

## GENETIC STRUCTURE AND IMMIGRATION IN FRENCH SEA BEET

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In this study we examined accessions of sea beet (*Beta vulgaris* subsp. *maritima* (L.) Arcang.), collected along the Mediterranean Sea and the Atlantic coast of France. The aim was to identify the scale and magnitude of differentiation and diversity in these accessions using both molecular and quantitative traits. Data filtering (allowing only one missing locus per multilocus genotype) reduced the final sample size from 336 (12 individuals each for 28 accessions) to 277 individuals. With SSR data, the observed heterozygosity was high across the accessions (mean 0.48), the mean inbreeding coefficient was fairly high (0.13) and significantly greater than zero. Inbreeding increased northward and heterozygosity increased southward. The mode value for K (number of genetic clusters) was found to be 2. Phenotypic foliar traits were significantly different among accessions in a one way ANOVA. Leaf length/width ratio, petiole length/width ratio and leaf thickness were significant at the 0.001, 0.05 and 0.001 levels respectively. Combining all three traits into a multivariate discriminant analysis using group assignments based on the genetic clusters resulted in a statistically significant discriminant function that could correctly predict group membership 75% of the time. Migration rate was estimated among three classes of genotypes (Mediterranean, Atlantic and Atlantic immigrant) using a Bayesian approach. The rates of migration were quite low between the Mediterranean and Atlantic groups in both directions. The rate of migration from the Mediterranean group to the putative Atlantic immigrant group was 20 times higher than from the Mediterranean group to the Atlantic group. Migration was four times higher from the Atlantic immigrant group to the Atlantic group than the reverse.