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Phylogenomic analyses of sex chromosomes highlight the perils of ancestral state reconstructions of bryophyte mating systems

LE JEUDI 21 MARS 2019 À 12 H

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

The mating system is widely believed to be a key factor shaping genome architecture, the distribution of genetic variation within species, and long term patterns of diversification. Most well-studied lineages of eukaryotes, however, are relatively homogeneous in their mating system (e.g., angiosperms are mostly hermaphroditic, while most vertebrates have separate males and females), precluding comparative studies within groups. The bryophytes are unusual in this regard because they contain nearly equal numbers of hermaphroditic species and species with chromosomally-determined separate sexes. Previously, we conducted an ancestral state reconstruction of dioecy in the mosses. In contradiction to expectations, dioecy appeared to evolve frequently from hermaphroditic ancestors, suggesting that sex chromosomes similarly evolved frequently in this group, much like in the angiosperms. We have now used phylogenomic analyses of transcriptomes from numerous mosses and liverworts to reconstruct the evolutionary history of the bryophyte sex chromosomes. Remarkably, these analyses indicate that the bryophyte sex chromosomes formed more than 300 mya, and that our earlier ancestral state reconstructions of frequent transitions from hermaphroditism to dioecy were incorrect. Nevertheless, although these data demonstrate that sex chromosomes and dioecy are far more ancient than we first inferred, they also show that bryophyte sex chromosomes are highly dynamic in gene content and patterns of molecular evolution.

Lunch et breuvages seront offerts.

**SVP confirmer votre présence sur : <https://doodle.com/poll/r392ew3w83nvc127>
avant le mercredi 20 mars, 10 h**

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