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Atlantic and Indo-Pacific separation in *Palythoa* sibling species: phylogenomic analyses using ultraconserved elements

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SUPPLEMENTARY MATERIAL

Supplementary Table 1. Number of UCE loci recovered per sample across different taxon occupancy thresholds (45%, 55%, 65%, and 70%).

Sample ID	45% matrix (loci)	55% matrix (loci)	65% matrix (loci)	70% matrix (loci)
<i>P. mizigama</i> (Oki)	265	102	20	12
<i>P. tuberculosa</i> (Oki)	210	88	20	12
<i>P. tuberculosa</i> (NewCal)	179	74	17	12
<i>S. marsupialis</i> (Brunei)	201	81	17	11
<i>P. tuberculosa</i> (Red)	205	80	19	11
<i>P. tuberculosa</i> (Red)	193	73	17	11
<i>P. tuberculosa</i> (Red)	189	79	18	11
<i>P. tuberculosa</i> (Red)	169	72	18	11
<i>P. tuberculosa</i> (Red)	161	72	20	11
<i>P. tuberculosa</i> (NewCal)	146	69	17	11
<i>P. caribaeorum</i> (Brazil)	181	72	16	11
<i>P. caribaeorum</i> (Brazil)	269	93	17	10
<i>M. occultus</i> (Oki)	169	72	17	10
<i>P. elongatus</i> (Chile)	175	78	17	10
<i>P. tuberculosa</i> (Red)	144	62	15	10
<i>P. tuberculosa</i> (Oki3)	153	67	18	10
<i>P. tuberculosa</i> (NewCal)	150	66	18	10
<i>P. tuberculosa</i> (NewCal)	155	68	13	10
<i>P. tuberculosa</i> (NewCal)	180	79	18	10
<i>N. harenaceus</i> (Oki)	201	80	17	9
<i>Z. sociatus</i> (Atlantic)	177	75	14	9
<i>P. heliodiscus</i> (Taiwan)	152	70	17	9
<i>P. tuberculosa</i> (Red)	171	69	17	9
<i>P. tuberculosa</i> (NewCal)	146	58	12	9
<i>E. illoricator</i> (Oki)	142	62	16	8
<i>P. tuberculosa</i> (Oki)	129	56	13	8
<i>P. tuberculosa</i> (NewCal)	158	61	14	8
<i>P. tuberculosa</i> (NewCal)	160	66	16	8
<i>P. tuberculosa</i> (NewCal)	168	66	17	8
<i>P. caribaeorum</i> (Brazil)	97	44	12	8
<i>P. swiftii</i> (Atlantic)	155	63	14	7
<i>H. gracilis</i> (Oki)	188	73	16	7
<i>P. tuberculosa</i> (Oki)	140	62	13	7
<i>P. tuberculosa</i> (Oki)	138	58	11	7
<i>P. tuberculosa</i> (Red)	126	58	13	6
<i>P. caribaeorum</i> (Brazil)	82	38	9	5
<i>P. caribaeorum</i> (Brazil)	78	28	7	4

Supplementary Table 2. Summary statistics (median, mean, and range) for phylogenetic support metrics across inferred trees, including ultrafast bootstrap support (UFboot), gene concordance factors (gCF), site concordance factors (sCF), and local posterior probabilities (LPP) from ASTRAL analyses.

Metric	Median	Mean	Range
UFBoot	74.5	73.9	38 - 100
gCF	3.79	18.60	0 - 83.5
sCF	40.30	43.21	27 - 91.2
ASTRAL LPP	0.60	0.66	0.20 - 1.00