



Dosage compensation by upregulation of maternal X alleles in both males and females in young plant sex chromosomes

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A recommendation – based on reviews by three anonymous reviewers – of Muyle A, Zemp N, Fruchard C, Cegan R, Vrana J, Deschamps C, Tavares R, Picard F, Hobza R, Widmer A and Marais GAB. 2018. Genomic imprinting mediates dosage compensation in a young plant XY system. bioRxiv 118695, ver. 6 peer-reviewed by Peer Community In Evolutionary Biology. doi: <https://doi.org/10.1101/179044>

Sex chromosomes evolve as recombination is suppressed between the X and Y chromosomes. The loss of recombination on the sex-limited chromosome (the Y in mammals) leads to degeneration of both gene expression and gene content for many genes [1]. Loss of gene expression or content from the Y chromosome leads to differences in gene dose between males and females for X-linked genes. Because expression levels are often correlated with gene dose [2], these hemizygous genes have a lower expression levels in the heterogametic sex. This in turn disrupts the stoichiometric balance among genes in protein complexes that have components on both the sex chromosomes and autosomes [3], which could have serious deleterious consequences for the heterogametic sex.

To overcome these deleterious effects of degeneration, the expression levels of dosage sensitive X-linked genes, and in some organisms, entire X chromosomes, are compensated, the expression of the single copy of in the heterogametic sex being increased. Dosage compensation for such genes has evolved in several species, restoring similar expression levels as in the ancestral state in males and/or equal gene expression in males and females [4-8]. The mechanisms for dosage compensation are variable among species and their evolutionary paths are not fully understood, as the few model sex chromosomes studied so far have old, and highly degenerate sex chromosomes [4-7].

Muyle et al. [9] studied the young sex chromosomes of the plant *Silene latifolia*, which has young sex chromosomes (4 MY) and highly variable dosage compensation [10, 11]. The authors used both an outgroup species without sex chromosomes for obtaining a proxy for ancestral expression levels before Y degeneration, and implemented methods to identify sex-linked genes and disentangle paternal versus maternal allele expression [12]. Using these elements, Muyle et al. [9] reveal upregulation of maternal X alleles in both males and females in the young *S. latifolia* sex chromosomes [9], possibly by genomic imprinting. The upregulation in both sexes of the maternal X alleles likely yields non-optimal gene expression in females, which is strikingly consistent with the theoretical first step of dosage compensation as postulated by Ohno [8], which predicts restoration of ancestral expression in males, over-expression in females, and unequal expression in the two sexes. These findings provide surprising insight into the earliest stages of dosage compensation, one of the most intriguing aspects of evolutionary biology.

References

- [1] Bachtrog D. 2013. Y chromosome evolution: emerging insights into processes of Y-chromosome degeneration? *Nature Reviews Genetics* 14: 113–124. doi: <https://doi.org/10.1038/nrg3366>
- [2] Malone JH, Cho D-Y, Mattiuzzo NR, Artieri CG, Jiang L, Dale RK, Smith HE, McDaniel J, Munro S, Salit M, Andrews J, Przytycka TM and Oliver B. 2012. Mediation of *Drosophila* autosomal dosage effects and compensation by network interactions. *Genome Biology* 13: R28. doi: <https://doi.org/10.1186/gb-2012-13-4-r28>
- [3] Pessia E, Makino T, Bailly-Bechet M, McLysaght A and Marais GAB. 2012. Mammalian X chromosome inactivation evolved as a dosage-compensation mechanism for dosage-sensitive genes on the X chromosome. *Proceedings of the National Academy of Sciences of the United States of America*. 109: 5346–5351. doi: <https://doi.org/10.1073/pnas.1116763109>
- [4] Graves JAM. 2016. Evolution of vertebrate sex chromosomes and dosage compensation. *Nature Reviews Genetics* 17: 33–46. doi: <https://doi.org/10.1038/nrg.2015.2>
- [5] Mank JE. 2013. Sex chromosome dosage compensation: definitely not for everyone. *Trends in Genetics* 12: 677–683. doi: <https://doi.org/10.1016/j.tig.2013.07.005>
- [6] Pessia E and Engelstädter J. 2014. The evolution of X chromosome inactivation in mammals: the demise of Ohno's hypothesis? *Cellular and Molecular Life Sciences* 71: 1383–1394. doi: <https://doi.org/10.1007/s00018-013-1499-6>
- [7] Muyle A, Shearn R and Marais GAB. 2017. The evolution of sex chromosomes and dosage compensation in plants. *Genome Biology and Evolution* 9: 627–645. doi: <https://doi.org/10.1093/gbe/evw282>
- [8] Ohno S. 1967. *Sex chromosomes and sex linked genes*. Springer, Berlin Heidelberg New York.
- [9] Muyle A, Zemp N, Fruchard C, Cegan R, Vrana J, Deschamps C, Tavares R, Picard F, Hobza R, Widmer A and Marais GAB. 2018. Genomic imprinting mediates dosage compensation in a young plant XY system. *bioRxiv* 118695, ver. 6 peer-reviewed by Peer Community In Evolutionary Biology. doi: <https://doi.org/10.1101/179044>
- [10] Papadopulos AST, Chester M, Ridout K and Filatov DA. 2015. Rapid Y degeneration and dosage compensation in plant sex chromosomes. *Proceedings of the National Academy of Sciences of the United States of America* 112: 13021–13026. doi: <https://doi.org/10.1073/pnas.1508454112>

[11] Bergero R, Qiu S and Charlesworth D. 2015. Gene loss from a plant sex chromosome system. *Current Biology* 25: 1234–1240. doi: <https://doi.org/10.1016/j.cub.2015.03.015>

[12] Muyle A, Kafer J, Zemp N, Mousset S, Picard F and Marais GAB. 2016. SEX-DETECTOR: a probabilistic approach to study sex chromosomes in non-model organisms. *Genome Biology and Evolution* 8: 2530–2543. doi: <https://doi.org/10.1093/gbe/evw172> <https://doi.org/10.1093/gbe/evw172>

Appendix

Reviews by three anonymous reviewers: <http://dx.doi.org/10.24072/pci.evolbiol.100044>