



Extreme Weather Events Driven (Summer Droughts; Winter Sea Floods) Salinization of Freshwater Coastal Ecosystems: Possible Impacts on Genetic Diversity of *Brachionus calyciflorus* Populations

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Abstract

Increased evaporation, low flow regimes together with climate change induced sea level rise and higher frequency of extreme weather events intensify the salinization of coastal freshwater ecosystems. Salinization of freshwater ecosystems through extreme weather events such as summer droughts and winter sea floods are prominent in temperate countries. This salinization may compromise the resilience of natural populations inhabiting coastal regions by decreasing their genetic diversity. This work intended to understand the effects of salinization on the genetic diversity of populations of the rotifer, *Brachionus calyciflorus* under different temperature regimes. Six lineages of *B. calyciflorus* (D, G, P, N, F, H) differing in lethal sensitivity to salinity were selected and lab-populations of each clonal lineage were maintained under optimal conditions until reaching a steady state (carrying capacity). At this point, they were exposed to predetermine salinity level (9.7 mS/cm) which was LC₇₀ of most tolerant genotype (H), for at least 30 days. Population densities were monitored across the exposure period. These long-term assays were conducted under 3 temperatures: (i) 17±1°C to simulate salt water intrusion during winter; (ii) 20±1°C the optimal temperature (control), since organisms were cultured in the laboratory at this temperature and (iii) 23±1°C to simulate seawater intrusion in freshwater ecosystems during summer. Continuous exposure to 9.7 mS/cm salinity level affected survival and reproduction of *B. calyciflorus*, leading to extirpation of some genotypes after long-term exposures. Under 17°C, F, H and P were the first three genotypes disappeared, and their LT₉₀ were 229±11.35h, 276.7±35.53h and 282.2±19.19h respectively. H, G and N genotypes showed an LT₉₀ of 418.5±34.35h, 536.6±71.82h and 555.7±78.90h respectively at 20°C. Under 23°C; F, D, and H genotypes disappeared first and their LT₉₀ values were 405.1±64.77h, 458.9±68.00h and 460.2±36.81h respectively. These different patterns of sensitivity observed due to long-term exposures, could be most probably due to acclimation-driven population recovery. Temperature differences influenced response to salinity. These results and its consequences at the population



level was discussed in the light of the genetic erosion hypothesis, through natural selection due to small within-genotype variability

Key words: *acclimation, genetic Erosion, long-term exposure, population recovery, salinization.*

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