YY males of the dioecious plant \textit{Mercurialis annua} are fully viable but produce largely infertile pollen

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\textbf{Abstract}

- The suppression of recombination during sex-chromosome evolution is thought to be favoured by linkage between the sex-determining locus and sexually antagonistic loci, and leads to the degeneration of the chromosome restricted to the heterogametic sex. Despite substantial evidence for genetic degeneration at the sequence level, the phenotypic effects of the earliest stages of sex-chromosome evolution are poorly known.
- Here, we compare the morphology, viability and fertility between XY and YY individuals produced by crossing seed-producing males in the dioecious plant \textit{Mercurialis annua}, which has young sex chromosomes with limited X–Y sequence divergence.
- We found no significant difference in viability or vegetative morphology between XY and YY males. However, electron microscopy revealed clear differences in pollen anatomy, and YY males were significantly poorer sires in competition with their XY counterparts. Our study suggests either that the X chromosome is required for full male fertility in \textit{M. annua}, or that male fertility is sensitive to the dosage of relevant Y-linked genes.
- We discuss the possibility that the maintenance of male-fertility genes on the X chromosome might have been favoured in recent population expansions that selected for the ability of females to produce pollen in the absence of males.

\textbf{Introduction}

Sex chromosomes have evolved numerous times in eukaryotes, showing a number of features that are remarkably common. They include the suppression of recombination around the sex-determining locus, and the genetic degeneration of this nonrecombining region, including the loss of genes, impairment of gene function, and the accumulation of repetitive elements (Charlesworth, 1991; Charlesworth \textit{et al.}, 2005; Bachtrog \textit{et al.}, 2011; Ming \textit{et al.}, 2011; Bachtrog, 2013; Abbott \textit{et al.}, 2017). The evolutionary genetic reasons for this degeneration are reasonably well understood (Charlesworth & Charlesworth, 2000; Bachtrog, 2008). For instance, purifying selection is much less efficient in regions of low recombination because of Hill–Robertson interference between linked loci (Hill & Robertson, 1966; McVean & Charlesworth, 2000), and processes such as genetic hitchhiking (Maynard-Smith & Haigh, 1974; Rice, 1987a), background selection (Charlesworth \textit{et al.}, 1995; Kaiser & Charlesworth, 2009) and Muller’s ratchet result in the accumulation of deleterious mutations (Muller, 1918; Gordo & Charlesworth, 2001; Bachtrog & Gordo, 2004; Engelstädter, 2008). The effects of such processes on the nonrecombining region of sex chromosomes have been documented at the genomic and transcriptomic levels in a diverse range of organisms (Rice, 1996; Steinemann & Steinemann, 1998; Berlin \textit{et al.}, 2007; Kaiser & Charlesworth, 2010), including plants (Filatov \textit{et al.}, 2000; Liu \textit{et al.}, 2004; Hough \textit{et al.}, 2017). By contrast, their phenotypic effects in terms of morphology, life history, viability and fertility have received little attention beyond potentially associated patterns of sexual dimorphism.

Although we expect nonrecombining regions of the genome to be prone to degenerative processes, they may also be targets of positive selection, conferring advantages on individuals of one or both sexes (Bachtrog, 2006; Ellegren & Parsch, 2007; Zhou & Bachtrog, 2012). Indeed, alleles that confer an advantage on one sex and a disadvantage on the other (‘sexually antagonistic’, or SA, alleles) are thought to be one of the reasons for the evolution of suppressed recombination around the sex-determining locus in the first place (Charlesworth & Charlesworth, 1980; Rice, 1987b, 1992; van Doorn & Kirkpatrick, 2007). For instance, alleles that are advantageous to males but detrimental to females will increase in frequency if in tight linkage with the male-determining locus (and vice versa for female-advantageous mutations), because recombination would place them in a genetic background in which their expression is deleterious. The sexual antagonism hypothesis also provides a plausible explanation for the existence of ‘evolutionary strata’ on sex chromosomes, where regions close to the sex-determining locus, for which

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recombination was suppressed first, are more divergent than those further away that stopped recombining more recently (Charlesworth et al., 2005; Bergero & Charlesworth, 2009). However, despite its conceptual plausibility, there is still limited empirical evidence for SA selection on sex chromosomes (Ironside, 2010). In the guppy (Poecilia reticulata), attractive colouration increases male siring success but would be deleterious in females that would be rendered more visible to predators (Brooks, 2000). Male colouration factors are linked to the sex-determining region of the Y chromosome in guppy populations prone to high predation (Lindholm & Breden, 2002; Charlesworth, 2018), pointing to the possibility that the nonrecombining region may have expanded as a result of SA selection. However, recent work has dismissed the idea of evolutionary strata on the Y chromosome in guppies because recombination is suppressed in males generally, and not just around the sex-determining locus (Bergero et al., 2019).

More widely, the enrichment of genes with sex-biased expression on the sex chromosomes is also consistent with the SA hypothesis (Ellegren & Parsch, 2007; Bachtrög et al., 2011; Connallon & Clark, 2013). This is because differential gene expression between the sexes points to a response to sex-specific selection (Connallon & Clark, 2010; Meisel et al., 2012). In the dioecious plant Silene latifolia, for instance, quantitative trait loci associated with sexual dimorphism that have the potential to resolve intralocus sexual conflicts, show sex-specific expression (Scotti & Delph, 2006; Delph et al., 2010) and are enriched on the sex chromosomes (Zemp et al., 2016). Similarly, in the subdioecious plant Fragaria virginiana, linked sex-limited QTL underlie sexually dimorphic traits (Spigler et al., 2011). Importantly, sex chromosomes in which recombination has ceased recently may come to harbour sex-specific variation before accumulating deleterious mutations, with a possible net positive effect on the corresponding sex.

The detection of phenotypic effects of Y-chromosome evolution, whether negative or positive, is likely to differ between the haploid and diploid phases of the plant life cycle. In the haploid phase of the life cycle, notably during pollen-tube growth, deleterious mutations should have an immediate effect on the phenotype. Haploid expression should therefore subject genes to strong purifying selection (Bergero & Charlesworth, 2009; Chibalina & Filatov, 2011), resulting in a slower rate of Y chromosome degeneration in plants than in animals (Chibalina & Filatov, 2011; Charlesworth, 2015; Krasovec et al., 2018). Nevertheless, the gradual accumulation of deleterious Y-linked mutations might eventually become detectable in the form of reduced competitiveness of Y-chromosome-bearing pollen tubes (Charlesworth, 2002b; Sandler et al., 2018), a phenomenon known as ‘certation’ (Smith, 1963; Lloyd, 1974). Such effects on gametophyte fitness have been invoked to explain female-biased sex ratios in the wind-pollinated dioecious plant Rumex nivalis (Stehlík et al., 2008). By contrast to their effects on the haploid phase of the plant life cycle, recessive mutations on the Y chromosome will tend to be masked in the diploid phase as a result of the expression of functional alleles on the X, and even partially dominant mutations might become hidden by dosage compensation (Charlesworth, 1996; Wilson & Makova, 2009; Vyskot & Hobza, 2015).

Although it will often be difficult to detect the effects of Y-linked mutations on diploid individuals, they should in fact become apparent through comparisons between XY and YY males. YY males can be generated by crossing XY males that have been artificially feminised (Durand & Durand, 1984; Khryyanov, 2002) or that show natural ‘leaky’ or ‘inconstant’ sex expression (Ehlers & Bataillon, 2007; Cossard & Pannell, 2019). Such manipulations have typically resulted in nonviable YY progeny in most animals with old sex chromosomes (Graves, 2006). By contrast, YY individuals are viable and fertile in animals with nondegenerate Y chromosomes such as a variety of fish species (Yamamoto, 1963, 1975; Chevassus et al., 1988; Scott et al., 1989; Kavumpurath & Pandian, 1993). A notable exception to this pattern is provided by WW individuals of the androdioecious clam shrimp Euclimnadia texana, in which ZW and WW hermaphrodites naturally co-occur with ZZ males. Here, WW hermaphrodites are viable but have substantially lower fitness than their ZW counterparts, pointing to recessive deleterious effects of W-linked alleles (Sassaman & Weeks, 2002). In plants, YY individuals are nonviable in both Silene latifolia (Janoušek et al., 1998; Soukupova et al., 2014; Veltsos & Delph, 2019), which has highly divergent heteromorphic sex chromosomes (Krasovec et al., 2018), and in Carica papaya, which has homomorphic sex chromosomes at the cytological level but shows XY divergence at the sequence level (Liu et al., 2004; Yu et al., 2008b). Viable YY males have been reported in Asparagus officinalis (Harkess et al., 2017), Spinacia oleracea (Yamamoto et al., 2014; Watlington & Ming, 2018), Cannabis sativa (Peil et al., 2003), Phoenix dactylifera and Actinidia chinensis (reviewed in Ming et al., 2011) Yet all these records provide limited details about the performance of YY individuals, and we are aware of no phenotypic comparisons between XY and YY individuals.

Here, we investigate the phenotypic consequences of early sex-chromosome evolution in adult males of the wind-pollinated dioecious plant Mercurialis annua L. (Euphorbiaceae). The M. annua species complex includes monoeocious and androdioecious polyploid lineages, but diploid populations (which are widespread across eastern, central and western Europe) are exclusively dioecious (Oubbard et al., 2006). Dioecy is ancestral in the genus Mercurialis (Krähenbühl et al., 2002), where all the dioecious species display common sexual dimorphism in their inflorescences, with male flowers developing on long peduncles held above the plant canopy and female flowers usually placed on much shorter pedicels in the leaf axils (Pannell, 1997; Buggs & Pannell, 2007). Mercurialis annua and its dioecious or androdioecious annual relatives share the same XY sex-determination system (Russell & Pannell, 2015). Veltsos et al. (2018, 2019) estimated that recombination has been suppressed over one-third the length of the M. annua Y chromosome, a region measuring c. 15 Mb with c. 500 genes and estimated to be younger than 1 Ma. About half of the c. 30 genes that show male-specific expression in M. annua occurs in the nonrecombining region of the Y, and the possession of the pedunculate male inflorescence, a likely sexually antagonistic trait (Santos del Blanco et al., 2018), is also
Y-linked (Russell & Pannell, 2015; Veltsos et al., 2018). Consistent with its relative youth, the Y chromosome shows signs of only mild sequence degeneration, with pseudogenisation of only a single Y-linked allele (as a result of a premature stop codon) and a modest excess in the ratio of nonsynonymous to synonymous mutations compared with autosomal genes (Veltsos et al., 2019).

Because the *M. annua* Y chromosome shows some signs of degeneration, we might expect YY individuals that lack an X complement to have reduced viability and/or fertility. They might also suffer fitness consequences from a dosage imbalance, as the YY genotype is rarely tested by selection. Alternatively, multiple features of the sex-linked loci, such as an enrichment in female-biased genes and the elevated sex-biased expression in male-biased genes, point to the possibility of ongoing sexually antagonistic selection shaping the Y chromosome (Veltsos et al., 2019). We might therefore also expect YY individuals to have a ‘super-male’ phenotype, if the Y-linked alleles are not completely dominant. To evaluate the phenotypic consequences of the recently evolved Y chromosome in *M. annua*, we compared the phenotypes of typical XY males with experimentally induced YY males for a range of vegetative and reproductive traits. We found limited phenotypic differences in the vegetative phenotypes or in viability and vigour between XY and YY males. By contrast, the pollen produced by YY males showed signs of partial sterility, which was confirmed by the progeny sex ratio of the number of XY and YY brothers to that of their XX sisters produced under open pollination. To our knowledge, our results represent the first account of the diploid-stage phenotypic effects of divergence between X and Y chromosomes of a plant species.

### Materials and Methods

#### Generation of YY males in *Mercurialis annua*

Two approaches were taken to generate YY males in *M. annua*. In the ‘hormone’ experiment, we germinated diploid *M. annua* seeds and kept 38 male seedlings in a growth chamber. Femising cytokinin (6-benzylaminopurine) was diluted in HCl at 10 mM for stock solution, then in ddH2O at 2 μM for use. Seedlings were sprayed with the femising cytokinin solution once a day, following a protocol modified from Louis & Durand (1978), which led to the production of a large number of pistillate flowers in the male inflorescences. We allowed the modified males to polli- nate one another, and then bulk-harvested the seeds. In total, we collected 443 seeds from these crosses.

In the ‘pruning’ experiment, we stimulated female-flower production through severe pruning on 2000 diploid *M. annua* males grown in a common garden, prompted by the observation reported by Kuhn (1939) that such pruning elicits increased lea- kiness in sex expression. After 10 wk of growth under open polli- nation, we harvested 496 seeds from the pruned males.

#### Identification and characterisation of YY vs XY males

All the seeds collected from the male crosses of both experiments were germinated and raised to maturity at the University of Lausanne. Seeds from the hormone experiment were grown in an outdoor field in 2015, and seeds from the pruning experiment were grown under glasshouse conditions in 2017. When the plants began flowering, we recorded the numbers of male and female seedlings among the progeny. In addition, a restriction enzyme-based assay was developed based on X- and Y-specific single nucleotide polymorphisms (SNPs) to distinguish between XY and YY males (see Supporting Information Methods S1; Fig. S1). Briefly, a sex-linked PCR product was digested with two restriction enzymes (BceI and Rsd) which cut only the X- or Y- linked sequence, therefore allowing individuals with or without an X to be distinguished. The Y-specific sequence characterised amplified region (SCAR) marker (Khakda et al., 2002) was used as a positive control for PCR amplification.

The following traits were measured on all XY and YY males: plant height, male flower biomass, peduncle biomass and total biomass. We also calculated the biomass/height ratio and the relative male reproductive allocation (MRA) as the proportion of total biomass allocated to reproductive organs, that is the biomass of flowers and pederuncles divided by the total reproductive and vegetative biomass.

We used linear mixed-effect models to compare phenotypic traits between XY and YY individuals using the lme4 library (v.1.1-17; Bates et al., 2015) in R v3.5.1. We conducted principal component analysis (PCA) to eliminate covariance between traits and applied linear mixed-effect models to the first four principal components of normalised independent phenotypic measurements. All data analysis was performed using R v3.5.1 (R Development Core Team, 2008) and the summary tables from the models were generated using the R package sjPlot v.2.4 (Lüdecke, 2017).

#### Assessment of the relative viability of YY males

We assessed the relative viability of YY and XY males by comparing the ratio of XY and YY progeny from the crosses among femi- nised males, with the ratio expected from random mating and equal survival of progeny genotypes (see scheme in Fig. 1a). Given the known XY sex determination in *M. annua*, crosses between parental XY males should result in a 1 : 2 : 1 ratio of XX female to XY male to YY male zygotes. Under the null hypothesis of complete YY viability, we therefore expect 75% of the F1 progeny to be males (p1 in Fig. 1a); by contrast, we expect 67% males under the assumption of complete YY nonviability (p2 in Fig. 1a). An intermediate value suggests partial YY inviability. We assessed the proportion of male progeny for significant deviations from expected values using chi-squared and likelihood-ratio tests (Etz, 2018).

#### Assessment of pollen morphology and anatomy in YY and XY males

We compared the morphology and gross internal structure of pollen grains from air-dried flowers produced by 9 YY and 9 XY male progeny of leaky males from the hormone experiment, using both scanning electron microscopy (SEM) and
transmission electron microscopy (TEM). We also included a mixed sample from five fresh normal diploid *M. annua* males as a further control. Whole flowers were used for SEM, while anthers were isolated for TEM. Multiple observations were applied to verify the results. Pollen size (polar and equator diameters) was measured on SEM images using ImageJ v.1.49 (Schneider et al., 2012).

Assessment of the relative fertility of YY and XY males
We compared the fertility of YY and XY males by assessing their relative siring success in competition with one another in a common garden, using progeny sex ratios to infer fertility (Fig. 1b). Specifically, we grew all progeny produced from the XY crosses from the hormone experiment in a single common garden, that is crossing XX sisters with their XY and YY brothers via open pollination. Mature seeds from the female plants were collected and grown to estimate the F2 sex ratio (i.e. the proportion of males among the progeny). We reasoned that all seeds sired by YY males would be males, whereas those sired by XY males would have a 50% sex ratio. Given that YY individuals made up 1/3 of the male plants in the F1 progeny of XY parents (see Results), we therefore expected 67% of the F2 progeny to be males if there was equal fertility of YY and XY males (p1 in Fig. 1b); by contrast, if YY individuals were completely sterile, all F2 progeny should be sired by XY males, with a corresponding 50% sex ratio (p2 in Fig. 1b). We applied both chi-squared and likelihood-ratio tests to test for deviation of the observed F2 sex ratio from these two extreme scenarios, adjusting for the actual F1 XY : YY ratio based on our molecular genotyping described above.

### Results

Mating among hormone-feminised males (hormone experiment) or among males with pruning-induced female-flower production (pruning experiment) yielded 939 seeds, of which 278 survived until maturity. Of these, there were 203 male and 75 female progeny (73% males). Recall that random mating among XY males should produce a proportion of 75% male progeny if YY and XY individuals are equally viable (Fig. 1a). The observed F1 sex ratio is therefore consistent with the scenario of equivalent viability of the two male types (i.e. we failed to reject the null hypothesis p1: $X^2_{1[1]} = 0.58, P = 0.45$). Alternatively, inviability of all YY progeny would have yielded a sex ratio of 67% males; our results are inconsistent with this scenario (p2: $X^2_{1[1]} = 5.05, P = 0.02$). Fully YY viability was 1.8 times more likely than complete YY lethality (Fig. S2a). The restriction enzyme genotyping assay confirmed the presence of 57 YY and 106 XY males in our sample of progeny. A chi-squared test revealed no significant deviation from the expected 2:1 ratio of XY:YY male progeny ($X^2_{1[1]} = 0.20, P = 0.66$).

### Comparisons between YY and XY phenotypes
We found almost no phenotypic differences between YY and XY males, irrespective of whether they had been generated by the hormone experiment or the pruning experiment (Tables 1, 2; Fig. S3). Specifically, YY males were identical to normal XY progeny from the hormone experiment in plant height, biomass/height ratio, absolute biomass allocated to different organs (flower, peduncle and vegetative parts), MRA, and the flower/peduncle ratio (P > 0.05 for all comparisons; Table 1). Nor were there any differences between the two male genotypes in terms of their principal components from a PCA analysis (Table S1; Figs S4, S5). The results from the pruning experiment were similar, except that YY males had a slightly higher MRA than XY males (n = 53, P = 0.025), as well as higher relative reproductive biomass allocation to male flowers (n = 61, P = 0.024 for flower/peduncle ratio; Table 2).

### Comparisons of pollen between YY and XY males
SEM revealed clear differences in the morphology and exine ornamentation of pollen produced by YY vs XY males (Fig. 2,
Table 1 Summary of linear mixed models for the effect of genotype on male phenotypes from the hormone experiment of *Mercurialis annua* L., with sampling date and sampler as random variables

<table>
<thead>
<tr>
<th>Predictors</th>
<th>Plant height</th>
<th>Biomass/height ratio</th>
<th>Male flower biomass</th>
<th>Peduncle biomass</th>
<th>Total biomass</th>
<th>Male reproductive allocation (MRA)</th>
<th>Flower/peduncle ratio</th>
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Bold values represent $P$ value < 0.05.

Table 2 Summary of linear mixed models for the effect of genotype on male phenotype from the pruning experiment of *Mercurialis annua* L., with family as a random variable.

<table>
<thead>
<tr>
<th>Predictors</th>
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Bold values represent $P$ value < 0.05.
In general, pollen grains were small, with a polar diameter range of 15–28 μm and an equatorial diameter range of 13–20 μm (Table S2). Dried fresh pollen grains from XY males were prolate elliptic, tricolpate monads, with a mainly reticulate exine sculpture (Fig. 2a). Apertures were invisible due to the constricted colpori. By contrast, dried pollen grains of XY males were elliptic (Fig. 2b), with one aperture located in the middle of each slightly infolded lolongate colporus. The ornamentation was granulate and reticulate, with small holes distributed on parts of the pollen wall. Irregular attachments were occasionally observed on the pollen surface. Pollen grains produced by YY males were nearly spheroidal, with mainly granulate ornamentation and more frequent surface presentation of verrucae (Fig. 2c).

TEM revealed more significant differences in the internal ultra-structures between pollen grains produced by XY and YY males (Fig. 2, bottom row). Both fresh (Fig. 2d) and air-dried pollen grains (Fig. 2e) from XY males maintained an internal matrix and had a distinct cell boundary. By contrast, many pollen grains from YY males (Fig. 2f) had a thicker exine layer, lacked starch storage within the grain, and presented an indistinct separation of intracellular and intercellular substrates. Other organelles such as the Golgi apparatus and mitochondria were also much less apparent in pollen from YY than from XY individuals. Interestingly, some YY anthers had pollen that resembled that of XY individuals, that is the differences just mentioned were not completely categorical at the individual plant level. Perhaps significantly, any differences between pollen grains among YY individuals were always from different anthers (i.e. we did not observe the two types of pollen in the same anther). Among the 23 biological replicates of single anther specimen from YY males, 12 samples showed abnormal pollen characters, while only two out of 11 samples from XY males were different from control XY samples (Table S2).

**Relative fertility and siring success of YY and XY males**

Results from mating arrays suggested that YY males were less fertile than XY males. We obtained 192 F₂ seedlings from seeds produced from mating among the F₁ progeny of hormone-treated parents. If we assume that the F₁ population comprised XY and YY males at a 2 : 1 ratio (along with XX females), the F₂ generation should comprise 67% males if XY and YY males are equally capable of siring ovules (Fig. 1b). The observed F₂ sex ratio was 56% (107 males, 85 females), representing a significant deficit.
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consistent with the conclusion, reached on the basis of DNA appears to be at least partly sterile. Together, our results are con-
dult sporophyte. By contrast, pollen produced by YY males double Y-chromosome dosage for some reproductive traits of the functional. We also observed minor potentially positive effects of genes on the Y chromosome affecting vegetative growth remain anatomy and siring ability of their pollen. YY and XY males were
indistinguishable for almost all traits investigated, indicating that genes on the Y chromosome affecting vegetative growth remain functional. We also observed minor potentially positive effects of double Y-chromosome dosage for some reproductive traits of the adult sporophyte. By contrast, pollen produced by YY males appears to be at least partly sterile. Together, our results are consistent with the conclusion, reached on the basis of DNA sequence analysis (Veltsos et al., 2018, 2019), that the nonrecom-
bining region of the M. annua Y chromosome is only mildly degenerated. They also indicate that the earliest consequences of Y-chromosome evolution in M. annua involve fertility.

Discussion

To evaluate the phenotypic consequences of Y-chromosome evolu-
tion, we compared the viability and fertility of YY and XY males of the plant M. annua, as well as the morphology, internal anatomy and siring ability of their pollen. YY and XY males were indistinguishable for almost all traits investigated, indicating that genes on the Y chromosome affecting vegetative growth remain functional. We also observed minor potentially positive effects of double Y-chromosome dosage for some reproductive traits of the adult sporophyte. By contrast, pollen produced by YY males appears to be at least partly sterile. Together, our results are consistent with the conclusion, reached on the basis of DNA sequence analysis (Veltsos et al., 2018, 2019), that the nonrecom-
bining region of the M. annua Y chromosome is only mildly degenerated. They also indicate that the earliest consequences of Y-chromosome evolution in M. annua involve fertility.

No difference in viability or vegetative morphology between YY and XY males

The similar vegetative morphology and viability of YY and XY males of M. annua indicated that an X chromosome is not required for effective growth, and that a double dosage of the Y chromosome has little or no effect on the diploid vegetative phe-
totype. Previous work has documented mild degeneration of the M. annua Y chromosome at the sequence level, with a slightly inflated dNdS ratio for Y-linked genes, implying the accumula-
tion of mildly deleterious mutations, and clear evidence for the pseudogenisation of only one gene of unknown function (Veltsos et al., 2019). It would appear that any Y-chromosome degeneration does not affect sporophyte growth. Given that the Y chro-
mosome accounts for at least an eighth of the genome of M. annua, and that a third of the Y chromosome is nonrecom-
bining (Veltsos et al., 2018, 2019), it seems unlikely the absence of phenotypic effects of Y-chromosome evolution is due to a paucity of genes on the Y that affect growth and rather points simply to very mild degeneration.

While it is possible that YY individuals suffer from mildly dele-
terious effects that we were unable to detect, or from effects on traits that we did not measure, the viability and phenotypic simi-
larity between individuals with and without an X chromosome (or with a single or double dose of the Y) are in striking contrast with studies that show substantially poorer performance of YY males compared with their XY counterparts. For instance, Y-
chromosome degeneration has led to YY lethality in many animal species (Graves, 2006), as well as in the plants Rumex hastatus (Smith, 1963), Silene latifolia (Westergaard, 1958; Janousek et al., 1998; Soukupová et al., 2014; Veltsos & Delph, 2019), and Carica papaya (Liu et al., 2004; Ming & Moore, 2007; Yu et al., 2008a). These species probably have older sex chromo-
somes than M. annua, with a longer history of Y-chromosome degeneration. For instance, tetraploid Y1Y1Y2Y2 plants of Rumex hastatus are inviable (Smith, 1963), a species for which chro-
mosomes probably evolved 15–16 Ma (Navajas-Pérez et al., 2005). Much of the Y chromosome of S. latifolia may have ceased recombining with the X 11 Ma (Krasovec et al., 2018). In Carica papaya, the divergence between X and Y chromosomes has been more recent than in S. latifolia, estimated between 0.6 and 2.5 Myr (Yu et al., 2008b), but may still be older than that in M. annua, in which the nonrecombining region is likely < 1 Myr old (Veltsos et al., 2019). The vegetative performance of YY com-
pared with XY individuals of M. annua is perhaps similar to that for Asparagus officinalis (Harkess et al., 2017) and Spinacia oleracea (Wadlington & Ming, 2018), which also have viable YY and nascent sex chromosomes. However, we are unaware of any direct comparisons between YY and XY phenotypes for any plant species other than M. annua.

Difference in reproductive traits and fertility between YY and XY males

By contrast to the purely vegetative traits, we found differences between YY and XY males for certain reproductive traits: YY males had higher reproductive allocation and a greater flower/pe-

duncle ratio than XY males in the pruning experiment. These results are compatible with a scenario in which homozygosity at one or more loci on the Y chromosome results in elevated male flower production, suggesting potential male-beneficial effects on the Y for at least one component of reproductive success. Such ‘super-male’ effects of the YY genotype for both nonreproductive and reproductive traits have been found in some animals, for example mating behaviour and siring success in Oryzias latipes (Hamilton et al., 1969), but we are not aware of similar reports for any plant species.

Notwithstanding the potentially positive effects of the YY con-
figuration on reproductive traits, our results point clearly to the infertility of YY males. Crossing results indicated that F2 progeny were sired more by XY than YY males, and YY males produced a substantial proportion of pollen grains that differed from pollen produced by XY males in external and internal morphological traits. It is noteworthy that pollen development of YY males var-
ied between anthers of the same individual, with some anthers producing only defective pollen and others producing only pollen with normal appearance. It therefore appears that the YY configu-
ration compromises the stability of pollen development at the anther level, a suggestion that is coherent with the widely observed temperature sensitivity of male sterility in other plants, where low (e.g. Imin et al., 2004) or high temperatures (e.g. Sakata et al., 2010) render otherwise fertile plants sterile. Although the normal appearance of some of the pollen from YY plants suggests partial fertility, our crossing results do not rule out complete sterility of YY males.

There are two possible explanations for the observed pollen sterility of YY males in M. annua. One possibility is that the Y
carries a partially penetrant loss-of-function mutation of a gene that is functional on the X, consistent with the mild degeneration of the Y (Veltos et al., 2018, 2019). If so, our results would imply that Y-chromosome degeneration can have deleterious effects even on an essential male function. Such an implication runs counter to the expectation that the X chromosome should harbour alleles under sexually antagonistic selection that promote female fertility and/or suppress male function, although the X may still contain recessive male-fertility genes (Ellegren & Parsh, 2007). Indeed, the X is known to contain genes associated with spermatogenesis in humans (Ross et al., 2005). An alternative explanation is that the pollen sterility of YY males represents an effect of dosage: a Y-linked gene with male-biased or male-limited expression, of which there are several (Veltos et al., 2019), may impair pollen development when expressed at a double dose, which is normally not tested by selection. Although we cannot distinguish between these two possibilities without gene expression comparisons between XY, YY and XXY individuals, our results point unambiguously to a divergence in gene function between an X- and Y-linked allele affecting pollen development.

Importantly, the effects of Y-chromosome evolution on pollen development of YY males in M. annua differ from the effect of certation, that is the poorer performance of Y- than X-bearing pollen tubes, as has been reported for dioecious species of Rumex (Stehlik & Barrett, 2005; Stehlik et al., 2008; Sandler et al., 2018). Certation biases the progeny sex ratio towards more daughters, possibly the result of the expression of deleterious mutations in the haploid genome of Y-bearing haploid pollen tubes (Smith, 1963; Lloyd, 1974); such mutations are expected to accumulate through the process of Muller’s ratchet, or because purifying selection is weakened in nonrecombining regions by background selection and Hill-Robertson interference (Nei, 1970; Charlesworth, 2002a; Vyskot & Hoba, 2004). By contrast, the poor performance of pollen from YY individuals in M. annua may be the outcome of a quasineutral process, because the vast majority of pollen production in wild populations is by XY individuals (YY individuals are very rare in nature, Cossard & Pannell, 2019), that is the effects we have observed would almost never be exposed to purifying selection in the wild. Moreover, by contrast with observations of sex-ratio bias in Rumex, the consistently equal sex ratio in dioecious populations of diploid M. annua indicates that the Y-bearing pollen grains compete on equal terms with X-bearing pollen in their race to fertilize ovules. We therefore have no evidence for effects of the Y chromosome on the haploid gametophytic phase in M. annua, be they deleterious and associated with chromosome degeneration, or beneficial and associated with the accumulation of male-beneficial alleles (Scott & Otto, 2017).

Conclusion

To our knowledge, this report is the first to describe male sterility associated with the absence of an X chromosome in plants that are otherwise completely viable. It joins evidence from the effects of certation on progeny sex ratios for early phenotypic effects of sex-chromosome evolution (Stehlik & Barrett, 2005; Stehlik et al., 2008), albeit in the context of (diploid) microsporogenesis rather than on (haploid) pollen-tube growth. The cause of the pollen defect is unclear, but the sterility of YY males would seem to suggest either: (1) that at least one gene required for the proper development of fertile pollen is compromised on the Y and remains functional on the X; or (2) that a double dose of one or more genes on the Y chromosome that has evolved male-biased male-limited gene expression impairs pollen-grain development. Future work comparing patterns of gene expression for such genes between XY and YY males will help to distinguish between these possibilities.

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Author contributions

JRP, XL and PV conceived the study. XL, PV and GGC conducted the experiments and collected the data. PV and JG analysed the molecular tests; Antonio Mucciolo, Damien De Bellis from the Electron Microscopy Facility at the University of Lausanne provided technical support for electron microscopy. The research was funded by grants from the Swiss National Science Foundation and studentships awarded to XL and JG from the Faculty of Biology and Medicine, University of Lausanne.

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References


Supporting Information

Additional Supporting Information may be found online in the Supporting Information section at the end of the article.

**Fig. S1** Restriction enzyme assay to distinguish XY and YY individuals.

**Fig. S2** Likelihood-ratio tests for progeny sex ratios.
Fig. S3 Comparison in phenotypic traits between XY and YY males of the F1 progeny.

Fig. S4 Summary of PCA for phenotypic measurements of F1 males from the hormone-induced experiment.

Fig. S5 Summary of PCA for phenotypic measurements of F1 males from the pruning-induced experiment.

Methods S1 Identification between XY and YY males with a restriction enzyme-based assay based on sex-specific SNPs.

Table S1 Summary of generalised linear model (GLM) comparison XY with YY males in terms of the first four principal components for morphology traits.

Table S2 Pollen observation under electron microscopy.

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