Diversification of Mediterranean Cystoseira (Fucales, Phaeophyceae) using a RAD-Seq approach

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The brown algal genus *Cystoseira* represents a very important component of shallow water coastal environments in the Mediterranean Sea. The plants typically form dense vegetations, creating a habitat for a multitude of vertebrate and invertebrate species. About 29 different taxa (species and intraspecific taxa) have been recognized. Resolving their evolutionary relationship however proves very difficult, due to the recency of their origin and most probably ongoing hybridisation between closely related taxa. In this study we aim to investigate the evolutionary history of the *Cystoseira* (clade-5 *sensu* Draimsa et al. 2010) and disentangle the roles of geography versus and ecology in the diversification process. Seven species have been selected: *C. amentacea* var. *stricta*, *C. brachycarpa*, *C. crinita*, *C. funki*, *C. mediterranea*, *C. tamariscifolia* and *C. zostertoides*. Most of the individuals sampled were located across the Mediterranean Sea, with few of them collected from the Atlantic coasts of Spain and France.

Restriction site Associated DNA (RAD) tags, were used, as a cost-effective polymorphism identification method, to be up to par with the evolving Next Generation Sequencing Techniques (Davey *et al.*, 2011). RAD tags are genome wide, short DNA sequences, associated with a specific restriction enzyme. We used *Sbf*1to generate thousands of markers from which gene and species will be constructed under a multispecies coalescent framework.

Our study presents the first RAD-Seq approach for algal species. Results are expected to provide new insights on *Cystoseira's* phylogeny and diversification in the Meditteranean basin following the end of the Messinian salinity crisis (5 mya).

References

Davey J.W., P.A. Hohenlohe, P.D. Etter, J.Q. Boone, J.M. Catchen and M.L. Blaxter. 2011 Genome-wide genetic marker discovery and genotyping using next-generation sequencing. Nature Reviews Genetics 12:499-510.

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