was computed using Welch's t-test. Sizes of chromatin areas covered by the hybridization signal in synapsed and unsynapsed autosomes were compared by Analysis of Variance (ANOVA) with Tukey's correction for multiple testing. Differences between cellular phenotypes were determined with χ² test. All computations were done using R 2.15.0 or Graphpad Prism (http://www.graphpad.com/scientific-software/prism/#1).

**Supporting Information**

**Figure S1** Mapping of Hstx1 locus on Chr X. The fertility of males with PWD/B6 single recombination declined with the recombination breakpoints in the interval DXMit76 (64.75 Mb) and DXMit143 (69.28 Mb), indicating the position of the Hstx1 gene. (EPS)

**Figure S2** Gene map of the Hstx2/Hstx1 critical region on Chr X. Predicted genes and pseudogenes are not included in this map. See text for details. (EPS)

**Figure S3** Expression profiling of protein-coding genes within Hstx1/Hstx2 critical region. (A) Log fold-change of expression ratio of PWD versus B6 protein-coding genes in flow sorted testicular cells. Data from Affymetrix GeneChip Mouse Gene 1.0ST Array do not show any significant differences between both strains in expression levels in primary spermatocytes. Abbreviations: Z-EP – Zygotene Early Pachytene, M-LP – Mid-Late Pachytene, ST – Spermatids. (B) qRT PCR of expression levels of six candidate genes in testes of 14.5 d reciprocal F1 hybrid males (PWD×B6)F1 and (B6×PWD)F1. None of the differences is significant. (EPS)

**Figure S4** The effect of Hstx2 on spermatogenic differentiation and synopsis of meiotic chromosomes. (A) Histological crossovers
of spermatogenic tubules of B6 control and (B6.PWD-Chr X.1×PWD)F1, abbreviated here DX.1PF1, and (B6.PWD-Chr X.1s×PWD)F1, abbreviated DX.1sPF1 hybrids. Note the vacuolar degeneration, heteropycnotic cells and absence of sperm cells in DX.1sPF1 hybrids. (B) Unsynapsed autosomes and sex chromosomes visualized by HORMAD2 and SYCP3 immunostaining. Early pachynemmas with high and low frequency of autosomal univalents are shown. (C) Frequency of primary spermatocytes at various stages of meiotic progress in males of different genotype. (PWD×B6)F1, abbreviated PB6F1, and (B6.PWD-Chr X.1×PWD)F1 (abbreviated DX.1sPF1) sterile males display the same profile of primary spermatocyte stages. (D, E) Frequency of pachynemmas with asynapsis and number of unsynapsed autosomes per cell are similar in PB6F1 and DX.1sPF1 sterile males. In DX.1PF1 males asynapsis occurs with lower frequency and the pachynemmas with asynapsis have lower number of univalents.

**Figure S3** Pachytene asynapsis in sterile F1 hybrid males prepared by different combinations of *Mus musculus* and *M. m. domesticus* inbred strains. (A) Over 90% of pachytene spermatocytes in all three strain combinations (PWD×B6)F1 – abbreviated PB6F1, (STUS×B6)F1 – STB6F1 and (PWD×SCHEST)F1 - PSCHF1) carry one or more asynapsed chromosome pair. Frequency of asynapsis of four analyzed autosomes varied between genotypes. Average number of univalents per cell was highest in PSCHF1 and lowest in PB6F1. (B) Distribution of pachynemmas with a given number of unsynapsed chromosome pairs. Asynapsis varies widely within each genotype. A significant excess of cells with one unsynapsed pair occurs in PB6F1 hybrids.

**References**


**Table S1** Coordinates of the introgressed PWD sequence in B6.PWD-Chr X subconsomics (GRCmm38).

**Table S2** Meiotic stages of adult testes of B6.PWD-Chr.X# and PWD hybrids.

**Table S3** Tests weight and sperm count in male progeny of B6×(STUS×PWD), B6×(PWD×STUS) and reciprocal crosses (STUS×PWD)×B6, and (PWD×STUS)×B6.

**Table S4** Intervals and candidate genes of Chr X PWD-independent HS QTLs.

**Table S5** Fertility of parental and F1 hybrid females with different allelic combinations at Hstx1/Hstx2 loci.

**Table S6** Primers.

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