



Evolutionary Biology Group of Professor Jacek Radwan (<http://evobiolab.biol.amu.edu.pl>) at Adam Mickiewicz University, Poznań, is offering a Post-Doc in an NCN-funded project aiming to investigate effect of sexual selection on genome-wide genetic variation using a powerful approach of experimental evolution coupled with genome re-sequencing. The candidate should hold PhD degree in biological sciences or computer sciences and should have significant achievements in the area of evolutionary biology, molecular genetics or bioinformatics, published in international scientific journals. The employment is offered for three years, starting ideally in April 2019, but it is negotiable. Please apply before 1 March 2019.

Further information about the project and application procedure can be obtained from the project leader via email: jradwan@amu.edu.pl

Brief summary of the project:

Genetic variation is a fuel of evolution, therefore assessing the role of sexual selection in maintaining this variation is fundamental to our understanding of evolutionary processes occurring in sexual species. The rate and extent of adaptation depend on available genetic variation, which sexual selection has long been thought to deplete. However, recent theory predicts that, contrary to the traditional view, sexual selection may actually increase genetic variation due to sexual antagonism and other trade-offs associated with evolution of costly sexually-selected traits. Yet, the effect of sexual selection on the amount of genetic variation segregating in populations has not been investigated empirically. The aim of the proposed project is to investigate effect of sexual selection on genome-wide genetic variation using a powerful approach of experimental evolution coupled with genome re-sequencing.

The project will use a species very well suited for this purpose, the bulb mite *Rhizoglyphus robini*, a well-established model in sexual selection research. The project will benefit from the fact that the genome of this species has recently been assembled and annotated.

Replicate populations will be allowed to evolve for about 20 generations under treatments differing in (i) sex ratio, and thus intensity of sexual selection and (ii) the frequency of males bearing an elaborated sexually-selected trait: thickened legs used for intrasexual contests. Previous research demonstrated that the trait is associated with increased ontogenetic intersexual conflict and life history trade-offs. Genomes of mites from replicated experimental evolution lines will then be sequenced and used for testing whether evolution of costly, condition-dependent sexually selected traits depletes (as predicted by traditional theory) or helps to maintain genetic polymorphism in functional parts of the genome (amino-acid substitutions in protein coding genes, and nucleotide substitutions in cis-regulatory sequences). The results will be interpreted in the context of

intragenomic variation in recombination rate, a major determinant of genetic variation. The variation in recombination rate will be estimated in the proposed project.

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