Population genomics of local adaptation in the deep-sea amphipod *Hirondellea dubia* across abyssal and hadal ecosystems

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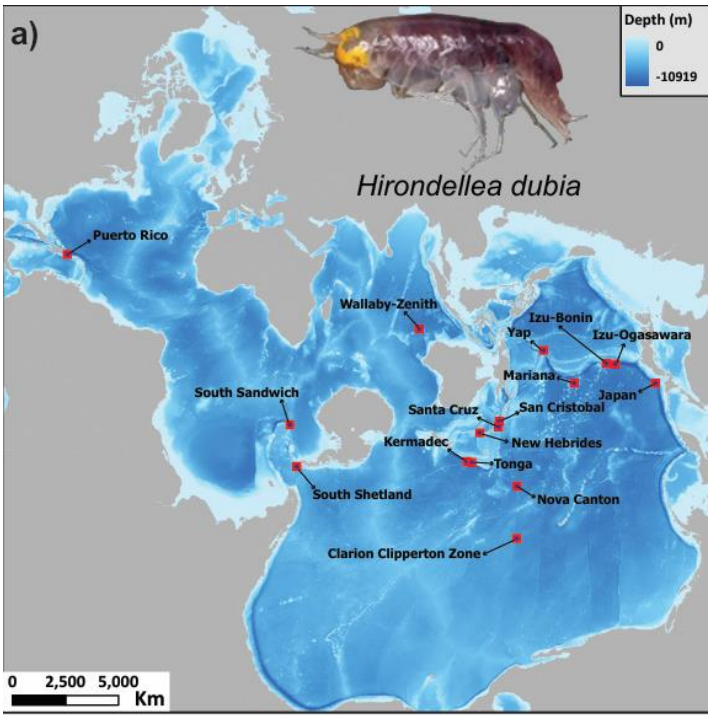
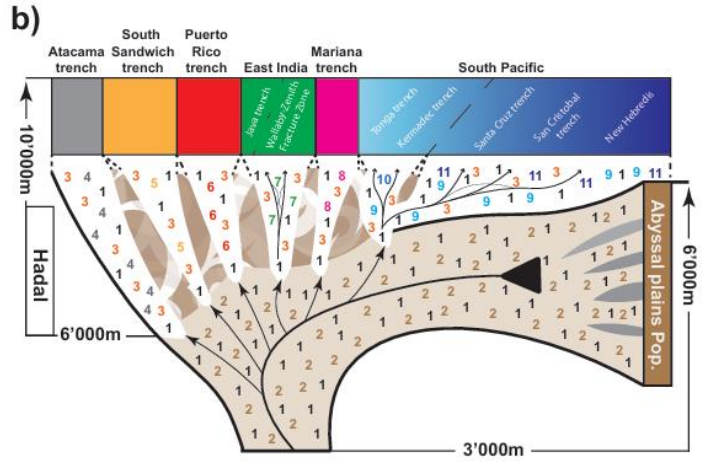
Hirondellea dubia is one of the most common and abundant scavenging amphipods in hadal ecosystems and, although less frequently, it is also known to inhabit abyssal plains. Its populations therefore span two contrasting depth zones, abyssal and hadal, and extend globally across deep-sea features with analogous environmental conditions. This makes *H. dubia* an ideal system for studying population dynamics and the evolution of local adaptation in the deep sea. The species is also practical to work with: it is distributed worldwide, small, abundant in the field, and easily collected with baited traps. This study includes specimens collected from 25 distinct deep-sea features across the Atlantic, Pacific, and Southern Oceans, at depths from 4,500 to ~11,000 m, covering both abyssal and hadal populations. Here, we aim to generate a high-quality reference genome for *H. dubia* and to resequence approximately 600 specimens across these locations. The project has three stages. First, we will use phylogenomics to reconstruct the diversification of the *H. dubia* lineage across depth and localities. Second, we will use comparative genomics to identify genomic regions associated with local adaptation that may drive population differentiation. Finally, we will use functional annotation to narrow down candidate coding regions linked to local adaptations in abyssal and hadal environments. Together, these analyses will establish the global population structure of *H. dubia* and identify molecular adaptations that enable its persistence across abyssal and hadal ecosystems.

Keywords: Abyssal, hadal, *Hirondellea dubia*, population structure, adaptive traits.


a)
Depth (m)
0
-10919
Hirondellea dubia
Puerto Rico
Wallaby-Zenith
Izu-Bonin
Yap
Izu-Ogasawara
Mariana
Japan
South Sandwich
Santa Cruz
San Cristobal
Kermadec
New Hebrides
Tonga
South Shetland
Nova Canton
Clarion Clipperton Zone
0 2,500 5,000
Km


b)
Atacama trench
South Sandwich trench
Puerto Rico trench
East India
Mariana trench
South Pacific
Java trench
Wallaby Zenith Fracture Zone
Tonga trench
Kermadec trench
Santa Cruz trench
San Cristobal trench
New Hebrides
10'000m
Hadal
6'000m
Abyssal plains Pop.
6'000m
3'000m

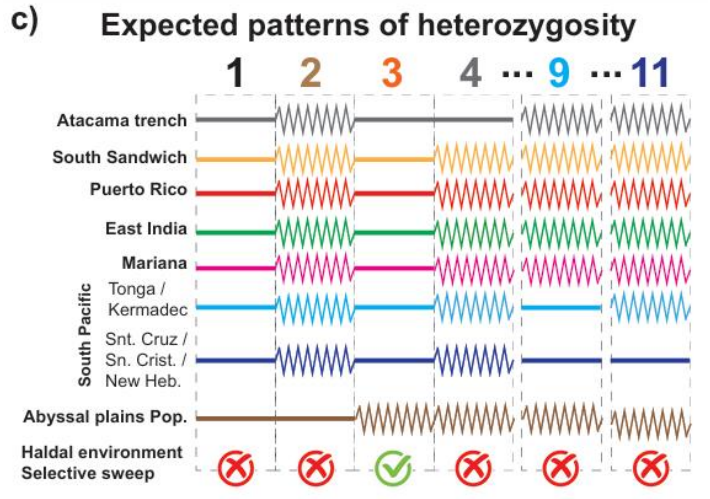

c)
Expected patterns of heterozygosity
1
2
3
4 ... 9 ... 11
Atacama trench
South Sandwich
Puerto Rico
East India
Mariana
South Pacific
Tonga / Kermadec
Snt. Cruz / Sn. Crist. / New Heb.
Abyssal plains Pop.
Haldal environment
Selective sweep

Figure 1. Overview of the study. (a) Maps show all currently known locations for the distribution of *H. dubia*, (b) Expected genomic landscape, and (c) Expected genetic heterozygosity, low and high represented as flat and zigzag lines. Numbers in (b) and (c) represent different genomic regions, “1” for ancestral regions, “2” for regions under selection at abyssal depths, “3” regions under selection at hadal depths, and “4” to “11” for regions shaped by local adaptation or by the “founder effect”. Map generate by Yakupjan Niyazi.