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Use of integrative taxonomy and DNA barcoding for characterization of ecological processes structuring marine benthic community assemblages in British Columbia

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Background: Human-induced disturbances generate strong selection pressures on the ecology and evolution of species, affecting community dynamics, ecosystem functioning, and global processes. In the marine environment, the taxonomy and distribution of most organisms are poorly known. As ecologists strive to understand increasingly complex processes, involving all species interacting within communities, reliable and accessible taxonomic tools to identify species in broad community-level datasets are needed. This study aims to document the species diversity of benthic marine communities in British Columbia, Canada, and to establish a molecular inventory including DNA barcodes to enable confident identification of species for ecological research. Results: Intertidal and subtidal sites were sampled across 700 km of BC coastline and 2000 specimens were collected. For marine shelled gastropods and brachyuran crabs, we used a high-throughput integrative taxonomic approach to generate fast and accurate species hypotheses based on the phylogenetic species concept. To date, 57 species have been delimited, including cryptic species that can cause difficulty in ecological studies because of taxonomic uncertainty. Rarefaction curves suggest 80%–100% of the actual diversity of macro-species living in sampled habitats was collected. However, the compilation of historic reports of species presence suggests that many micro and deep-sea species remain to be sampled in the North East Pacific. Overall, the four habitat types analyzed contained distinct species assemblages. Evidence of nonrandom co-occurrence patterns indicative of ecological relationships or reflecting preference for certain environmental conditions were observed in 35 species. Significance: This is the first study to assess marine species richness and ecological patterns in BC using a modernized approach to species hypotheses including the incorporation of DNA barcode data. The high-throughput taxonomic approach used should bring new opportunities for ecologists studying complex natural communities. The molecular inventory of native macro-species generated provides baseline data and will facilitate monitoring for invasive species in BC.