

Genetic differentiation and phenotypic characteristics of geographically separated populations of the *Alexandrium tamarense* North American ribotype

T.J. Alpermann¹, U. John¹, U. Tillmann¹, K.M. Evans², S. Nagai³, D.M. Anderson⁴, A.D. Cembella¹

¹ Alfred Wegener Institute for Polar and Marine Research, Bremerhaven, Germany

² Royal Botanic Garden Edinburgh, Scotland, UK

³ National Research Institute of Fisheries and Environment of Inland Sea, Hiroshima, Japan,

⁴ Woods Hole Oceanographic Institution, Massachusetts, USA

talpermann@meeresforschung.de

The '*Alexandrium tamarense* species complex' contains prominent paralytic shellfish poisoning (PSP) toxin producers that can be further discriminated either on the basis of morphological characteristics or by DNA sequence divergence. The North American clade, as defined by its LSU ribosomal DNA sequence, is the most widely distributed representative of the PSP toxin-producing *A. tamarense* clades. Populations of this clade cause recurrent blooms in many regions of the world. Natural populations from North America, Northern Europe and Japan exhibit notable genetic differentiation that can be detected by molecular markers with different resolution properties. Whereas molecular sequence analysis of ribosomal DNA yields only a coarse resolution pattern of regional subclades, mitochondrial DNA sequences and microsatellites, as well as Amplified Fragment Length Polymorphism (AFLP) analysis, allow the estimation of genetic differentiation between contiguous populations. No congruence of any of the genetic markers were found between the expression of PSP toxin phenotypes or allelochemical properties that can affect grazers or competing algal species, but inter-population differences in PSP toxin profile were apparent on a broad geographical scale. The variable expression of the allelopathic phenotype within a population from Northern Europe was used to experimentally test the protective benefit of allelochemical properties on bloom formation.