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Microsatellites reveal high population connectivity in eelgrass (Zostera marina) in two contrasting coastal areas

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ABSTRACT: Populations of marine angiosperms, or seagrasses, are at the basis of productive ecosystems thriving in shallow coastal areas around the world. Genetic markers allow important inferences on the connectivity of seagrass populations. Here, I compare the fine scale geographic structure in eelgrass (Zostera marina) at a regional scale (2-60 km) among two adjacent coastal areas, the northern Wadden Sea (N = 8), and the southwestern Baltic (N = 5). Plants were genotyped for eight highly polymorphic microsatellite loci displaying a total of 114 alleles. Consistent with their clonal mode of reproduction, populations in the Baltic were genetically less diverse compared to those in the Wadden Sea, suggesting an effective population size that is half compared to the Wadden Sea. Although I expected more gene flow among populations in the Wadden Sea where abundant seeds can be transported by strong tidal currents, no quantitative difference in population differentiation was detectable between both coastal areas. To the contrary, in the atidal Baltic, nonsignificant genetic differentiation (F<sub>57</sub> < 0.009) was present up to waterway distances of 54 km, compared to only 33 km in the Wadden Sea. Correlations between genetic and geographic distances were weak in both areas, and significant only in the Wadden Sea. I examined as one potential mechanism responsible for high population connectivity whether the genotypic composition of rafting reproductive shoots differed from resident Baltic populations (N = 2) using assignment tests. At one sampling occasion, at least 130 immigrant seeds m<sup>-1</sup> shoreline were identified based on their multilocus genotype. The results have implications for coastal management and restoration and suggest that local population history may be less crucial for explaining seagrass distribution than previously suggested.

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