

Kelp are large brown macroalgae in the order Laminariales that provide the foundation for some of the most productive habitats on earth. However, the lack of fundamental research in kelp when compared to other groups leads to naturally arising biases in the literature. This thesis attempts to bridge some of these disparities by addressing knowledge gaps, reconciling conflict regarding some of these theoretical assumptions, and identifying overarching trends in the research.

The first systematic review of kelp population genetics in the north-east Atlantic was conducted in Chapter 2, with an emphasis on identifying overarching patterns of biogeography between species as well as biases in sample geography and methodologies. This review identified knowledge gaps and research biases in the literature, and proposes future research avenues. It also provides a foundational basis for new researchers and collaboration opportunities, and addresses a fundamental gap in the path forward towards the recently proposed European Board of Macroalgal Genetic Resources (EBMGR).

In Chapter 3 and 4, the three most abundant Irish species were studied, *Saccharina latissima*, *Laminaria digitata*, and *Laminaria hyperborea* using high quality Single Nucleotide Polymorphism (SNP) markers generated using Genotyping By Sequencing (GBS). These were sampled along projected Irish glacial retreat patterns from the Last Glacial Maximum (LGM) in order to identify glacial refugia, as well as connectivity, genetic structure, and genetic diversity. Ireland was found to likely harbour numerous glacial refugia, and showed high diversity, but population structure was species specific. Evidence for outbreeding was identified, indicating that a greater emphasis on the role of the neglected gametophyte stage may be prudent in population genetic research of kelp. An extensive morphometric analysis of *Laminaria* samples using traits typically used in species discrimination between *L. digitata* and *L. hyperborea* found that identification by morphology alone is unreliable for species identification in this genus in the north-east Atlantic, and that molecular testing is required for the consistent delineation between these two sister species.

Chapter 5 synthesises the findings of the data in light of the identified knowledge gaps, and proposes theoretical and methodological avenues for future research to explore. Ultimately, this research identifies and addresses some of the knowledge gaps in European kelp population genetic research, and challenges some of the historic assumptions of kelp natural history in light of the theoretical framework shifts in recent decades. This holistic reconciliation comes at an appropriate time given the context of increased environmental pressures on natural kelp populations and a rapidly developing kelp aquaculture industry in Europe.