

## **MASTS Deep Sea Small Grant Award. DSSG16: Phylogenetics of heat-shock proteins in deep-sea amphipods**

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The funding provided by the MASTS Deep Sea Small Grant Award covered the costs of laboratory reagents and the DNA sequencing required to characterise two heat-shock protein genes in a number of deep-sea amphipod species.

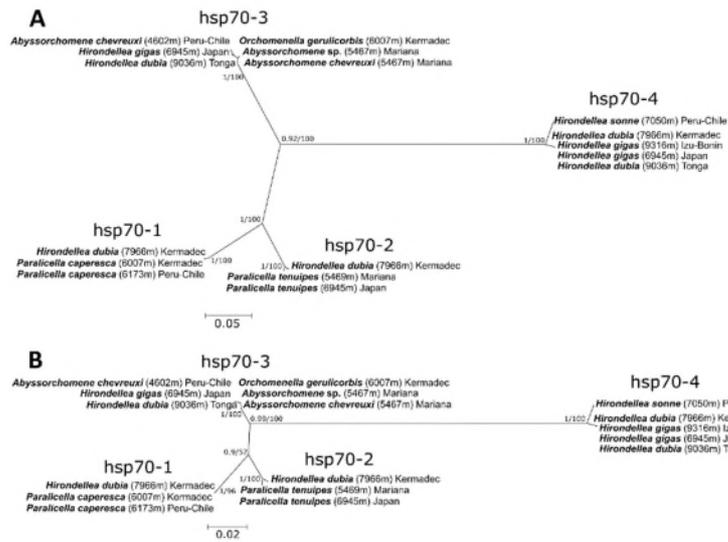
Heat-shock protein genes (HSPs) are a family of cellular chaperones that form a key component of the stress response where molecular adaptation to extreme environmental stressors has been shown across a wide-range of taxa. The aim of this study was to examine patterns of adaptation of two prominent heat-shock protein genes (hsp70 and hsp90) to the high hydrostatic environment of the deep sea, across a number of deep-sea amphipod species from the Izu-Bonin, Japan, Kermadec, Mariana, New Hebrides, Peru-Chile and Tonga trenches. Characterising these genes can allow us to examine their evolutionary history in deep-sea amphipods by identifying their phylogenetic patterns, examining copy number variation and testing for signatures of selection.

DNA sequences were obtained using a PCR approach performed at the University of Aberdeen before sequencing was conducted at MWG Eurofins, Ebersberg, Germany. From the sequencing data we successfully characterised four phylogenetically distinct isoforms in both hsp70 (Figure 1) and hsp90 (Figure 2), across 13 species of deep-sea amphipods from seven hadal trenches. The discovery of multiple copies in both genes that were examined is itself a signature of selection. Furthermore, one isoform in each gene (isoform 4 in hsp70 and isoform 2 in hsp90) was shown to be exclusive to the hadal genus *Hirondellea* which suggests these isoforms may be hadal specific. Purifying selection was also shown to be acting on all isoforms suggesting they are well adapted to deal with the selection pressures associated with the abyssal and hadal environments.

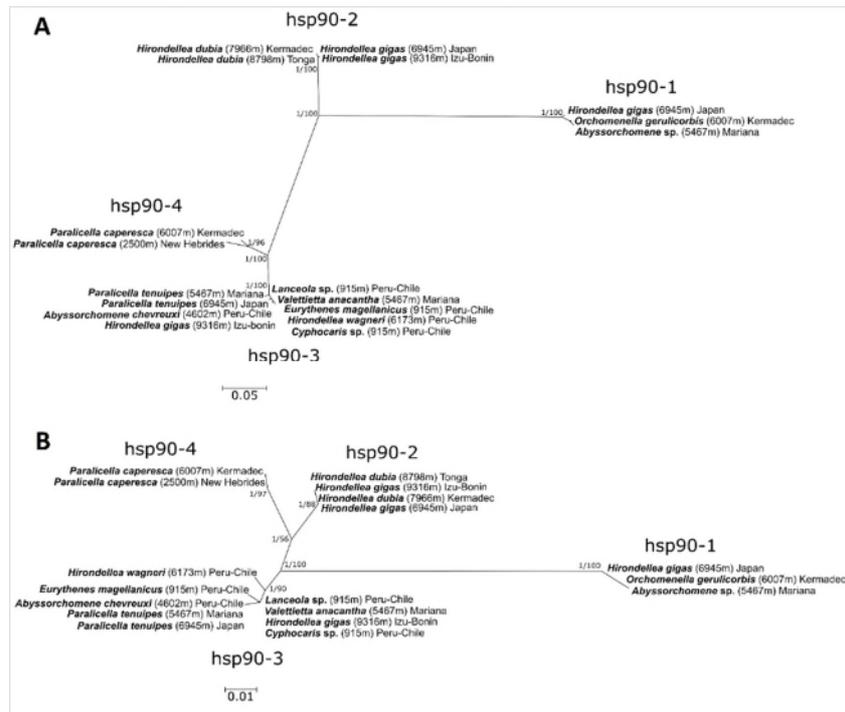
By using the DNA sequence data collected here we were able to elucidate the evolutionary history of two heat-shock protein genes by examining their phylogenetic patterns and testing for signatures of adaptation in deep-sea amphipods. These data are an important contribution to our understanding of adaptation to the extreme hydrostatic pressure of the deep-sea environment and they offer an insight into the molecular underpinnings required for life in the abyssal and hadal zones.

This research has been submitted for publication as:

Ritchie, H., Jamieson, A. J., Piertney, S. B., (2017) Heat-shock protein adaptation in abyssal and hadal amphipods. *Deep Sea Research II (resubmitted)*.



**Figure 1.** Unrooted maximum-likelihood tree showing the relationship between four deep-sea amphipod isoforms in the hsp70 gene for both A) nucleotide sequences and B) amino acid sequences. Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on major branch nodes.



**Figure 2.** Unrooted maximum-likelihood tree showing the relationship between four deep-sea amphipod isoforms in the hsp90 gene for both A) nucleotide sequences and B) amino acid sequences. Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on major branch nodes.