Genealogy of zebra finch lab populations: Results from call for DNA samples

Two years ago, in the ISBE Newsletter I reported about a workshop 'Zebra finches – *status quo* and where we go' (Rutkowska 2005). Workshops that focus on a single study organism typically lead to lively discussions about why research findings often differ between the various research labs. Is it the details of the experimental procedure, the conditions of how the birds are kept and reared, or could it be that the different lab populations have diverged genetically due to inbreeding and drift? To address the latter possibility, Wolfgang Forstmeier (Max Planck Institute for Ornithology, Seewiesen Germany) made a call, which I announced in the ISBE newsletter, to contribute DNA samples for a study of genetic differentiation of the various captive zebra finch populations. The call was very successful and as a result, he was able to compare 1000 zebra finches from 2 wild Australian and 18 captive populations used in behavioral research. The findings have just been published in Molecular Ecology (Forstmeier at al. 2007).

The authors used 10 microsatellite markers to provide a tree of the genetic similarity of zebra finch populations and to study the possible genetic bottlenecks that captive populations might have gone through. For the two natural zebra finch populations the research revealed the highest allelic richness and heterozygosity in microsatellites ever reported for wild bird populations. Consequently, most of the alleles present in these natural populations had very low frequencies and captive populations have lost different alleles therefore significantly diverging from each other. However, the process of zebra finch domestication did not cause dramatic bottlenecks. The loss of genetic diversity in captive as compared to wild populations is comparable to what is expected to occur in an isolated island population bottlenecked for 50 generations with an effective population size of 200 individuals.

These findings have important implications for interpretation and planning of research. First, disparities in results from different populations may be explained by different origin of birds and should be especially pronounced between populations from continents that markedly differ in allelic content. Interestingly, the Vancouver population is very 'cosmopolitan' as its individuals cluster to Europe to the same extent as to North America. Second, information on genetic differences may be purposely used to design crosses between populations to ultimately map quantitative trait loci.

Here is zebra finch *status quo*. Where we go? The genome of the zebra finch is expected to be published some time next year. It will be (after the chicken) the second bird genome sequenced, and this will open exciting possibilities for studying genes that affect, for example, sexually selected ornaments, personality traits or genetic compatibility. Thus, while already serving as a model organism in neurobiology and behavioral ecology, the zebra finch is now entering the world of genomics.

Joanna Rutkowska
Department of Psychology
Cornell Univeristy
Ithaca, NY 14853 USA

References

Forstmeier W, Segelbacher G, Mueller JC, Kempenaers B. 2007. Genetic variation and differentiation in captive and wild zebra finches (*Taeniopygia guttata*). Mol Ecol. 16: 4039-4050, doi:10.1111/j.1365-294X.2007.03444.x

Rutkowska J. 2005. Maternal effects in zebra finches - status quo and where we go. ISBE Newsletter. Supplement to Behavioral Ecology 17:14–5