Diving deep into kelp forest food webs using dietary DNA metabarcoding

Bonnie Bailet[1], Jean-Charles Leclerc[2], Thibaut De Bettignies[3], Pascal Provost[4], Yannis Turpin[5], Martial Laurans[6], Pierre Thiriet[7], and Erwan Quemere*[1]

[1]UMR DECOD "Dynamique et durabilité des écosystèmes : de la source à l'océan" – INRAE – France
[2]Station biologique de Roscoff = Roscoff Marine Station – CNRS – France
[3]UMS Patrinat – OFB – France
[4]Réserve Naturelle Nationale des Sept-Iles – Ligue pour la Protection des Oiseaux (LPO), France – France
[5]Parc naturel marin d'Iroise – OFB – France
[6]UMR DECOD "Dynamique et durabilité des écosystèmes : de la source à l'océan" – Institut Français de Recherche pour l'Exploitation de la Mer (IFREMER) – France
[7]UMS Patrinat – Muséum National d'Histoire Naturelle (MNHN) – France

Résumé

Kelp forests are iconic coastal ecosystems, harbouring highly diverse communities of algae, meiofauna, and macrofauna, valued for their ecological, economic, and cultural significance. These ecosystems confront multiple threats including pollution, overfishing, seaweed harvesting, over-grazing events, and temperature anomalies linked to climate change. These have led to large-scale episodes of deforestation worldwide, often accompanied by disruptions in ecosystem functioning. Understanding the intricate interaction network within these communities is critical for predicting the cascading effects of such pressures. Kelp forests have been the subject of numerous studies on their level of primary production, their genetic characteristics and the associated communities. However, precise knowledge regarding their structure and trophic functioning remains lacking. For example, traditional methods such as stable isotope analyses provide insights on dominant trophic pathways, but they do not provide adequate taxonomic resolution to assign species-specific interactions. In this study, we used a multi-marker metabarcoding approach to reconstruct food webs within kelp forests in two protected areas in Britany: the Iroise Marine Natural Park and the natural reserve of the Seven Islands. We examined the diet (both animal prey and algae) of twenty keystone species including seals, cormorants, fish and invertebrates such as urchins, starfish, and crabs. Our findings revealed a remarkable diversity of prey with the vast majority identified at the species level. We also uncovered cryptic dietary niche partitioning in fish that likely contributes to stabilizing species coexistence. Additionally, dietary DNA metabarcoding data provided information on the trophic dependency levels of the studied species on kelp forests, offering valuable insights for conservation efforts.

Mots-Clés: trophic interactions, dietary niche partitioning, ecological network, kelp forests, high-throughput sequencing, DNA metabarcoding

---

*Intervenant