

# **Implications of life history transitions on population genetic structure of the toxic marine dinoflagellate *Alexandrium tamarense***

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Few studies on harmful microalgae have employed genotypic or phenotypic markers for population characterization, focussing primarily on differentiation. We uncovered significant genetic substructure and low but significant multilocus linkage disequilibrium (LD) within a planktonic population of the toxigenic species *Alexandrium tamarense*. Among molecular genotyping approaches, only amplified fragment length polymorphism (AFLP) revealed cryptic genetic population substructure by Bayesian clustering, whereas microsatellite markers failed to yield concordant patterns. Both markers, however, gave support for genetic differentiation of population subgroups as defined by AFLP. A considerable portion of multilocus LD could be attributed to population subdivision, but the remaining linkage disequilibrium within population subgroups was interpreted as an indicator of frequency shifts of clonal lineages during vegetative growth in the plankton. Directional selection on phenotypic characters such as cellular PSP toxin content and composition and allelochemical properties may contribute to differentiation of annual planktonic populations, if clonal lineages that express these characters are selectively favoured. Nevertheless, significant phenotypic differentiation for these characters among genetically differentiated subgroups could only be detected for cellular PSP toxin content in two of the four population subgroups. We developed a conceptual model to explain the importance of life history transitions in the evolutionary ecology of these dinoflagellates.