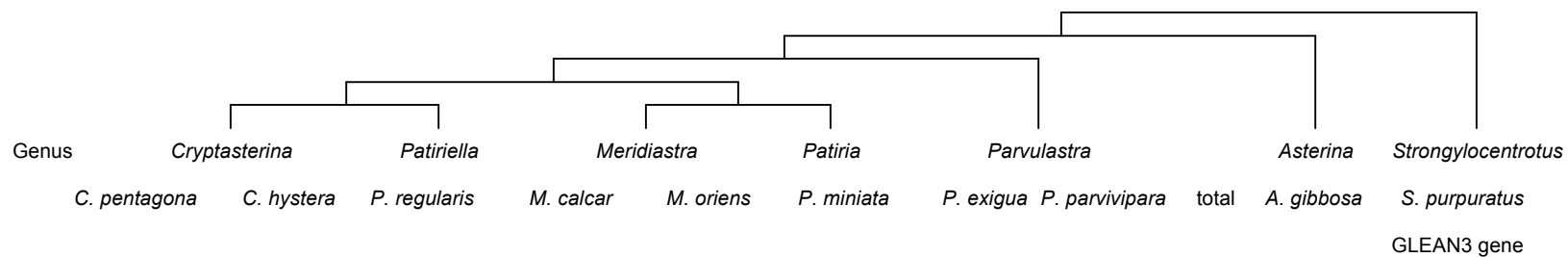


## Appendix 11: Microsatellite Cross Amplification Patterns



A4	-	-	-	181	+	-	-	-	2	
A102	-	214	-	-	-	-	-	-	1	
A104	-	-	-	137	-	-	-	-	1	
A108	179	+	-	-	-	-	-	-	2	
A110	-	-	-	-	-	-	+	226	2	
B3	-	-	-	-	-	122	-	-	1	
B4a	-	-	-	+	123	-	-	-	2	
B6	+	+	-	-	+	+	249	-	5	-
B11	-	-	-	-	-	154	-	-	1	
B101	-	-	-	-	234	-	-	-	1	(Ap-Zic)
B105	-	-	-	+	273	-	-	-	2	
B106	+	+	-	-	-	-	-	-	2	

B110	-	-	-	-	-	286	-	-	1		
B114	-	-	-	256	-	-	-	-	1		28470: <i>anosim-1</i>
B201	-	-	-	-	-	294	-	-	1		
B202	+	+	+	+	+	+	+	+	8	+	22573: <i>Sp-Nk7</i>
B209	-	-	-	-	-	148	-	-	1		
B212	-	-	299	-	+	-	-	-	2		
B222	-	-	-	+	+	-	-	-	2		
B227	180	+	-	-	-	-	-	-	2		
B228	-	-	-	-	-	208	-	-	1		
B231	193	-	-	-	-	-	-	-	1		
B234	+	-	-	+	+	-	+	-	4	-	
B236	+	+	+	+	+	+	+	+	8	-	07839: <i>SRCR</i>
C8	+	-	-	+	151	+	-	-	4	+	
C104	-	-	-	-	-	-	-	230	1		
C107	-	-	-	264	-	-	-	-	1		
C111	-	+	-	+	109	-	-	-	3		
C112	-	-	-	+	+	-	+	+	4	-	
C113	-	-	+	+	+	266	+	+	6	+	
C114	-	-	-	+	292	+	+	-	4		
C115	-	-	-	-	-	-	-	249	1		
C204a	-	-	+	+	199	+	-	-	4	+	
C207	-	-	-	-	-	-	287	-	1		
C210	-	-	-	-	-	231	-	-	1		

C212	-	-	-	-	-	-	-	272	1	
C213	-	-	-	-	194	-	-	-	1	
C216	-	-	-	202	-	-	-	-	1	
C219	+	+	165	-	+	+	+	+	7	-
C227	-	-	+	-	187	+	+	+	5	+
C231	-	-	-	283	-	-	-	-	1	
C232	-	-	+	143	+	-	+	-	4	
D8	-	-	+	-	279	-	+	+	4	-
D114	-	-	232	-	-	-	-	-	1	
D127	-	200	-	-	-	-	-	-	1	
assigned	3	2	3	7	10	8	2	4	39	
cross-amplified	7	8	7	12	11	8	11	7	71	

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Successful (+) and unsuccessful (-) cross-amplification of each microsatellite is indicated. Locus names are the same as in Appendix 1. Numbers under taxon names are PCR product size for clones from that species. Empty cells for *Asterina gibbosa* indicate amplifications not attempted. Row totals show the number of successful amplifications among Indo-Pacific asterinid species; column totals show number of clones isolated from each species and number of additional cross-amplifications. Homologies of four clones to sea urchin or sea star protein-coding genes are shown in the last column (and explained in the text). The branching diagram above the genus names shows well-known phylogenetic relationships based on mtDNA sequences (see Keever and Hart, 2008).

