



Spring bloom development, genetic variation, and population succession in the planktonic diatom *Ditylum brightwellii*

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ABSTRACT: We determined spatial and temporal variation in abundance, distribution, and genetic composition of the planktonic marine diatom *Ditylum brightwellii* in 21 water samples collected between February and June from five locations in Puget Sound and the Strait of Juan de Fuca, Washington. Four blooms with cell abundances of $>1,000$ cells L^{-1} were detected during the sampling period. The blooms were comprised of two genetically distinct populations identified by analyzing up to three microsatellite loci from 707 individual cells. One population was detected at all locations from February to April and comprised three blooms. In May and June, it was gone, replaced by a second, genetically distinct population that comprised a different bloom. Both populations had high levels of diversity: on average, 94% of cells in each sample were genetically distinct. The two populations contained cells with identical 18S and 5.8S rDNA sequences and 1.1% sequence divergence at the internal transcribed spacer regions, which suggests that both populations were members of the same species. The populations detected in early and late spring were composed of cells with average valve diameters of 22 and 69 μm , respectively. The population sampled in late spring, comprised of large-diameter cells, had a distinct genetic composition, indicating that it did not arise from a sexual reproduction event in the population sampled in early spring. Both populations were associated with significantly different exposures to solar irradiance and silicic acid concentrations, suggesting that environmental selection may regulate bloom dynamics of distinct populations.

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