The genetic population structure of multiple species of *Daphnia* waterfleas

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We studied the genetic population structure of European *Daphnia* waterfleas of 46 ponds and lakes and 1626 individuals across the whole of Europe. By using a genetic marker system of 12 so-called microsatellites we were able to divide these individuals into genetically similar groups without prior information on their sampling locations and to infer assignment to one of three species, and within species to one of several populations. This task required a computationally intensive sequence of independent but repeated analyses. The HPC infrastructure of the Baden-Württemberg bwHPC-C5 initiative provided us with the resources to parallelise these otherwise serial analyses and arrive at a useful solution both faster and more accurate as otherwise possible. Specifically, we used the Bayesian clustering algorithms implemented in the software Structure 2.3.4 on the bwUniCluster by using bash scripts and the command 'parallel'. The three *Daphnia* species, *D. longispina*, *D. cucullata* and *D. galeata*, displayed distinct population structures which lead to the inference of differences in the reaction to anthropogenic pressure to which they are exposed, depending on, for example, level of eutrophication or stocking of fish for industrial food production. These were linked to known ecological and life history traits and were discussed in the framework of global environmental change and its potential influence on natural food webs in fresh water habitats.