

Can you eat your cake and have it too? Theory (and common sense) tell us you cannot, at least when it comes to reproduction. On one hand, asexual reproduction has clear advantages, such as the lack of the cost of producing males (who do not produce offspring, so it is better to produce only daughters who all can produce more daughters), no risks stemming from mating (time costs of mate searching, injuries in fights for mates, increased predation risk due to flamboyant sexual ornaments and mating, sexually transmitted diseases, etc.), and higher dispersal potential (a single female is sufficient to colonise a new environment). On the other hand, theory predicts that sexual lineages should be more persistent and successful over evolutionary timescales than asexual ones, because recombination (mixing parental genes when sperm and egg fuse into a zygote) and sexual selection (an evolutionary process in which usually males compete for females and only some are able to father the offspring) are thought to facilitate both the spread of good genes through populations. That is why it is expected that abandoning sexual reproduction with all its shortcomings, even though initially may be beneficial, it inevitably leads to the accumulation of bad mutations, which results in lineage extinction. Hence, it has been predicted and observed that asexual lineages represent short-lived twigs on the phylogenetic tree of life, scattered among old large and widely spread branches of sexually reproducing lines. Importantly, however, there are notable exceptions to this pattern, such as bdelloid rotifers or oribatid mites, often termed as ‘evolutionary scandals’ exactly because their existence clashes with our understanding of evolution. In other words, the question is why are some asexual lineages able to persist over long evolutionary time, whereas the majority of them seem to be evolutionary dead ends? Are they examples of when you actually can eat your cake and have it too, i.e. benefit from characteristics of both asexual and sexual reproduction without producing males and all costs it involves? Until very recently there were no tools which would allow for reliable testing whether these ancient asexuals may genetically compensate for the lack of males, either by unknown means of recombination or horizontal gene transfer from unrelated organisms.

Therefore, I propose a large-scale project that takes advantage of the cutting-edge methodology of genome sequencing and analysis of tardigrades, a poorly explored animal group known to a wider audience thanks to their adorable looks and abilities to withstand extreme environmental conditions (even the outer space), to test whether ancient asexuals found a way around to circumvent the costs of losing sex while benefiting from clonal reproduction. To achieve this, we will use two groups of tardigrades: among one of them no males have ever been found, so they are considered ancient asexuals, whereas the other group comprises a mixture of sexually and parthenogenetic (asexual) species, which indicates the asexuality in this group is recent and evolved independently multiple times. The main hypothesis to be tested in the project is that ancient asexuals have been able to persist because they compensate the loss of males by other means of genetic recombination. The prediction, therefore, is that ancient asexuals exhibit genomic signatures of recombination, whereas recent ones do not. Thus, the project will provide first large scale, systematic comparative analysis of the genomic architecture of ancient and recent asexuals and may help us understand why both sexual and asexual reproduction co-exist. Importantly, thanks to the very recent advancements in genome sequencing of microscopic animals (which do not have much DNA), tardigrade genomes will be obtained from single individuals (to date, the very few available tardigrade genomes were obtained from pooling thousands of animals to provide sufficient amounts of DNA for analysis).

In addition to the main goal, the project will also result in the first experimental estimation of mutation rates in tardigrades and the first tardigrade phylogeny based on genomes. Finally, a large number of barcoding data collected in the project will translate to a tardigrade biodiversity survey of an unprecedented geographic and taxonomic resolution and accuracy, which will constitute important information from the point of view of nature conservation and will be a sound reference point for monitoring future changes in micrometazoan communities, which is of especial importance in the face of the current biodiversity crisis.