

MASTS Deep Sea Small Grant Award. DSSG15:

Genome size variation in deep-sea amphipods

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The funding provided by the MASTS Deep Sea Small Grant Award was used to underpin the laboratory reagents and technical support for undertaking genome size estimation of a number of deep-sea amphipod species using flow cytometry.

Genome size varies considerable across taxa and considerable research effort has been invested in trying to understanding the evolutionary causes and ecological consequences of differences across taxa. The aim of this study was to use deep sea amphipods as a model to examine how species with a common evolutionary history, equivalent life-history traits in a common ecological niche had canalised genome sizes. We examined genome size variation across 13 species from the Mariana, Kermadec and New Hebrides trenches and generate multi-locus mitochondrial DNA sequence data to allow for a phylogenetically controlled analysis of genome size diversification rates across taxa, and how genome size varies with a number of variables such as location and species' maximum depth.

Genome size estimates were obtained using a flow cytometry approach which was further verified by fluorescent microscopy analysis for all species (Figure 1). All sample preparations, protocol optimisation and flow cytometer data collection and analysis were conducted at the Institute of Medical Science (IMS), University of Aberdeen. We identified that genome size ranged from 3.97 gigabase pairs in *Paralicella caparesca* to 34.2 gigabase pairs in *Alicella gigantean* (Table 1). This highlights a broad range of genome sizes for deep sea amphipods, and highlights some extraordinarily large genomes in some deep sea taxa. The observed variation in genome size argues against a single underlying driver of genome size such as environmental stress mediated through hydrostatic pressure or common evolutionary history. Indeed, *Alicella* displayed a significantly elevated rate of genome size diversification relative to other Lyssaianassoid amphipods, indicating taxonomically localised selection pressures underpinning genome size variation. By dovetailing these data with ongoing genome sequencing for deep-sea amphipods it is possible to identify the mechanistic basis of genome size variation, and for *Alicella* it is clear that its large genome reflects a large component of transposable elements proliferation.

Overall, these data are an important contribution to our understanding of genome size evolution both in deep-sea amphipods specifically, and more generally across crustaceans which are currently underrepresented as a group in databases of genome size. The work is currently being prepared as a stand-alone publication to be submitted to the primary, peer-reviewed literature.

TABLE 1: C values for 13 deep sea amphipod samples, mitochondrial DNA sequence accessions used in phylogenetic analysis, and associated ecological metadata.

Species	C-Value \pm SE	Genome Size (Gb)	Genbank Accession Numbers			Depth Range (m)	Max. Depth (m)	Median Depth (m)	Max. Body Length (mm)
			16S	COI	18S				
<i>Lanceola</i> sp.	-	-	KP456062	KP713953	KT372894	-	-	-	-
<i>Abyssorchomene</i> sp.	9.81	9.59	KX034333	KX365238	KX365242	1010	2500	1995	9
<i>Abyssorchomene chevreuxi</i>	16.46	16.10	KX034329	KP713882	KP347454	3300	5400	3750	14
<i>Abyssorchomene distinctus</i>	15.30 \pm 0.04	14.96	KX034327	KP713886	KT372892	3800	6007	3004	14
Unidentified amphipod	9.09	8.89	KX034299	KX365239	KX365243	4984	7484	4992	-
<i>Alicella gigantea</i>	34.79 \pm 1.43	34.02	KX034290	KP713894	KP347467	5280	7000	4360	340
<i>Cyclocaris</i> sp.	4.73	4.62	KX034301	KP713899	KT372890	1907	6007	5034	15
<i>Eurythenes magellanicus</i>	18.35 \pm 0.74	17.95	KX034311	KP713957	KP347469	1229	5329	3486	85
<i>Eurythenes maldoror</i>	18.86 \pm 3.56	18.45	KX034310	KX365240	KX365244	3160	6230	4650	100
<i>Hirondellea dubia</i>	4.74 \pm 0.56	4.64	KX034251	KP713906	KP347459	6218	11,000	7891	12
<i>Paracallisoma</i> sp.	19.54	19.11	KX034319	KX365241	KX365245	1726	5100	4237	28
<i>Paralicella caperesca</i>	4.06 \pm 0.54	3.97	KX034272	KP713921	KP347463	5925	7415	4453	18
<i>Paralicella tenuipes</i>	4.13 \pm 0.59	4.04	KX034284	KP713931	KP347464	4915	7415	4958	14
<i>Valettietta anacantha</i>	7.80	7.63	KX034322	KP713950	KT372893	6007	6007	3004	15

FIGURE 1: Representative photomicrograph of florescent PI and DAPI double-stained cells a) *Gallus domesticus* erythrocytes (2C= 2.5pg) and b) *Eurythenes maldoror* (2C = 37.72pg) taken at 20x magnification. 6.1B) Representative fluorescence emission histogram from a DNA flow cytometric assay of a) reference cells from *Gallus domesticus* and b) *E. maldoror*.



