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Cover: Statue of Ardhanarishvara, the half-male, half-female form of Shiva, India 11th century A.D.

NEW TOOLS FOR ANALYSIS AND VISUALIZATION OF RAD-SEQUENCING DATA FOR THE EXPLORATION OF SEX DETERMINATION SYSTEMS.

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How sex determination evolved still remains a key evolutionary question because of our current fragmented view. Improvements in recent genomics approaches, including sequencing based technologies, now enable the investigation of genetic sex determination evolution in a much broader perspective. One widely-used technology to investigate sex determination systems in novel species, is restriction site-associated DNA sequencing (RAD-seq). This reduced representation approach is relatively easy to implement and inexpensive enough to compare genomic populations or sexes in different species simultaneously. However, most bioinformatic tools for analysis of RAD-seq data, such as STACKS software, which was developed for finding allelic variation in complex analyses of multiple populations, are not easy to use for this purpose mainly because of the need to fine-tune numerous parameters that influence results. We thus developed simpler approaches to analyse sex determination based on RAD-seq data, including visualization tools allowing an easier exploration of the results. We used these straightforward tools to study sex determination in many fish species and found that they were not only efficient to decipher simple XX/XY and ZZ/ZW monofactorial sex-determination systems, but also highly effective to detect both large or discrete sex-biased signatures in biological datasets containing potential sex-phenotyping errors, environmentally sex-reversed animals, and even species with complex polygenic systems. Our novel bioinformatics tools provide a new efficient and user-friendly way to analyse RAD-seq datasets to investigate the evolution of genetic sex determination in many eukaryote species.