

The core-periphery hypothesis (CPH) predicts that genetic diversity is greatest at the centre and lowest at the edges of a species' distribution because genetic diversity is a function of a species' abundance, which is also expected to be greatest at the centre and lowest at the edges of the distribution. Variants of the CPH include the 'Ramped North' (greatest variation in the north), the 'Ramped South' (greatest in the south), and the 'Abundant Edge' (greatest at the distributional edges). Here, we present the first standardised multi-phylum analysis of the CPH using nine indices of genetic diversity for New Zealand's marine biota, covering 52 species. Based on 80 studies across eight phyla, spatial variation in the genetic indices was tested against four models (Normal (N), Ramped North (RN), Ramped South (RS), Abundant Edge (AE)). Only 22.7% of all individual taxon-specific tests were statistically significant: Ramped North (10.5%), Ramped South (7.4%), Abundant Edge (2.6%) and Normal (2.2%). Nonetheless, amongst the Chordata (Ramped North and Ramped South), Arthropoda (Ramped South) and Mollusca (Ramped North), a reasonably consistent pattern of genetic variation was observed within each phylum. Spatially-explicit genetic diversity of the remaining taxa fitted different models but without any obvious pattern across the phyla. Generalised binomial testing of observed p-values for each genetic index across all studies revealed that 10 of 29 tests were significant (5 RN, 2 N, 2 RS, 1 AE). Overall, our meta-analysis revealed no real support for the CPH and only limited support for a Ramped model (either Ramped North or Ramped South) of spatially-explicit genetic diversity. For New Zealand coastal marine taxa, we conclude that consistently strong patterns of genetic variation across multiple taxa do not exist and the CPH requires extensive testing from multiple other regions before we can say that such patterns exist, let alone explain them.

