PhD position: Evolutionary ecology of genome size

Despite an explosive increase of genomic information during the last decade the ultimate causes of genome size variation in eukaryotes are still controversial. At the core of this controversy is the puzzling genome size variation across eukaryotic taxa, which spans approximately five orders of magnitude. The goal of this project is to investigate the mechanisms and significance of genome size variation at short evolutionary timescales, such as variation among closely related species, among populations, and among individuals within a population. Our model system is the facultative asexual rotifer *Brachionus plicatilis*, a cryptic species complex consisting of at least 14 closely related species. Within this complex we focus on a lineage that has undergone a 1.9-3.5 fold increase in genome size relative to its sister-species (e.g., http://www.biomedcentral.com/1471-2148/11/90/abstract). Within this lineage we also study a population that exhibits a remarkable 25% continuous variation in genome size.

The project aims are:

- 1) to elucidate the mechanisms of genome size variation by comparative genome sequencing
- 2) to experimentally determine how variation in genome size is maintained within populations and inherited during sexual reproduction, and
- 3) to test assumptions and predictions of general hypotheses on genome size evolution using intra-population genome size variation, e.g., that clones with small genome size are favored by selection for maximum population growth rates under nutrient limitation, that clones with large genome size accumulate deleterious mutations faster than clones with small genome size, or that genome size variation at the population level significantly co-varies with cell size, body size and egg development time.

The PhD candidate will be involved in all three project aims, in particular aims (1) and (3). On the methodological level, the PhD project will include experimental work with rotifer cultures, genome size measurements using flow cytometry, basic molecular genetic techniques (e.g., PCR), genome sequencing and bioinformatics. The latter will be done in close collaboration with Dr. David Mark Welch at the Josephine Bay Paul Center (MBL, Woods Hole, USA). This will involve a stay at the MBL for a training in genomic analysis of approximately two weeks duration. The main work will be done at the research institute for limnology in Mondsee (http://www.uibk.ac.at/limno/), which is part of the University of Innsbruck. The project is funded by the Austrian Science Funds (FWF) and salary is according to their regulations (https://www.fwf.ac.at/en/research-funding/personnel-costs/).

The Research Institute for Limnology is located in Mondsee, a small town in the Salzkammergut lake district, which lies approximately 30 km east of the City of Salzburg and 200 km east of the City of Innsbruck. The Salzkammergut area is among the most popular regions in Austria. It offers a high quality of life and exceptional opportunities for all kinds of outdoor activities. The Institute has a staff complement of approximately 30, including 8 research scientists, who work on various areas in evolutionary ecology of aquatic organisms.

Applicants should have a M.Sc. degree and a good background in evolutionary biology. Previous experience in experimental work is also advantageous. To apply for this position, please provide: (i) a letter of motivation (in English) including a statement of your research

interests, relevant skills and experience; (ii) a short CV including publications (if applicable); (iii) the names of at least two independent referees.

All materials should be emailed as a single PDF to claus-peter.stelzer@uibk.ac.at with the subject heading "EVOL_GS_PHD".

Application deadline is the 04 Apr 2015. The University of Innsbruck is an equal opportunity employer and particularly encourages applications from women.

For more details, please contact: Dr. Claus-Peter Stelzer (claus-peter.stelzer@uibk.ac.at)