Rank change and growth within social hierarchies of the orange clownfish, *Amphiprion percula*

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Electronic Supplementary Figures

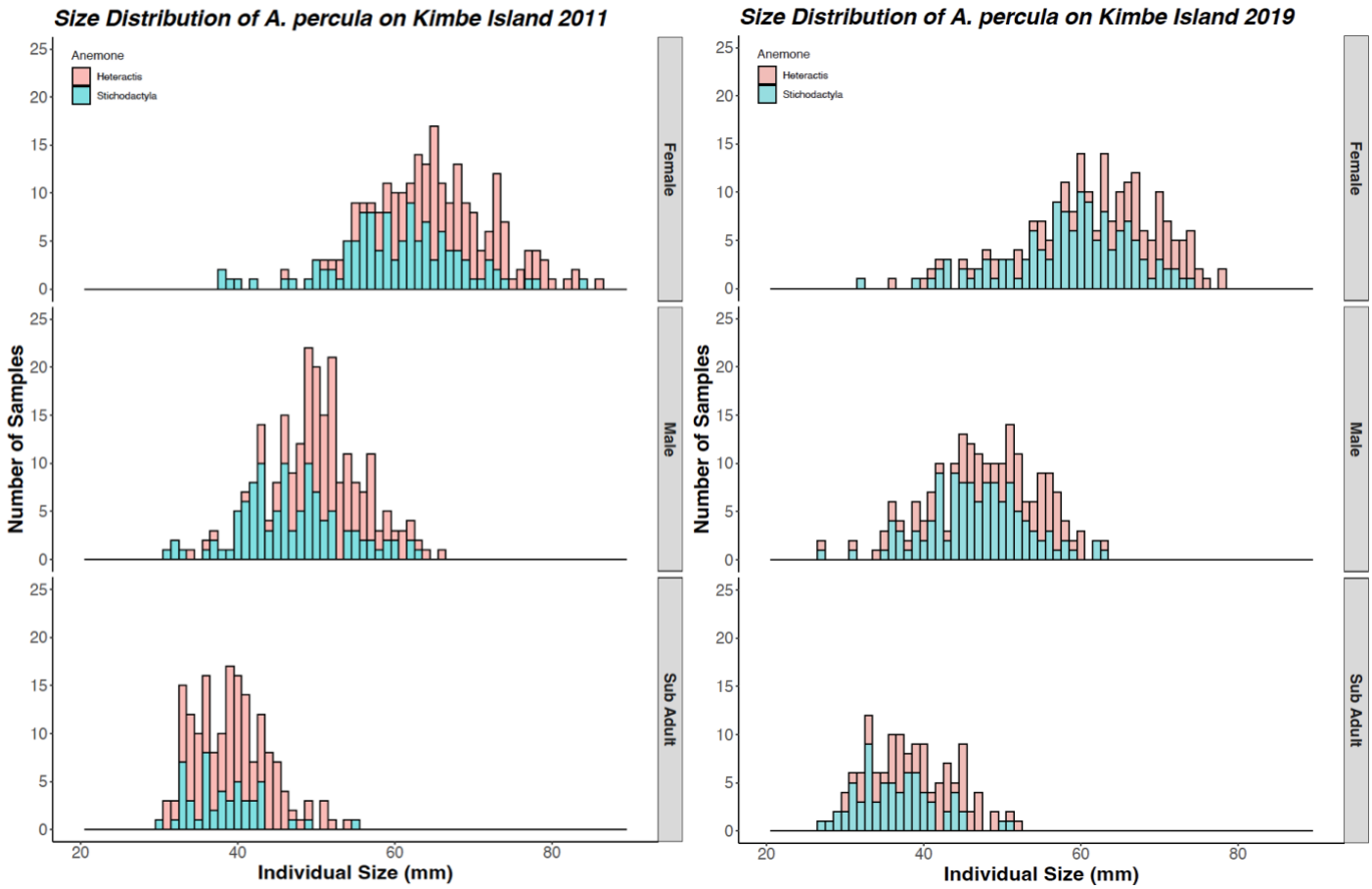

Figure S1: Size distribution between 2011 (n = 660) and 2019 (n = 533) within group members (sub-adult, male and female). In 2011, females (n = 246) were on average 66.9 ± 7.30 mm (SD) on *H. magnifica*, and 60.2 ± 8.07 mm (SD) on *S. gigantea,* and males (n = 239) were on average 51.6 ± 5.27 mm (SD) on *H. magnifica*, and 46.9 ± 6.64 mm (SD) on *S. gigantea,* and sub-adults (n = 175) were on average 39.7 ± 4.93 mm (SD) on *H. magnifica* and 38.3 ± 4.73 mm (SD) on *S. gigantea*. In 2019, females (n = 246) were on average 63.9 ± 9.19 mm (SD) on *H. magnifica*, and 58.7 ± 7.84 mm (SD) on *S. gigantea* and males (n = 239) were on average 49.0

± 7.61 mm (SD) on *H. magnifica*, and 46.8 ± 6.38 mm (SD) on *S. gigantea,* and sub-adults (n = 175) were on average 40.1 ± 5.46 mm (SD) on *H. magnifica* and 36.6 ± 5.03 mm (SD) on *S. gigantea*.

Table S1: Summary of the 20 microsatellite markers amplified in this study for *A. percula*. The primer sequence, motif, fluorescent dye, number of alleles, size range, and multiplex are indicated below.

Locus	Primer Sequence (5'-3')	Motif	Dye	Number of Alleles	Size (base pair)	Multiplex
CF27	F: TGCAATTATGTTAGCACCTG R: TGGCCAGATTAGATGGTTAC	$(TCTA)_{16}$	PET	15	190 - 240	A
79	F:GCATGGATGGTCACAGAGGAGCT R: CTCTGAAGTTCAAGGCTGCAGAC	$(GT)_{37}$	NED	17	210 - 260	A
perc06	F: GTGCTATGAAGAAGTGGGCG R: CTGCACACACAACTACCTCC	$(AC)_{14}$	VIC	11	235 - 270	A
perc21	F: TTGTGTGAGTTCCTGACCCG R: AAATGGAGAGGCTGGCGTC	$(AC)_{11}$	6-FAM	11	220 - 270	A
perc41	F: TTTGCATGTTCTCCCTGTGC R: TGACAGGAATGCTGGAGGAG	$(ATCC)_{12}$	6-FAM	9	330 - 380	A
CF9	F: CTCTATGAAGGTGAGATTTTT R: GTACATGTGTGGGTTTCCTC	$(TCAA)_8TGAA(TCAA)_{15}$	NED	18	270 - 360	B
CF36	F: TTTACAGATGTACCTACACG R: GGTACAAACACACACACTG	$(CA)_{23}$	6-FAM	32	190 - 340	B
perc07	F: TTACGCTGCAGGAACAACTC R: CGAAAGGCAGGAGAAGACAC	$(AGAT)_{22}$	PET	24	190 – 280	B
perc02	F: CCTGAGTCCCTGGTGCTAAG R: AGTGTAAGGACTAGCGCAGG	$(AG)_{10}$	PET	12	370 - 440	B
perc38	F: TGCTACTGACAGATCTGCCC R: ATCTTTGCGGAAACAGGCAG	$(ATCC)_{10}$	VIC	7	300 - 350	B
120	F: TCGATGACATAACACGACGCAGT R: TGTGTCCGCTCCAGCTCTAC	$(GT)_{18}N_{20}(GT)_{14}$	VIC	9	380 - 420	C
70	F: AGATGATTGGGCAGCCTCACACT R: GATTATTGTCTTGTCGGGAGTCA	$(GT)_{13}(GT)_5$	6-FAM	14	360 - 380	C
perc17	F: TGAGGGCTTCTAAGTATGGCTC R: GTACGACACTCCAGAGACCC	$(AC)_{13}$	NED	7	90 - 150	C
perc42	F: TGTGGCTGATTTGTGTACGC R: ACCTCCATTGTTCCTCTGCC	$(AC)_{14}$	PET	11	130 - 220	C
perc16	F: GCCACTCATGTTTACTCGGC R: TGACATCTGCTGACAAAGGC	$(AC)_{10}$	NED	8	100 - 260	C
CF11	F: GCTGGTTACAACACCTTG R: GACAGGCAGCCATATGAG	$(CT)_{15}(CA)_{16}$	PET	13	100 - 300	D
CF3	F: GTTCAGCCCTGTATGACATT R: TGCTCTCATTCCTCTAGTCC	$(CA)_{17}$	PET	22	190 - 400	D
44	F: TTGGAGCAGCGTACTTAGCT R: ATGTGGCACTCAGCCTCCT	$(GT)_{13}$	6-FAM	15	200 - 340	D
CF39	F: CCGGACAGCCAGAGCAAAGA R: CCTAATCGATCGGTGGTGACAT	$(AC)_{10}(GC)(AC)_{26}(AGAC)_{11}(AGAT)(AGAC)_2(AC)_{11}(AGAC)_2$	VIC	27	310 - 400	D
CF42	F: TGCAGTCCAACAACCTGAAA R: ATGTGCACACAAGGTCCAAA	$(AGAT)_4(AGAC)_{18}(AGCC)(AGAC)_6(AC)(AG)_2$	VIC	20	170 - 260	D

Table S2: Characteristics of the 20 microsatellite markers amplified in this study for *A. percula* for 2011 and 2019. N, number of individuals genotyped; Na, the total number of alleles; Ho, observed heterozygosity; He, expected heterozygosity; F*is*, fixation index; *p*-value from Hardy-Weinberg Equilibrium.

	Amphiprion percula 2011 population (n = 660)					*Amphiprion percula* 2019 population (n = 533)				
Locus	**Na**	**Ho**	**He**	**Fis**	***p* value**	**Na**	**Ho**	**He**	**Fis**	***p* value**
CF27	10	0.800	0.813	0.16	ns	12	0.812	0.807	-0.006	$p < 0.001$
79	18	0.661	0.764	0.134	$p < 0.001$	19	0.633	0.764	0.172	$p < 0.001$
perc06	4	0.716	0.695	-0.031	ns	4	0.741	0.683	-0.085	$p < 0.001$
perc21	6	0.593	0.593	0.000	ns	5	0.603	0.622	0.031	ns
perc41	5	0.548	0.538	-0.017	$p < 0.001$	7	0.606	0.580	-0.045	ns
CF9	17	0.887	0.900	0.014	$p < 0.001$	17	0.872	0.897	0.028	$p < 0.001$
CF36	22	0.753	0.821	0.083	$p < 0.001$	22	0.731	0.827	0.116	$p < 0.001$
perc07	20	0.744	0.768	0.032	$p < 0.05$	15	0.788	0.766	-0.028	ns
perc02	7	0.387	0.589	0.343	$p < 0.001$	5	0.528	0.604	0.125	$p < 0.001$
perc38	5	0.587	0.579	-0.016	ns	5	0.593	0.584	-0.015	$p < 0.05$
120	4	0.695	0.685	-0.014	ns	4	0.583	0.669	0.129	$p < 0.001$
70	9	0.634	0.621	-0.022	$p < 0.001$	7	0.614	0.600	-0.022	$p < 0.001$
perc17	5	0.540	0.545	0.009	ns	4	0.553	0.550	-0.005	ns
perc42	7	0.558	0.578	0.035	ns	6	0.583	0.610	0.044	ns
perc16	6	0.529	0.528	-0.001	$p < 0.001$	6	0.546	0.533	-0.024	ns
CF11	9	0.715	0.725	0.014	ns	9	0.702	0.743	0.055	$p < 0.001$
CF3	23	0.781	0.815	0.042	$p < 0.001$	27	0.738	0.893	0.174	$p < 0.001$
44	9	0.523	0.554	0.056	$p < 0.001$	8	0.570	0.567	-0.005	$p < 0.001$
CF39	20	0.890	0.886	-0.004	ns	21	0.887	0.893	0.008	ns
CF42	9	0.847	0.843	-0.005	ns	9	0.826	0.826	0.001	ns