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Genetic Basis of Floral Organ Variation in *Spergularia Marina*

*Spergularia marina*, a member of the Caryophyllaceae, harbors an unusually high level of variation in stamen number. *S. marina* also boasts a relatively high frequency of chimeric organs, or organs containing both petal and stamen tissue. The genetic basis for such variation in floral organ identity is poorly understood. My work investigates the potential role of floral homeotic genes in the production of floral organ variation in *S. marina*. Primers that were successful in amplifying the floral homeotic gene *APETALA3* (*AP3*) in the Caryophyllaceae member *Silene latifolia* were used to amplify the *AP3* ortholog in *S. marina* in order to characterize its expression in the future. Furthermore, analysis of the phylogenetic relationship between *S. marina* and other members of the Caryophyllaceae was carried out. DNA barcoding of *maturase K* and internal transcribed spacer (ITS) sequences was used to identify a recently collected *Spergularia* plant that could possibly be used as an outgroup species with less variation in stamen number for future comparisons.