Disentangling the Causes for Faster-X Evolution in Aphids

Julie Jaquiéry[1,2,*], Jean Peccoud[3], Tiphaine Ouisse[2], Fabrice Legeai[1,4], Nathalie Prunier-Leterme[1], Anais Gouin[1,4], Pierre Nouhaud[5], Jennifer A. Brisson[6], Ryan Bickel[6], Swapna Purandare[7], Julie Poulain[8], Christophe Battail[9], Claire Lemaitre[4], Lucie Mieuzet[1], Gael Le Trionnaire[1], Jean-Christophe Simon[1,†], and Claude Rispe[10,†]

[1]INRA UMR IGEPP Domaine de la Motte, Le Rheu, France

[2]CNRS UMR 6553 ECOBIO, Université de Rennes 1, France

[3]CNRS UMR 7267 Ecologie et Biologie des Interactions, Equipe Ecologie Evolution Symbiose, Université de Poitiers, France

[4]INRIA Centre Rennes – Bretagne Atlantique, GenOuest, Rennes, France

[5]Institute of Population Genetics, Vetmeduni Vienna, Vienna, Austria

[6]Department of Biology, University of Rochester

[7]Multidisciplinary Center for Advance Research and Studies (MCARS), Jamia Millia Islamia, New Delhi, India

[8]Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Genoscope, Evry, France

[9]Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Centre National de Génotypage (CNG), Evry, France

[10]BIOEPAR, INRA, ONIRIS, La Chantrerie, Nantes, France

*Corresponding author: E-mail: julie.jaquiery@inra.fr.

Accepted: January 18, 2018

[†]These authors contributed equally to this work.

Data deposition: This project has been deposited at NCBI under the following accessions. RP022905 and PRJNA385573: The resequencing of genomes of individuals from one strain (respectively, adult males and adult females) (Illumina Hiseq 2000, at a >40× coverage for each sex). PRJNA385897: The transcriptome sequencing of *Acyrthosiphon svalbardicum* (Illumina Hiseq 2000, 44 GB of sequences). PRJNA385905: The resequencing of genomes for a pool of 60 individuals (Illumina HiSeq 2000, ~85× coverage).

Abstract

The faster evolution of X chromosomes has been documented in several species, and results from the increased efficiency of selection on recessive alleles in hemizygous males and/or from increased drift due to the smaller effective population size of X chromosomes. Aphids are excellent models for evaluating the importance of selection in faster-X evolution because their peculiar life cycle and unusual inheritance of sex chromosomes should generally lead to equivalent effective population sizes for X and autosomes. Because we lack a high-density genetic map for the pea aphid, whose complete genome has been sequenced, we first assigned its entire genome to the X or autosomes based on ratios of sequencing depth in males (X0) to females (XX). Then, we computed nonsynonymous to synonymous substitutions ratios (d*N*/d*S*) for the pea aphid gene set and found faster evolution of X-linked genes. Our analyses of substitution rates, together with polymorphism and expression data, showed that relaxed selection is likely to be the greatest contributor to faster-X because a large fraction of X-linked genes are expressed at low rates and thus escape selection. Yet, a minor role for positive selection is also suggested by the difference between substitution rates for X and autosomes for male-biased genes (but not for asexual female-biased genes) and by lower Tajima's *D* for X-linked compared with autosomal genes with highly male-biased expression patterns. This study highlights the relevance of organisms displaying alternative chromosomal inheritance to the understanding of forces shaping genome evolution.

Key words: sex chromosome, sex-biased expression, evolutionary rates, hemizygosity, selection, drift.

Introduction

Sex chromosomes are major players in evolution. Besides their role in sex determination, sex chromosomes contribute to genomic conflicts (Rice 1984; Meiklejohn and Tao 2010; Soh et al. 2014), genetic incompatibilities, and reproductive isolation (Coyne and Orr 2004; Saether et al. 2007;

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Kitano et al. 2009; Johnson and Lachance 2012). A pair of sex-determining chromosomes typically evolves toward reduced recombination (crossing over), which eventually causes one of the sex chromosomes to gradually lose most of the chromosomal regions (loci) present in the alternate one (Charlesworth et al. 2005). These loci will thus be found in single copy in the sex that carries the degenerate, smaller sex chromosome. When the heterogametic sex is the male, sex chromosomes are denoted X and Y (e.g., in mammals), whereas when it is the female, sex chromosomes are noted W and Z (e.g., in birds). Alleles of loci present only on the X (or Z) are more exposed to selection in individuals of the heterogametic sex, facilitating the fixation of beneficial mutations and the purging of deleterious ones (Charlesworth et al. 1987). On the other hand, because males (XY) bear and transmit a single X chromosome, the effective population size is smaller for the X compared with autosomes (Wright 1931; Caballero 1994, 1995). This can increase the rate of fixation of slightly deleterious mutations on the X by genetic drift (Kimura 1983) (the same principles apply to ZW systems, so we ignore these in the following). Consequently, X-linked genes may evolve faster than autosomes ("faster-X" evolution) due to higher levels of positive selection (rate of fixation of beneficial mutations) and/or genetic drift (rate of fixation of slightly deleterious mutations) (Vicoso and Charlesworth 2009; Mank, Vicoso et al. 2010). The faster evolution of X-linked proteins is supported by observations from a large panel of species (e.g., *Drosophila*, nematodes, mammals, birds, see Meisel and Connallon 2013 for a review). In some species, drift appears to play the dominant role in causing faster-X evolution (Mank, Nam et al. 2010; Avila et al. 2010), whereas positive selection appears to predominate in other species (Baines et al. 2008; Hvilsom et al. 2012; Langley et al. 2012; Mackay et al. 2012; Kousathanas et al. 2014; Sackton et al. 2014; Avila et al. 2015).

In this context, organisms with atypical sex chromosome inheritance can greatly facilitate inferences about the processes contributing to the evolution of sex chromosomes (Bachtrog et al. 2011). Aphids, which have X0 males and XX females, reproduce by cyclical parthenogenesis, such that males and sexual females constitute only a short part of their life-cycle, which is dominated by apomictic parthenogenetic (clonal) XX females (fig. 1). Males are produced asexually via the elimination of one X from the germ line (Wilson et al. 1997; Caillaud et al. 2002). As a result, X-linked recessive alleles are exposed to selection in male aphids, just like in other X0 or XY males. However, because all sexually produced aphid eggs are XX females, all progeny inherit their X from males and sexual females in equal proportions, just as with autosomes. This difference from other heterogametic systems, where progeny present even sex ratios, has deep consequences for the evolutionary trajectory of the aphid X chromosome (Jaquiéry, Stoeckel, Rispe, et al. 2012). This peculiar, autosomal-like inheritance of the X predicts similar effective population sizes for X chromosomes and autosomes. This prediction was borne out under the parameters used in the simulations performed by Jaquiéry, Stoeckel, Rispe, et al. (2012). Thus, aphids are interesting models to test causes for faster-X effects, since they are likely unaffected by confounding factors linked to the smaller effective population size of the X. Furthermore, in contrast to standard systems, variance in reproductive success between sexes, population expansion, bottlenecks, and sex-biased dispersal should not differentially affect aphid sex chromosomes and autosomes since the X is transmitted with equal probability through fathers and mothers (see Jaquiéry, Stoeckel, Rispe, et al. 2012 for further explanations). Mutation and recombination rates are also expected to be equal across chromosomes because of their similar mode of inheritance and the complete absence of crossing overs in males (Jaquiéry, Stoeckel, Rispe, et al. 2012). These similarities between X chromosomes and autosomes make aphids exceptionally useful to pinpoint the causes of faster-X evolution, since the factors mentioned above need not be accounted for. Still, a notable difference between X and autosomes in aphids is the theoretical propensity of the X to accumulate sexually antagonistic mutations beneficial for males and detrimental to asexual females, which is the consequence of cyclical parthenogenesis combined with X inheritance patterns (Jaquiéry et al. 2013). Importantly, the X should always adapt more rapidly than the autosomes, regardless of the dominance coefficient of alleles, as long as there is ongoing selection on males (Jaquiéry et al. 2013).

Empirical analyses on a small subset of pea aphid (*Acyrthosiphon pisum*) genes showed that X-linked genes evolve faster than autosomal genes (Jaquiéry, Stoeckel, Rispe, et al. 2012) and that genes expressed predominantly in males (hereafter "male-biased" genes) were predominantly locate on the X (Jaquiéry et al. 2013). Subsequent genome-wide analyses did not, however, support faster-X evolution (Purandare et al. 2014), and found a lesser degree of enrichment of male-biased genes on the X (Purandare et al. 2014; Pal and Vicoso 2015). These discrepancies likely stem from the fact that these two studies did not assign individual genes to chromosome types, but entire scaffolds, which contain assembly errors (as shown by Bickel et al. 2013 and suggested by Jaquiéry et al. 2013). Misassignment of genes to chromosomes would artificially decrease the contrast between X-linked and autosomal genes.

Here, we aimed to overcome these shortcomings in order to fully disentangle the causes for faster-X evolution in aphids. For this, we first assigned genes to the X or to autosomes at the scale of the entire genome in the pea aphid. On a large set of genes, we then combined estimates of substitution rates at the interspecific level with polymorphism data in pea aphid populations and gene expression levels in the various genders and morphs. This allowed the assessment of how relaxed

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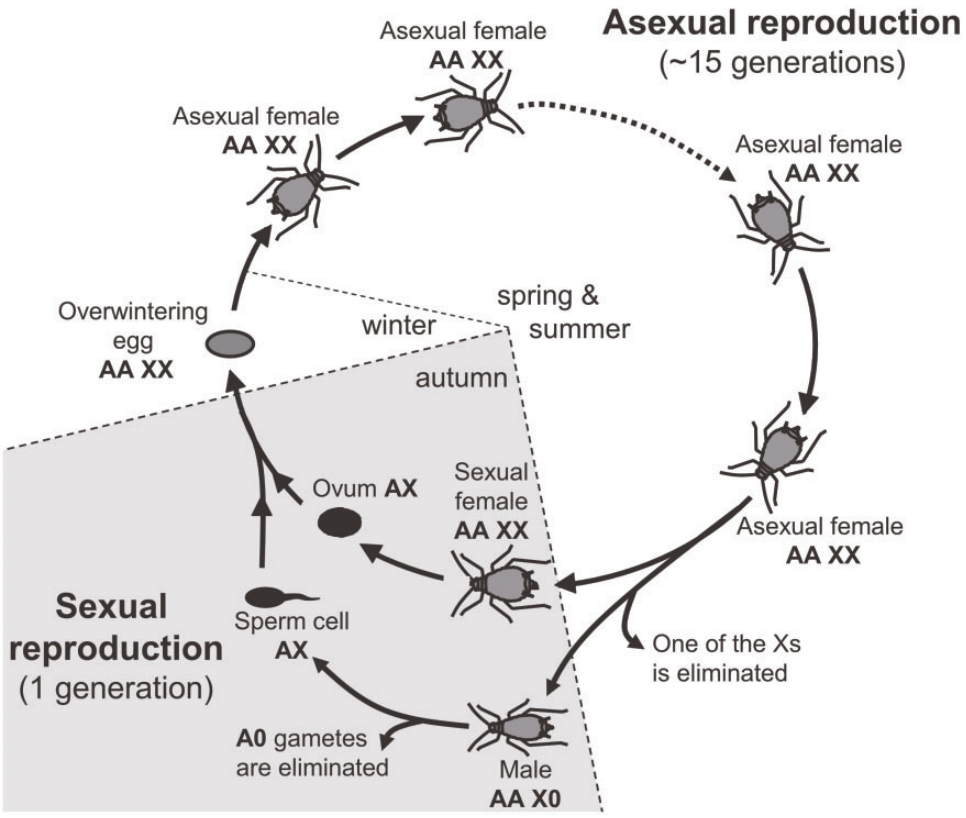


Fig. 1.—Life-cycle of the pea aphid and ploidy levels for autosomes (*A*) and the sex-chromosome (X) (adapted from Jaquiéry et al. 2013).

selection (genetic drift) and adaptation contribute to the faster evolution of the X chromosome in this system.

Materials and Methods

Assignment of Scaffold Regions to the X and Autosomes

Full-Genome Sequencing of Females and Males

An asexual aphid mother has the same diploid autosomal genome as her sons, but has two X chromosomes instead of just one (fig. 1). We took advantage of this XX/X0 system to assign pea aphid genome sequences (Acyr 2.0, Genbank accession GCA_000142985.2, IAGC 2010) to the X or to the autosomes by comparing sequencing depth along assembled scaffolds between mapped reads from females and males of the same parthenogenetic lineage (clone). DNA from five asexual females, five winged males and five wingless males of clone P123 (Simon et al. 2011) was extracted with the Qiagen DNeasy Blood and Tissue kit, following the manufacturer's protocol. The male wing polymorphism in this clone was used to determine the X copy that each male carried, based on the knowledge that the locus that controls this trait is X-linked (Caillaud et al. 2002) and is heterozygous in clone P123 (Frantz et al. 2010). Each individual was genotyped at seven polymorphic microsatellite markers (Peccoud et al. 2008) to confirm its clonal identity. One of those markers, which is known to be X-linked (Caillaud et al. 2002), allowed us to confirm the nature of the X copy inherited by each male. The three DNA extracts (P123 asexual females and the two types of P123 males) were sequenced on the Illumina Hiseq 2000 platform yielding 100-bp pair-end reads at ~43× coverage for the females sample and 25–30× coverage for each male type. Reads from each sample were mapped to scaffolds of the pea aphid genome assembly (Acyr 2.0) and to genome sequences of the bacterial symbionts of this pea aphid clone using the method described in Gouin et al. (2015) using Bowtie 2 (Langmead and Salzberg 2012) with proper insert sizes and parameters set as default. Depth of coverage at each nucleotide position of the reference genome was recorded and single nucleotide polymorphisms (SNPs) were identified using GATK's Haplotype Caller (McKenna et al. 2010; DePristo et al. 2011). The raw sequence data have been deposited in the SRA division of Genbank (project accession: ERP022905 and PRJNA385573).

Comparison of Sequencing Depth between Males and Females

The following analysis was performed in R (R Development Core Team 2015). We analyzed genome positions covered by 20–70 reads in the asexual female sample, a range chosen to

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eliminate regions with low-coverage and regions with suspiciously high coverage (potentially duplicated or repeat-rich regions). Since overall coverage was slightly higher for one of the male types (~30×) than for the other (~25×), we normalized the depth of coverage data of the second male type (multiplying coverage estimates by a 30/25 ratio). We then averaged depth of coverage at each base position over male types. The ratio of male median coverage depth to female median coverage depth was calculated on 10-kb scaffold windows sliding by 2-kb steps. A single window was used for scaffolds shorter than 10 kb. We expected the ratio of median coverage depth to be two times larger for autosomal regions than for X chromosome regions. Accordingly, this ratio had a clearly bimodal distribution (supplementary fig. S1, Supplementary Material online), with modes at 0.34 and 0.66. We assigned each 10-kb window to the X if its ratio ranged between 0.2 and 0.445, and to autosomes if it ranged between 0.53 and 1, whereas the region was tagged as "ambiguous" if it ranged between 0.445 and 0.53. Windows assigned to the same chromosome type and which were separated by less than four consecutive "ambiguous" windows were aggregated into a scaffold region we call a "block." A whole block, including its "ambiguous" windows, was assigned to the corresponding chromosome type.

Comparison of Male and Female Genotypes

The inheritance of single nucleotide polymorphisms (SNPs) is also informative about the type of chromosome carrying a scaffold block. SNPs that are heterozygous in females but are also heterozygous in males are necessarily located on autosomes. Conversely, SNPs which are heterozygous in females but homozygous (hemizygous) in males must be on the X. This SNP-based approach is, however, expected to be less powerful than the depth of coverage-based method for genomic regions with low heterozygosity. Thus, we only used SNP data to validate X/A assignments based on depth of coverage ratio (supplementary fig. S2, Supplementary Material online). A position was determined as heterozygous if the rarest allele was represented in at least 25% of the reads, otherwise it was considered homozygous. Assignment of SNPs to chromosome types was performed according to the genotypes of males, as described earlier. SNPs showing inconsistent genotypes (e.g., females and males of one type are both heterozygous while males of the other type are homozygous) were not assigned. Assignments based on depth of coverage were then visually compared with SNP-based assignments (supplementary fig. S2, Supplementary Material online) and to a set of 305 microsatellite markers assigned to chromosomes (Jaquiéry et al. 2014; supplementary file S1, Supplementary Material online).

Assignment of Predicted Genes to the X and Autosomes

We used the 36,990 genes (v2.1) predicted from the Acyr 2.0 genome assembly available at http://bipaa.genouest.org/is/aphidbase/ (last accessed January 25, 2017). Each of these genes was determined to be X-linked or autosomal if the full length of its coding sequence (CDS) was found in a single scaffold block or was spread over several scaffold blocks assigned to the same type (either X, or A). Genes that could not be unambiguously assigned (mainly because they were located on "ambiguous" blocks) were removed from further analyses. We also excluded 589 predicted genes that corresponded to rRNA (noncoding DNA).

Sex-Biased Gene Expression

We used the eight RNAseq libraries from Jaquiéry et al. (2013) to characterize gene expression patterns between morphs. Briefly, these eight libraries correspond to whole insects, with three male libraries, three parthenogenetic female libraries and two sexual female libraries—different libraries in each morph representing biological replicates—using adults of a single clone of *A. pisum* (clone LSR1). Details regarding aphid rearing, library preparation, and sequencing are provided in Jaquiéry et al. (2013). Libraries were mapped to Acyr 2.0 as described previously. The number of reads covering each CDS was then counted. Read counts were normalized with the R package DESeq with default parameters (Anders and Huber 2010). For each gene, the effect of the morph (a three-level factor comprising male, sexual female, and asexual female) on expression was tested with a GLM (R package MASS, Venables and Ripley 2002) with a quasi-poisson distribution of residuals, considering the different libraries for each morph as replicates. *P* values were corrected for multiple testing using the Benjamini–Hochberg method implemented in R. Genes differentially expressed between morphs ($P < 0.05$ after adjusting for multiple testing) were then categorized according to their pattern of expression in the different morphs as described in table 1.

Evolutionary Rates

To assess substitution rates in X-linked and autosomal genes, sequences from another aphid species were necessary. *Acyrthosiphon svalbardicum* was chosen to limit the risk of mutational saturation and of chromosomal rearrangements between the two species. Note that rearrangements should not increase the contrast between X and autosomes (i.e., if there is a chromosome type effect on evolutionary rates, rearrangements will only decrease the observed differences, so our tests are conservative). Asexual females of *A. svalbardicum* were collected in Svalbard in 2009, and were then reared in the lab under 10:14 light:dark and 15°C on *Dryas octopetala*. Ten females were frozen in liquid nitrogen and kept for subsequent RNA extraction using the RNeasy plant mini

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Table 1
Number of X-Linked and Autosomal Genes and Frequency of X-Linkage for Classes of Genes with Contrasted Patterns of Expression between Morphs

Category of Genes	Number of X-Linked Genes	Number of Autosomal Genes	Frequency of X-Linkage	*P* Value[f]
All[a]	13,726	19,263	0.42	10^{-16}
Low expression[b] (<10 reads per kilobase)	10,995	8,136	0.57	10^{-16}
Expressed[c] (at least 10 reads per kilobase)	2,771	11,127	0.20	0.0001
Unbiased[d] (>10 reads per kilobase and *P*adj>0.1)	697	3,355	0.17	na
2-fold male-biased[e]	1,546	2,245	0.41	10^{-16}
5-fold male-biased[e]	962	948	0.50	10^{-16}
2-fold sexual female-biased[e]	448	1,369	0.25	10^{-10}
5-fold sexual female-biased[e]	148	407	0.27	10^{-7}
2-fold asexual female-biased[e]	244	1,023	0.19	0.10
2-fold asexual female-biased[e]	93	423	0.18	0.68

[a]All predicted genes that were assigned to the X or autosomes are included.
[b]Genes with on an average <10 reads per kilobase of exon (average over the three morphs).
[c]Genes with on an average ≥10 reads per kilobase of exon (average over the three morphs).
[d]Genes with on an average ≥10 reads per kilobase of exon (average over the three morphs) and with an adjusted *P* value ≥ 0.1 when tested for morph-biased expression.
[e]A gene was included in the morph-biased category (either male-, female-, or asexual-biased) if the adjusted *P* value for a morph effect was <0.05 and if it was at least x-fold (2 or 5) more expressed in one of the morph compared with the two other morphs.
[f]Deviation from expectation (given by the "unbiased" category) was evaluated with a test of proportion.

kit (Qiagen) according to manufacturer's instructions. Two separate RNA extractions of five adults were performed. RNA quality was checked by Bioanalyzer (Agilent) and quantified by Nanodrop (Thermo Scientific). One sample made of a pool of 2 µg of the two independent RNA extractions was sent to GATC Company for RNA paired-end sequencing. The raw sequence data have been deposited in the SRA division of Genbank (project accession: PRJNA385897).

A de novo transcriptome assembly for *A. svalbardicum* was obtained following the methods of Rispe et al. (2016). Low quality parts of the reads were trimmed from the right ends with prinseq-lite (http://prinseq.sourceforge.net/; last accessed January 25, 2017) when the mean of phred score in a 20-bp window was <20. Reads longer than 20 bp after trimming were reorganized by pairs (orphans were suppressed) and assembled with Trinity (Grabherr et al. 2011) using default parameters. Coding regions were predicted using FrameDP (Gouzy et al. 2009). Reciprocal BLASTN (Altschul et al. 1990) searches between CDSs of *A. svalbardicum* and of *A. pisum* were carried out with an e-value threshold of 10^{-8}. The following steps were performed with an R script. A reciprocal best hit criterion was used to identify putative orthologous genes between the two species. These were aligned by the pairWiseAlignment function of the Biostrings package (Pages et al. 2016). Indels were inspected to flag CDS regions where the two species did not present the same reading frame. Bases in these regions were replaced with Ns, and were trimmed by the Gblocks program (Castresana 2000; Talavera and Castresana 2007), alongside regions of unreliable alignment. We then estimated pairwise synonymous (d*S*) and nonsynonymous (d*N*) substitution rates for each gene, using the codon-based method of Li (1993), as implemented in the R package seqinR (Charif and Lobry 2007). Only the 9,696 genes (out of 9,924) with an alignment length of >90 nucleotides, d*N*<0.3 and d*S*<2 were kept. We also truncated d*N*/d*S* ratios to a maximal value of 2.5.

Estimates of Selection Intensity Based on Intraspecific Polymorphism

Polymorphism data for *A. pisum* were obtained from 60 genotypes originating from three alfalfa (*Medicago sativa*) fields located in France and Switzerland (Jaquiéry, Stoeckel, Nouhaud, et al. 2012). These fields can be considered to harbor a single large population of *A. pisum* (Peccoud, Ollivier, et al. 2009; Jaquiéry, Stoeckel, Nouhaud, et al. 2012). DNA was extracted from four asexual females of each clone using the method described earlier. Because the approach described below does not require reconstructing allele sequences or individual genotypes, sequencing the pooled individuals (Gautier et al. 2013) was used to save costs. After RNAse treatment on each sample and DNA dosage with Pherastar, DNA samples were pooled to attain equimolar proportions. Paired-end libraries were then sequenced on two lanes of Illumina HiSeq 2000 using the Illumina Sequencing Kit v3 (producing 100-bp reads) by Beckman Coulter Genomics (Danvers, MA). This yielded ~85× of sequencing coverage, hence an expectation of 0.71× per individual chromosome. Reads were mapped to Acyr 2.0 and symbiont genome sequences as described previously. The two alignment (BAM) files (one per sequencing lane) were filtered from PCR duplicates using SAMtools rmdup (Li et al. 2009) and reads realigned near indels using the Genome Analysis Toolkit (McKenna et al. 2010). The raw sequence data have been

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deposited in the SRA division of Genbank (project accession: PRJNA385905).

The two BAM files were merged and converted as pileup format using SAMtools (options -B -Q 0 –R) (Li et al. 2009). A modified estimator of Tajima's *D* (Tajima 1989) which takes into account sequencing errors (Achaz 2008) was then calculated from this mpileup with Popoolation 1.2.2 (Kofler et al. 2011), after subsampling at a uniform coverage (subsample-pileup.pl, options: –target-coverage 30 –max-coverage 120 –method withoutreplace). Computations were performed for each gene including introns (Variance-at-position.pl –pool-size 120). Tajima's *D* allows evaluating the type of selection at work, since selective sweeps and/or purifying selection tend to decrease it, and balancing selection tends to increase it.

The McDonald and Kreitman (1991) approach, which compares fixed mutations to polymorphic mutations in CDS, was adopted to further evaluate selection pressures on these different categories of genes, using the DoS estimate (Direction of Selection, Stoletzki and Eyre-Walker 2011). Positive, null, and negative values of DoS, respectively, suggest adaptive evolution, neutral evolution, and purifying selection. Fixed mutations between species were counted from alignments we previously generated for *A. svalbardicum* and *A. pisum* CDSs. We restricted the analysis to regions of reliable alignments, as given by the Gblocks txts outputs. In these regions, we called SNPs on the BAM files with LoFreq (Wilm et al. 2012), which offers a good compromise between speed, sensitivity, and accuracy in pools of multiple individuals (Huang et al. 2015). We used SAMtools mpileup (Li et al. 2009) to assess depth of coverage at all positions in these regions, polymorphic or not. We instructed mpileup to discard reads with mapping quality 0. The following was done in R. We discarded all positions covered by less than three reads (both BAM files combined). At each SNP, the number of polymorphic mutations was the number of different bases (alleles) found in the pea aphid population minus one. A fixed difference was counted if no base was shared at a position between the pea aphid population and *A. svalbardicum*. The number of polymorphic nonsynonymous mutations per codon was taken as the number of amino acids found in the pea aphid populations for that codon minus one. To count the number of fixed nonsynonymous differences per codon, we considered that a codon might differ between the two species by up to three mutations. Any of these may involve a change in protein sequence that we cannot ascertain without knowledge on the order of appearance of the mutations. We adopted parsimony and considered the minimum number of mutations required between the two codons. If several codons were present in the pea aphid population (due to a SNP), we considered the minimum number of coding changes that any pair of codons between the pea aphid and *A. svalbardicum* involves. For all these counts, we discarded rare codons showing more than one SNP, because the actual codons (and amino acids) present in the pea aphid population cannot be determined without phasing. We counted the following for each gene: the number of polymorphic nonsynonymous changes (*Pn*), the number of all polymorphic changes minus *Pn* (which is the number of polymorphic synonymous mutations, noted *Ps*), the number of fixed nonsynonymous differences (*Dn*), the number of all fixed differences minus *Dn* (which is the number of fixed synonymous changes, noted *Ds*). DoS was then calculated as $Dn/(Dn+Ds)-Pn/(Pn+Ps)$ for each gene. Similarly, we measured α (the proportion of amino acid substitution driven by positive selection) as $1-\frac{DsPn}{DnPs}$ (Stoletzki and Eyre-Walker 2011). For both indices, we considered only genes whose average depth of coverage, as given by mpileup, was between 20 and 150 (expected coverage was ~85) to avoid including genes presenting multiple collapsed copies that could artificially inflate polymorphism.

Statistical Analyses

Differences in expression levels between X-linked and autosomal genes in the different morphs, as well as differences in d*N*/d*S*, d*N*, and d*S* between X-linked and autosomal genes were tested with Mann–Whitney *U* tests. The latter analysis was done on all genes, and on genes grouped based on an average expression over the three morphs. To evaluate evolutionary forces responsible for faster-X evolution, we then compared d*N*/d*S*, Tajima's *D*, DoS, and α between X-linked and autosomal genes for classes of genes with different expression patterns (unbiased, male-biased, sexual female-biased, and asexual female-biased genes). For biased genes, we considered different fold changes in expression (2- to 5-fold, and > 5-fold). Statistical significance was evaluated with Mann–Whitney *U* tests. Finally, we tested the factors affecting log-transformed d*N*/d*S* using a complete linear model. Included variables in *model 1* were *CDS size, CAI* (the codon adaptation index, calculated with CAIcal, Puigbò et al. 2008), τ (a measure of morph specificity in expression, Yanai et al. 2005), *mean expression level* (averaged over the three morphs), and *chromosome*. To test whether d*N*/d*S* measures were significantly higher for X-linked male-expressed genes than for autosomal genes (expected if selection is more efficient on X due to the hemizygosity of this chromosome in males), we constructed a second model (*model 2*) including the following variables: *CDS size, CAI*, τ, *expression level in asexual female, expression level in sexual females, expression level in males, chromosome*, and the interaction between the last two terms. Significance was tested with permutations in the R package lmPerm (Wheeler and Torchiano 2016).

Results

Gene Assignment to the X and Autosomes

Based on the depth of coverage ratio based on reads from males versus females, 64% of the nucleotides assembled in

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the pea aphid reference genome (Acyr 2.0) were assigned to autosomes and 31% to the X chromosome, whereas only 5% could not be assigned (supplementary fig. S1, Supplementary Material online). Genotypes of males at SNPs that were heterozygous in the female generally confirmed the assignment from coverage depth data (supplementary fig. S2, Supplementary Material online), though confirmation was not possible in regions lacking such SNPs. These estimates roughly correspond to the expected size of the X chromosome in the pea aphid, which represents ~30% of the chromosome content based on karyotypes (Mandrioli and Borsatti 2007). This assignment revealed a high rate of misassembly in Acyr 2.0: 56% of scaffolds ≥150 kb (which represent 80% of the assembly length) contained blocks assigned to both chromosome types (supplementary fig. S3 and table S1, Supplementary Material online). Based on assigned scaffold blocks, 19,263 predicted genes were located on autosomes and 13,726 on the X chromosome, whereas 4,001 genes could not be unambiguously assigned. The X chromosome contained a higher fraction of predicted genes than expected from its relative size (42%, test of proportion, $P < 10^{-15}$).

Gene Evolutionary Rates

We assessed substitution rates by comparing pea aphid gene sequences to transcripts sequenced from a related species (*A. svalbardicum*). We found that X-linked genes had almost a twice higher nonsynonymous substitution rate, d*N* (mean $dN_X = 0.034$; $dN_A = 0.019$, Mann–Whitney $U = 4{,}839{,}860$, $P < 10^{-15}$, $n = 9{,}096$) and only slightly higher synonymous substitution rate, d*S* (mean $dS_X = 0.101$; $dS_A = 0.085$, Mann–Whitney $U = 6{,}190{,}137$, $P < 10^{-6}$), compared with autosomal genes. As a result, the evolution of X-linked genes involves more protein-sequence changes (in proportion) than the evolution of autosomal genes (mean $dN_X/dS_X = 0.390$; $dN_A/dS_A = 0.237$; Mann–Whitney $U = 5{,}026{,}170$, $P < 10^{-15}$, fig. 2*A* and supplementary table S2, Supplementary Material online).

Causes of Faster-X Evolution

High ratios of nonsynonymous to synonymous rates, d*N*/d*S*, can result from a decreased influence of selection—and thus an increased influence of drift—on amino acid substitutions (i.e., relaxed negative selection) and/or from more efficient selection of adaptive changes in the protein sequence (i.e., increased positive selection). To distinguish between these two hypotheses, we used gene expression levels as proxies for possible impacts on fitness, although we recognize that this proxy suffers limitations (Wall et al. 2005; Zhang and He 2005; Hart et al. 2014). The positive correlation between α (the proportion of amino-acid substitutions driven by positive selection) and expression demonstrates the relevance of this proxy in our data set (supplementary fig. S4, Supplementary Material online). Expression levels of X-linked genes were significantly lower than those of autosomal genes in all three aphid morphs: males, sexual females, and parthenogenetic females (fig. 2*B*). Expression level averaged over the 13,726 X-linked genes ranged from ~52 reads per kilobase in sexual and asexual females to 155 reads per kilobase in males, whereas expression level averaged over the 19,263 autosomal genes varied from 575 (in asexual females) to 648 reads per kilobase in males. Genes that are not expressed or expressed at a low level may have a reduced effect on the phenotype and may therefore accumulate nonsynonymous substitutions faster (reduced purifying selection), an hypothesis supported by the increase of α with expression (supplementary fig. S4, Supplementary Material online). We indeed observed that, for both X and autosomes, d*N*/d*S* ratios decrease with increasing expression levels (averaged over the three morphs, $P < 10^{-15}$ in table 2, *model 1*, supplementary fig. S4, Supplementary Material online), and that the contrast between X and autosomes tends to decline for highly expressed genes (fig. 2*A* and supplementary table S2, Supplementary Material online). The regression model also revealed that d*N*/d*S* decreases with gene length ($P < 10^{-11}$), increases with τ (a measure of morph specificity in expression, $P < 10^{-15}$) and *CAI* ($P < 10^{-15}$), and highlighted a significant chromosome effect ($P = 0.00015$), d*N*/d*S* being higher for X-linked genes (*model 1*, table 2). A slight contrast in d*N* ratios is still maintained for highly expressed genes, though (supplementary table S2, Supplementary Material online). Therefore, low expression levels of X-linked genes may not entirely account for faster-X evolution in aphids.

Selection may also be relaxed in genes that are predominantly expressed in rare morphs (males and sexual females), which constitute a minor fraction of the annual life cycle of aphids, which is dominated by asexual females. Relaxed selection on mutations affecting male-biased genes (Brisson and Nuzhdin 2008; Purandare et al. 2014), combined with the tendency of such genes to locate on the X (Jaquiéry et al. 2013; Pal and Vicoso 2015) could contribute to faster-X evolution. However, the influence of X-linkage could not properly be evaluated in Purandare et al. (2014) because misassembled scaffolds, rather than individual genes, were assigned to chromosomes. Our new data set of X-linked and autosomal genes unambiguously confirmed that the X is largely enriched for genes overexpressed in males, and to a smaller extent for those overexpressed in sexual females (table 1). Like Purandare et al. (2014), we observed higher d*N*/d*S* ratios in genes overexpressed in the rarer morphs (i.e., males and sexual females, fig. 3*B* and *C*) than in genes overexpressed in the common morph (parthenogenetic females, fig. 3*D*) when considering X-linked and autosomal genes together. The global analysis (*model 2*, table 2) further demonstrated that d*N*/d*S* decreases with expression in asexual females ($P < 10^{-15}$), but increases with expression in males and sexual females ($P < 10^{-8}$ and 10^{-6}, respectively) as well as with

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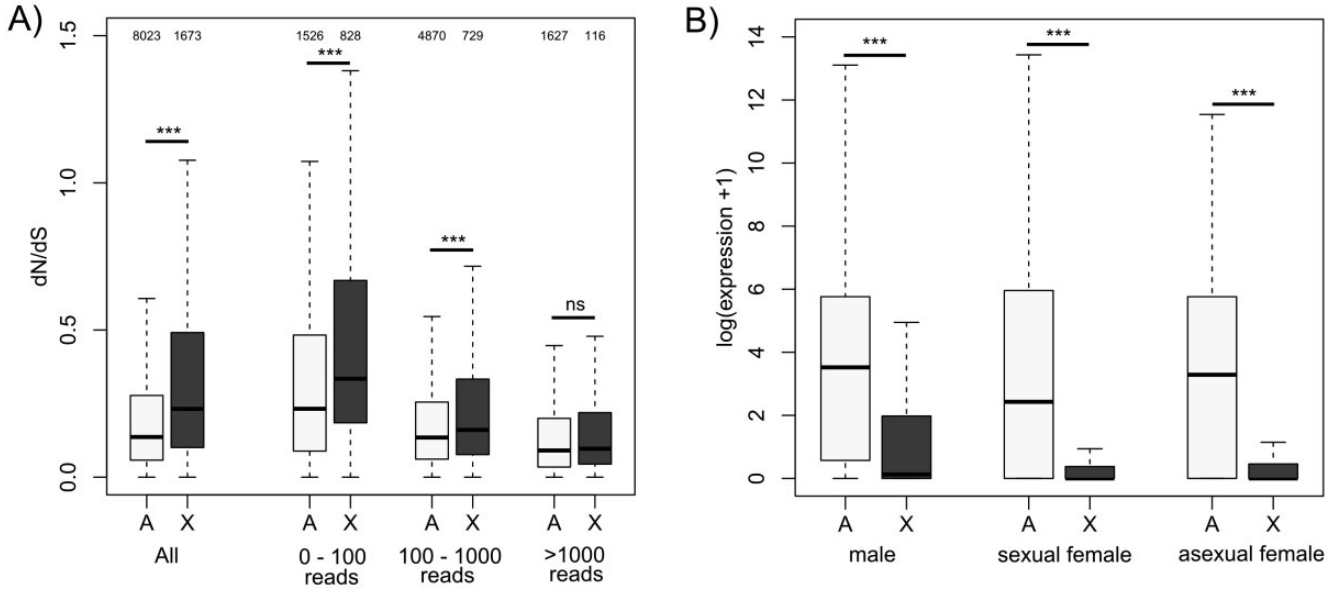


Fig. 2.—Evolutionary rates for autosomal and X-linked genes and gene expression in males, sexual and asexual females. (*A*) Evolutionary rates (d*N*/d*S*) are shown for all genes (expressed or not in *Acyrthosiphon pisum*) and for genes expressed at different levels (when averaged over male, sexual and asexual females): lowly expressed genes (i.e., covered by < 100 reads per kilobase of exon model); moderately expressed (from 100 to 1,000 reads per kilobase), highly expressed genes (>1000 reads per kilobase). The number of genes per category is shown above each boxplot. (*B*) Expression level for X-linked ($n = 13{,}613$) and autosomal genes ($n = 18{,}812$) in males, sexual females and asexual females. It should be noted that males carry only one X chromosome per cell and females carry two. Significance was tested with Mann–Whitney *U* tests.

Table 2

Results from the Linear Models Examining the Below Variables on Log-Transformed d*N*/d*S*

Variables	Estimate	*P* Value
Model 1		
CDS size	-1.0×10^{-5}	10^{-11}
CAI	0.33	$<10^{-15}$
τ	0.21	$<10^{-15}$
Log(Mean expression+1)	−0.019	$<10^{-15}$
Chromosome	−0.012	0.00015
Model 2		
CDS size	-9.4×10^{-6}	10^{-9}
CAI	0.19	10^{-11}
τ	0.14	$<10^{-15}$
Log(Asexual female expression+1)	−0.047	$<10^{-15}$
Log(Sexual female expression+1)	0.011	10^{-6}
Log(Male expression+1)	0.013	10^{-8}
Chromosome	−0.011	0.0007
Log(Male expression+1): Chromosome	−0.0012	0.37

morph specificity in expression τ ($P < 10^{-15}$). Tajima's *D* also tends to increase in genes overexpressed in the sexual morphs compared with unbiased genes (significantly so for all male-biased and for 2- to 5-fold female-biased genes, fig. 4*B*), but not in genes overexpressed in the common morph (where D is significantly lower compared with unbiased genes, fig. 4*D*), a pattern compatible with relaxed selection on genes expressed mainly in the rare morphs. Supporting this hypothesis, α (the proportion of amino acid substitutions driven by positive selection) is significantly lower for male- and sexual female-biased genes compared with unbiased genes, but not in genes overexpressed in the common morph (supplementary fig. S6, Supplementary Material online). However, the DoS did not differ significantly between these categories of genes, except for strongly female-biased genes (supplementary fig. S5, Supplementary Material online).

When analyses were done by chromosome type, d*N*/d*S* ratios of X-linked genes were significantly higher than those of autosomal genes for both sexual female- and male-biased genes (fig. 3*E–H*), but not for asexual females. Contrastingly, Tajima's *D* differed between chromosome types only for strongly male-biased genes (being lower for X-linked genes, suggesting more positive selection, fig. 4*F*) and for unbiased genes (being larger for X-linked genes, possibly revealing more balanced selection, fig. 4*E*). No signal was detected between chromosome types based on the DoS index or α (supplementary figs. S5 and S6, Supplementary Material online).

Alternatively, the faster evolution of X-linked male-biased genes compared with autosomal male-biased genes could result from the fact that the former are present in a hemizygous state in males. Nonsynonymous mutations on the X are thus more exposed to selection in males, since they are not masked by potentially dominant alleles, such that adaptive mutations on the X should more rapidly and more likely reach

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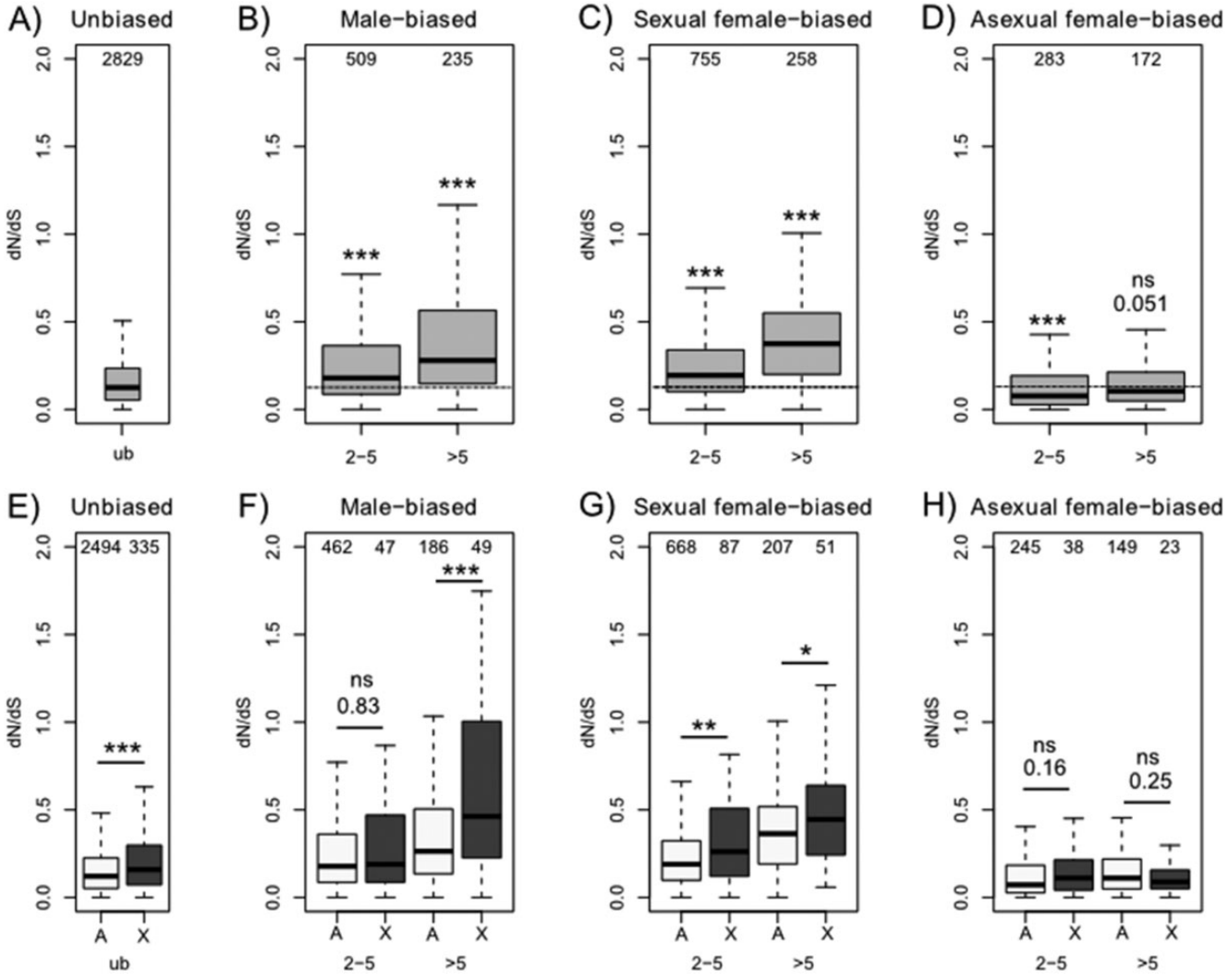


Fig. 3.—Substitution rates of genes (d*N*/d*S*, measured between *Acyrthosiphon pisum* and *A. svalbardicum*) according to the ratios of expression levels between morphs. Panels (*A–D*) consider all genes together (X-linked and autosomal), and panels (*E–H*) consider X-linked (dark gray) and autosomal (light gray) genes separately. The number of genes in each class is shown above each boxplot. Only genes supported by at least 100 reads per kilobase of exon model were retained. ub: unbiased genes (*P*adj > 0.1 for morph effect on expression), 2–5: levels of gene expression are two to five times higher in the specified morph (*P*adj <0.05 for morph effect), >5: levels of gene expression are at least five times higher in the specified morph (*P*adj < 0.05). Significance of differences: ns: $P > 0.05$; *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$ (Mann–Whitney *U* tests). For panels (*B–D*), differences correspond to comparisons with genes of the "unbiased" category, whereas X and autosomes were compared in panels (*F–H*).

fixation than adaptive mutations on autosomes. This hypothesis predicts that the contrast between substitution rates of X-linked genes and autosomal genes will be highest for male-biased genes, and lowest for sexual- and asexual female-biased genes, because in these morphs, the X is always diploid and adaptive mutations can be recessive. We indeed observed these patterns (fig. 3*F*), although the interaction between male expression level and chromosome in *model 2* (table 2) was not significant. Nevertheless, the significantly lower Tajima's *D* for X-linked male-biased genes compared with autosomal genes provides some support to this hypothesis (fig. 4*F*, $P < 0.01$) as do DoS and α (though not significantly, supplementary figs. S5*F* and S6*F*, Supplementary Material online).

Discussion

Here, we performed a genome-wide identification of X-linked genes, enabling us to locate a large number (13,726) and proportion (42%) of predicted genes on the X chromosome. We demonstrated that these genes tend to evolve faster than autosomal genes, on an average, confirming earlier results based on a much smaller set of genes (Jaquiéry, Stoeckel, Rispe, et al. 2012). We found that faster-X evolution mainly results from the low expression of a large fraction of X-linked

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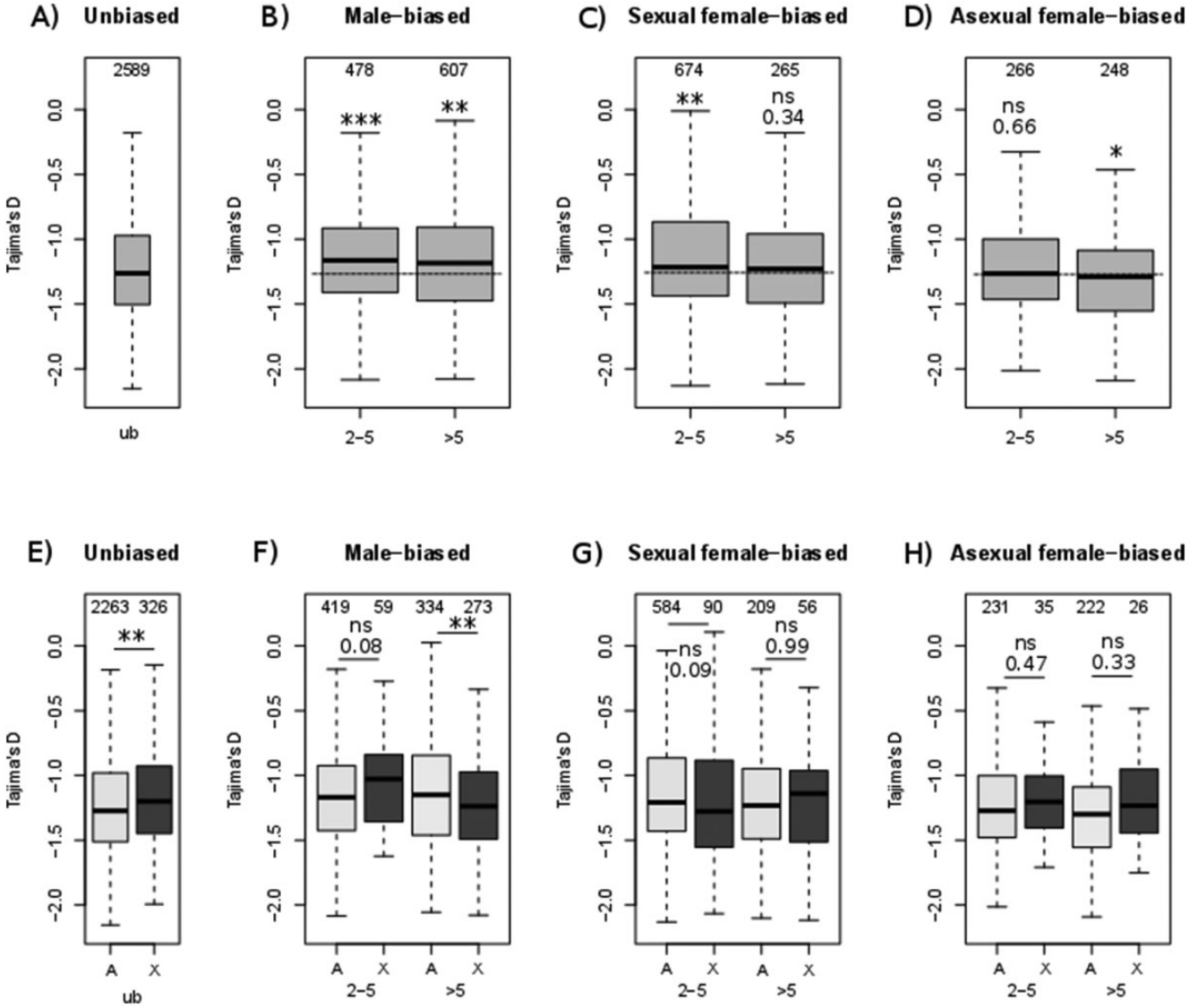


Fig. 4.—Tajima's *D* according to the ratios of gene expression levels between morphs. Panels (*A–D*) consider all genes together (X-linked and autosomal) and panels (*E–H*) consider X-linked (dark gray) and autosomal (light gray) genes separately. Terms are defined as in figure 3. Dashed lines show median values for unbiased genes. Significance of differences was tested with Mann–Whitney *U* tests.

genes, which likely have a lesser effect on phenotypes and may accumulate nonsynonymous mutations at a higher rate. The enrichment of the X chromosome with genes expressed in the rare male and sexual female morphs (which show signs of relaxed selection) might also contribute to faster-X evolution. Lastly, some of our analyses suggested that higher exposure of recessive X-linked alleles to selection in hemizygous males might also contribute to faster-X evolution via more efficient positive selection, although this hypothesis requires further testing.

We demonstrated clear faster-X evolution in the pea aphid based on a large set of X-linked and autosomal genes. The nonsynonymous to synonymous substitution ratio (d*N*/d*S*) for X-linked genes is 1.69 times greater than for autosomal genes. This clearly places aphids among species showing strong contrast between the evolution of X-linked and autosomal genes, as the d*N*/d*S* for X-linked genes is between ~0.9 and ~1.8 times that of autosomes in most species studied (i.e., *Drosophila*, mammals, birds and moths, review in Meisel and Connallon 2013; see also Sackton et al. 2014). In addition, both X and autosomes exhibit higher d*N*/d*S* for sex-biased genes, as previously shown in aphids (Purandare et al. 2014) and in several other organisms (Torgerson and Singh 2003; Ellegren and Parsch 2007; Parsch and Ellegren 2013; Kousathanas et al. 2014).

Remarkably, the pea aphid has the same effective population size for the X and autosomes under the demographic scenario investigated in Jaquiéry, Stoeckel, Rispe,

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et al. (2012), such that hemizygosity in males should be the only differentiating factor affecting the evolution of genes located on different chromosome types. However, our analyses revealed another key difference between X-linked and autosomal genes, in that the former are, on an average, four to ten times less expressed than the latter (fig. 2*B*), and expectedly show higher rates of substitution (supplementary fig. S4, Supplementary Material online). Such negative correlations between substitution rates and expression levels have already been observed in several species (Drummond et al. 2005; Nguyen et al. 2015; Zhang and Yang 2015). Therefore, enrichment of the X with lowly expressed genes is likely to explain, to a large extent, the faster-X evolution in aphids.

Gene expression differs between chromosome types in another dimension, as the X is enriched in genes that are mostly expressed in the rare morphs (i.e., males and sexual females) (Jaquiéry et al. 2013; Pal and Vicoso 2015). Such genes should evolve under more relaxed constraints as they are exposed to the selective environment only during a short period of the aphid life cycle (Brisson and Nuzhdin 2008; Purandare et al. 2014). Enrichment of the X chromosome with genes expressed in the rare male morph (which show signs of relaxed selection based on α) might also contribute to faster-X evolution in the pea aphid.

This leaves hemizygosity of the X chromosome in males, which exposes all X-linked alleles expressed in males to the selective environment, as another contributing cause. This hypothesis finds some support in the contrast in d*N*/d*S* between X-linked genes and autosomal genes, which is larger for male-biased genes than for sexual and asexual females-biased genes (fig. 3*F*–*H*), and in the lower Tajima's *D* for male-biased X-linked genes than for genes on autosomes (fig. 4*F* and *G*). The DoS or α also tend to support the hypothesis of positive selection on the X, but the effect of chromosome type proved not significant.

The mean expression levels of X-linked genes measured from the whole bodies were strikingly lower than those of autosomal genes, in all morphs studied. The difference we found is more pronounced than in previous observations (Jaquiéry et al. 2013; Pal and Vicoso 2015) probably due to more reliable gene assignments to chromosomes (we found that 10% of the 3,712 genes used in Jaquiéry et al. 2013 had been misassigned because of scaffold misassembly). Lower expression of X-linked genes compared with autosomal genes is observed in mammals (Nguyen et al. 2015), but not in *Drosophila* (Zhang and Presgraves 2016). To our knowledge, no other taxon displays such a strong contrast between the X and autosomal gene expression levels. This raises the question of why genes on the X are so lowly expressed in this species. We cannot rule out that the lower average expression of X-linked genes measured on whole bodies reflects expression patterns that are more tissue/organ-specific than those of autosomal genes. Another hypothesis from a theoretical model (Jaquiéry et al. 2013) predicts that the X chromosome is more easily invaded than autosomes by sexually antagonistic alleles beneficial to males and deleterious to females. Such evolution may have favored a global decrease in gene expression of this chromosome in the common morph (the asexual females) for which it could be harmful. Indeed, an analysis of the structure of the chromatin has revealed that the chromatin of the X is less accessible in females than in males, suggesting the existence of a global mechanism of regulation (Richard et al. 2017). Pseudogenization on the X chromosome would have ensued if genetic variation in lowly expressed genes has little effect on fitness. Yet, this chromosome carries one third of the genome and contains a higher fraction of genes than predicted by its relative size. Insights into the respective role of sexual antagonism or the breadth of gene expression on the peculiar expression patterns observed here could be gained by studying expression of X and autosomal genes in different male and female tissues. Particularly, transcriptomes of tissues subject to different sex-specific selection pressures (Parisi 2003; Khil et al. 2004; Yang et al. 2006; Huylmans and Parsch 2015) could help examine this hypothesis.

Assignments of scaffold blocks to chromosomes revealed widespread errors in the pea aphid genome assembly (Acyr 2.0). More than half of scaffolds >150 kb are clear chimeras of X and autosomes. This is a minimal estimate for the rate of misassembly, since our method only detects breakpoints between X and autosomes. Consequently, we confidently conclude that the genome of the pea aphid presents considerable assembly problems, to a degree that goes far beyond what current assembly pipelines typically yield (Salzberg et al. 2004; Muggli et al. 2015). Although the cause of these errors remains undetermined, they have important drawbacks for genomic studies on a species that is currently considered the model aphid, in particular those relying on the physical organization of the genome, ranging from high-resolution genome scans to studies of chromatin conformation, and genomic rearrangements. The results presented here should not be affected by misassembly because we were able to unambiguously assign almost 90% of the 36,990 predicted genes. Such a high number of genes compared with other arthropod genomes (Adams 2000; Colbourne et al. 2011; Mathers et al. 2017) could indicate errors in gene prediction in the official gene consensus set. There is, however, no doubt that many functional groups show an unusual high level of gene duplication in the pea aphid (IAGC 2010). Most importantly, we see no reason why prediction errors would be more common on the X than on autosomes, and so this should not affect our conclusions.

In conclusion, faster-X evolution of proteins in the pea aphid seems to be primarily explained by relaxed selection on lowly expressed genes, a class of genes more frequent on the X chromosome than on autosomes. We found little evidence that the exposure of X-linked recessive alleles to selection in hemizygous males plays an additional role in faster-X evolution, but this hypothesis deserves further investigation

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on more specific data sets. Importantly, the pea aphid forms a species complex, including races and cryptic species at different stages of divergence (Peccoud, Ollivier, et al. 2009; Peccoud, Simon, et al. 2009; Peccoud et al. 2015). This complex offers an excellent opportunity to investigate the tempo and mechanisms of chromosome evolution through comparative genomics. In particular, characterizing gene expression in morphs of closely and distantly related lineages could help disentangling the role of drift and selection in the low expression of the X and its masculinization.

Supplementary Material

Supplementary data are available at *Genome Biology and Evolution* online.

Acknowledgments

This work was supported by the Agence Nationale de la Recherche (grants ANR-09-GENM-017-001 to Denis Tagu, ANR-11-BSV7-005-01 to Denis Tagu and ANR-11-BSV7-007 to J.C.S.); INRA-AIP BioRessources (project Poly-Express to J.C.S. and Denis Tagu); the Fondation pour la Recherche sur la Biodiversité (grant AAP-IN-2009-020 to J.C.S.); the Institut Polaire Francais Paul-Emile Victor (IPEV project 426 Arctaphid to Maurice Hullé and J.C.S.); the Genoscope (project 62 AAP 2009/2010 to J.C.S.) and the Swiss National Science Foundation (grants PBLAA-122658 and PA00P3-139720 to J.J.). We would like to thank the GenOuest platform for the use of its cluster to perform the computational analyses, and two anonymous referees for their constructive comments on a previous draft of this manuscript.

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