Inferring the demographic history of *Cnesterodon brevirostratus* using bioinformatics tools

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Cnesterodon brevirostratus is a freshwater fish species occurring in highland grasslands in South Brazil. Recent genomic data have shown that this single taxon consists of four evolutionary different lineages. Some of these lineages may be found in the same river basins, sometimes sintopically, and the different lineages show morphological differences in the gonopodium, which can be related to sexual selection. However, details of its divergence and evolutionary history are still elusive. In this work we used genomic (RADSeq) data to fit alternative demographic models using the allele frequency spectrum (AFS) in the ∂a∂i software. We used 6841 SNPs from 133 individuals to construct the folded AFS for each lineage. We tested five models for each lineage: neutral (constant population size), growth (exponential size change), two epoch (an instantaneous size change), bottlegrowth (instantaneous size change followed by exponential growth) and three epoch (two size changes, the first during a specific period and the second begging some time ago in the past). The best-fitting model was chosen based on the Akaike Information Criterion. Preliminary results shows that the best model for lineages 1, 2 and 3 was the 'growth' model, while for lineage 4 was the 'two epoch'. For lineages 1 and 2, growth ratio was similar, from about 3,000 to 30,000 individuals (95% Confidence Interval ~ 20,000 – 60,000 individuals) starting around 10,000 years ago (95%CI ~2,500 – 20,000 years ago). Despite the broad confidence intervals, results for lineage 3 suggest an older and stronger growth, arriving at a population of ~41,000 individuals (95%CI ~3,000k – 130,000 individuals) since ~20,000 years ago (95%CI 500 – 68,000 years ago), coinciding with the Last Glacial Maximum. Finally, the best-fit model for lineage 4 suggests that by 13,000 years ago (95%CI 1,500 – 41,000 years ago) a small population of 5,000 individuals (95%CI 3,000 – 7,000 individuals) grow to 17,000 individuals (95%CI 5,000 – 38,000 individuals). These results suggest that Pleistocene glacial cycles were probably the drivers of population size change for these lineages, especially related to the colder and drier glacial periods, which favored the expansion of the grassland environments in which these lineages can be found. The next step is to analyze the joint allele frequency spectrum of two lineages to gain insights into their splitting times, and to test if divergence was followed by gene flow or not. Financial support: CAPES, CNPq, UFRGS.