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Larval fish dispersal in a coral-reef seascape

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Table S1. Numbers of juveniles assigned to parents by DNA parentage analysis for *Amphiprion percula* and *Chaetodon vagabundus* from Lolobau Islands (LO), Cape Huessner (CH), Kimbe Island (KI), Restoff/Schumann Islands (RS), Malu Malu Islands (MM), Tarobi (TI), Wulai Island (WU), and Walindi reefs (LD). Matrix rows show number of assignments from each of the sites, while matrix rows show number of assignments to each of the sites. Details include number of adults sampled (Adults), number of juveniles sampled (Juveniles), and total number of juveniles assigned by site (Σ assigned).

Sites	Adults	Juveniles	LO	CH	KI	RS	MM	TI	WU	LD	Σ assigned
<i>Amphiprion percula</i> 2009											
LO	384	167	47	3				4			54
CH	774	419	2	88	12	2		8		7	119
KI	505	280	3	12	120			2	1	2	140
RS	46	18		1	1						2
MM	11	13						1			1
TI	447	312	7	10	4	2		34	5	1	63
WU	253	131	1	3				1	12		20
LD	126	107		4	2					2	8
Total	2546	1447									407
<i>Amphiprion percula</i> 2011											
LO	323	151	37	3	1			3	1		45
CH	704	371	1	93	6			9	2		111
KI	414	177	2	7	99			4	3		115
RS	41	24									0
MM	19	9					1		1		2
TI	993	604	7	4	8			114	1	2	136
WU	290	135		3		1		2	16		22
LD	129	76		1				1		4	6
Total	2913	1547									437
<i>Chaetodon vagabundus</i> 2009											
LO	358	326	3	5	2		2	2			14
CH	336	30	2								2
KI	409	124	1	2	2			1			6
RS	3	1									0
MM	147	54	1	1							2
TI	486	193	2	2	4		2	2	1		13
WU	282	160	5		1			1	2		9
LD	0	97	1				3	3			7
Total	2021	985									53

Sites	Adults	Juveniles	LO	CH	KI	RS	MM	TI	WU	LD	Σ assigned
<i>Chaetodon vagabundus</i> 2011											
LO	713	317		1	2					4	7
CH	442	66			1				1		2
KI	367	92		2				2	1		5
RS	0	0									0
MM	336	53			1		1		1		3
TI	1078	190			1			1	2		4
WU	2012	215						3	6		9
LD	0	101	1					3	2		6
Total	4858	958									39

Table S2. Microsatellite DNA loci used in the current study for both focal species in 2009 and 2011. Details include: Number of alleles (Na), Allele size range in base pairs (Size), PCR Multiplex group (Mg), and reference (Ref).

Name	Primer sequences 5'-3'	Motif	Na	Size	Mg	Ref
<i>Amphiprion percula</i>						
2009						
79	F: GCATGGATGGTCACAGAGGAGCT R: CTCTGAAGTTCAAGGCTGCAGAC	(GT) ₃₇	18	223-257	1	50
CF27	F: TGCAATTATGTTAGCACCTG R: TGGCCAGATTAGATGGTTAC	(TCTA) ₁₆	14	195-243	1	51
CF12	F: CATGGGAGCCAAATGTAAGAA R: CTCTCCATTGATCTGCAGTGTC	(AC) ₁₅	13	175-207	2	52
CF21	F: AGAAGC-CTCCTCACACATTC R: GAAAAAGACGAAGGGAGTAAG	(AAAG) ₄ (ATAG)(AAAG) ₁₇ (AGA)(AAAG) ₄	23	184-230	2	52
CF9	F: CTCTATGAAGGTGAGATTTTT R: GTACATGTGTGGGTTTCCTC	(TCAA) ₈ TGAA(TCAA) ₁₅	21	245-365	2	52
120	F: TCGATGACATAACACGACGCAGT R: TGTGTCCGCTCCAGCTCTAC	(GT) ₁₈ N ₂₀ (GT) ₁₄	25	393-453	3	50
70	F: AGATGATTGGGCAGCCTCACACT R: GATTATTGTCTTGTCGGGAGTCA	(GT) ₁₃ (GT) ₅	21	278-380	3	51
CF29	F: AGTGTATGTGTGCAAGAGAG R: GGCAGTACAGTGGAACAA	(AC) ₆ (GC)(AC) ₂ (GC) ₄ (AC) ₃₉	34	245-347	3	52
44	F: TTGGAGCAGCGTACTTAGCT R: ATGTGGCACTCAGCCTCCT	(GT) ₁₃	26	240-342	4	50
CF11	F: GCTGGTTACACACCTTG R: GACAGGCAGCCATATGAG	(CT) ₁₅ (CA) ₁₆	18	142-174	4	53
CF3	F: GTTCAGCCCTGTATGACATT R: TGCTCTCATTCTCTAGTCC	(CA) ₁₇	23	229-271	4	51
CF39	F: CCGGACAGCCAGAGCAAAGA R: CCTAATCGATCGGTGGTGACAT	(AC) ₁₀ (GC)(AC) ₂₆ (AGAC) ₁₁ (AGAT)(AGAC) ₂ (AC) ₁₁ (AGAC) ₂	33	317-387	4	52
CF42	F: TGCAGTCCAACAACCTGAAA R: ATGTGCACACAAGGTCCAAA	(AGAT) ₄ (AGAC) ₁₈ (AGCC)(AGAC) ₆ (AC)(AG) ₂	28	189-245	4	52
CF19	F: CAG ATG GAC GTC TGA TATT R: AAG CCT GTA ACA CCT G	(GT) ₅ T(GT) ₂ GC(GT) ₁₄ GC(GT) ₂₄	30	158-236	5	52
CF36	F: TTTACAGATGTACCTACACG R: GGTACAAACACACACACTG	(CA) ₂₃	32	204-330	5	52
2011						

79	F: GCATGGATGGTCACAGAGGAGCT R: CTCTGAAGTTCAAGGCTGCAGAC	(GT) ₃₇	17	223-257	1	50
CF27	F: TGCAATTATGTTAGCACCTG R: TGGCCAGATTAGATGGTTAC	(TCTA) ₁₆	15	185-251	1	51
perc41	F: TTTGCATGTTCTCCCTGTGC R: TGACAGGAATGCTGGAGGAG	(ATCC) ₁₂	9	307-363	1	51
perc21	F: TTGTGTGAGTTCCTGACCCG R: AAATGGAGAGGCTGGCGTC	(AC) ₁₁	11	239-259	1	52
perc06	F: GTGCTATGAAGAAGTGGGCG R: CTGCACACACAACCTACCTCC	(AC) ₁₄	11	239-261	1	53
CF12	F: CATGGGAGCCAAATGTAAGAA R: CTCTCCATTGATCTGCAGTGTC	(AC) ₁₅	13	207-241	2	53
CF9	F: CTCTATGAAGGTGAGATTTTT R: GTACATGTGTGGGTTTCTC	(TCAA) ₈ TGAA(TCAA) ₁₅	18	288-356	2	53
perc07	F: TTACGCTGCAGGAACAACCTC R: CGAAAGGCAGGAGAAAGACAC	(AGAT) ₂₂	24	200-284	2	53
perc02	F: CCTGAGTCCCTGGTGCTAAG R: AGTGTAAGGACTAGCGCAGG	(AG) ₁₀	12	379-421	2	53
perc38	F: TGCTACTGACAGATCTGCC R: ATCTTTGCGGAAACAGGCAG	(ATCC) ₁₀	7	304-340	2	53
CF36	F: TTTACAGATGTACCTACACG R: GGTACAAACACACACACTG	(CA) ₂₃	32	202-334	2	53
120	F: TCGATGACATAACACGACGCAGT R: TGTGTCCGCTCCAGCTCTAC	(GT) ₁₈ N ₂₀ (GT) ₁₄	9	393-453	3	52
70	F: AGATGATTGGGCAGCCTCACACT R: GATTATTGTCTTGTGCGGAGTCA	(GT) ₁₃ (GT) ₅	14	278-380	3	51
perc17	F: TGAGGGCTTCTAAGTATGGCTC R: GTACGACACTCCAGAGACCC	(AC) ₁₃	7	126-138	3	51
perc42	F: TGTGGCTGATTTGTGTACGC R: ACCTCCATTGTTCTCTGCC	(AC) ₁₄	11	130-194	3	51
perc16	F: GCCACTCATGTTTACTCGGC R: TGACATCTGCTGACAAAGGC	(AC) ₁₀	8	175-231	3	51
perc14	F: GCCAACTCAGTGTCTGCTAAC R: CCCTCCAGAATCAGTGCGG	(AAAT) ₈	38	303-459	3	51
CF11	F: GCTGGTTACAACACCTTG R: GACAGGCAGCCATATGAG	(CT) ₁₅ (CA) ₁₆	13	142-182	4	51
CF3	F: GTTCAGCCCTGTATGACATT R: TGCTCTCATTCTCTAGTCC	(CA) ₁₇	22	229-281	4	51
CF42	F: TGCAGTCCAACAACCTGAAA R: ATGTGCACACAAGGTCCAAA	(AGAT) ₄ (AGAC) ₁₈ (AGCC)(AGAC) ₆ (AC)(AG) ₂	20	189-245	4	52

CF39	F: CCGGACAGCCAGAGCAAAGA R: CCTAATCGATCGGTGGTGACAT	(AC) ₁₀ (GC)(AC) ₂₆ (AGAC) ₁₁ (AGAT)(AGAC) ₂ (AC) ₁₁ (AGAC) ₂	27	311-385	4	52
44	F: TTGGAGCAGCGTACTTAGCT R: ATGTGGCACTCAGCCTCCT	(GT) ₁₃	15	298-330	4	50
<i>Chaetodon vagabundus</i>						
2009						
A114	F: GCCCACAAAATCCTTTTGAA R: TTGATGCAGGTCCACTGAAA	(CA) ₁₂	27	178-232	4	54
B11	F: CTCTGCTGACCCAACAGTC R: ATGCCCTGCTATGTCCAC	(AG) ₁₅	28	243-297	1	55
B6	F: GCGGCTGATACACTCTTGG R: GGGTTGGGAGGTAACCTGC	(AG) ₂₆	25	183-231	1	55
D2	F: TGCATGTTTTGTCTTTGACCA R: CAAGCCCTAAACCTGCTGAG	(AGAT) ₁₈	21	120-202	1	55
C4	F: TTGGGAGAGTGCTAGAGTGC R: ACGTGC GTTTCATTACAC	(ACAG) ₆	5	209-225	2	55
C9	F: GTATTGGCAACACCGTTTGG R: GTAGCATGTCGGTGGTCTGA	(GACA) ₇	13	111-159	2	54
D107	F: GTGCATGGTGGAGTTTTCT R: GAAGGGATTATGAGCCGTGA	(GACA) ₅ (GATA) ₁₄	33	181-317	2	55
D3	F: TGTCCCGAGCTGTGTGTA R: ATGGATGGAGGGTCGAAAG	(AGAT) ₉ (AC) ₂₂	21	127-215	2	55
A105	F: CAGTGGAAACAAACAATTGC R: TGCTGGACAATATCCACAG	(GT) ₁₆	33	152-220	3	54
D117	F: TCCCCTCCCTCTCTCTTT R: TGCATCACTCACAATGTCG	(AGAT) ₉	18	179-247	3	55
D06	F: TGGTTATTCCATGAACTCTTC R: GGTTGGAGGAGGTTGATG	(AGAT) ₉	14	251-303	3	55
D08	F: TGGCAATTCTGCATGTTTGT R: TGTATCCCTCCTTGCAGCTC	(AGAT) ₁₄	29	256-368	3	55
C5	F: AACGGAGTCACAAACACAAG R: GACGAGCACACTGAACAT	(ACAG) ₈	31	201-303	4	55
D111	F: GTAAATCTTCGCCTGGGACA R: TGAATTTCCCTTTGGGATGA	(GATA) ₁₈	37	100-250	4	55
D116	F: TCCATCAGTCCATCTGTCCA R: TGTGAGCTGTCCATCTGCAT	(TATC) ₆	17	181-245	4	55

		2011				
B6	F: GCCCCTGATACACTCTTGG R: GGGTTGGGAGGTAACCTTGC	(AG) ₂₆	27	173-231	1	55
D2	F: TGCATGTTTTGTCTTTGACCA R: CAAGCCCTAAACCTGCTGAG	(AGAT) ₁₈	21	120-200	1	55
B11	F: CTCTGCTGACCCAACAGTC R: ATGCCCTGCTATGTCCAC	(AG) ₁₅	33	237-317	1	55
A114	F: GCCCACAAAATCCTTTTGAA R: TTGATGCAGGTCCACTGAAA	(CA) ₁₂	29	176-234	1	55
D3	F: TGTCCCGAGCTGTGTGTAAA R: ATGGATGGAGGGTCGAAAG	(AGAT) ₉ (AC) ₂₂	20	127-203	2	55
C4	F: TTGGGAGAGTGCTAGAGTGC R: ACGTGCCTTTCATTACAC	(ACAG) ₆	6	205-225	2	55
C9	F: GTATTGGCAACACCGTTTGG R: GTAGCATGTCGGTGGTCTGA	(GACA) ₇	13	107-155	2	55
cvag96	F: ATGCATCGCTGACAGGTTTG R: GTGAACACACCACTGAGCTG	(AC) ₁₂	32	269-363	2	55
cvag82	F: AAAGGGACGCTGCTTGTTC R: ATCTTGGCTGGCTCTACGTG	(AC) ₁₂	24	142-190	2	55
C5	F: AACGGAGTCACAAACACAAG R: GACGAGCACACTGAACAT	(ACAG) ₈	30	220-340	2	55
D8	F: TGGCAATTCTGCATGTTTGT R: TGTATCCCTCCTTGCAGCTC	(AGAT) ₁₄	33	240-380	3	55
D6	F: TGGTTATTCCATGAAACTCTTC R: GGTGGAGGAGGTTGATG	(AGAT) ₉	14	250-304	3	55
D117	F: TCCCCTCCCTCTCTCTTT R: TGCATTCACTCACAATGTCG	(AGAT) ₉	21	175-249	3	55
A105	F: CAGTGGAAACAAACAATTGC R: TGCTGGACAATATCCCACAG	(GT) ₁₆	32	156-222	3	55

Table S3. Parameters and the log of odds ratio (LOD) score values for DNA parentage analyses performed using the Famoz software application. Details include number of microsatellite DNA loci used (NL), the exclusion probability for a single parent (SP Excl_p), LOD error in simulations to estimate LOD score thresholds (LOD_{err}), LOD threshold value for single parents (LOD_{sp}), LOD threshold value for parent couples (LOD_{pc}), probabilities of type I (Type I) and type II (Type II) errors in parental assignments, and mean LOD (± 1 standard deviation).

Species, year	NL	SP Excl _p	LOD _{err}	LOD _{sp}	LOD _{pc}	Type I	Type II	Mean LOD
<i>C. vagabundus</i> , 2009	15	1	0.001	8	20	0.0076	0.0265	9.76 (± 3.05)
<i>C. vagabundus</i> 2011	19	1	0.001	9	24	0.0098	0.0251	10.81 (± 3.21)
<i>A. percula</i> , 2009	15	0.999959	0.0001	6.5	15.2	0.0146	0.0437	10.36 (± 3.35)
<i>A. percula</i> , 2011	22	0.999965	0.0001	6.5	18	0.012	0.0411	13.09 (± 4.69)

Table S4. Summary of reef area and total population sizes of adult *Amphiprion percula* in 2009 and 2011. Details include total reef area (Reef area), total reef area sampled (Area sampled), estimated population size (Pop size), number of adults sampled (Adults sampled), and percentage of adults sampled (% sampled).

Sites	Reef area (km ²)	Area sampled (km ²)	Pop size	Adults sampled	% sampled
<i>2009</i>					
Lolobau Islands	1.04	1.04	384	384	100
Cape Huessner	0.44	0.44	774	774	100
Kimbe Island	0.43	0.43	505	505	100
Restoff/ Schumann Islands	0.42	0.42	46	46	100
Malu Malu Islands	0.47	0.47	11	11	100
Tarobi	0.47	0.11	1902	447	24
Wulai Islands	1.36	0.72	477	253	53
Walindi reefs	0.59	0.59	126	126	100
<i>2011</i>					
Lolobau Islands	1.04	1.04	323	323	100
Cape Huessner	0.44	0.44	704	704	100
Kimbe Island	0.43	0.43	414	414	100
Restoff / Schumann Islands	0.42	0.42	41	41	100
Malu Malu Islands	0.47	0.47	19	19	100
Tarobi	0.47	0.23	2014	993	49
Wulai Islands	1.36	1.12	435	290	67
Walindi reefs	0.59	0.59	129	129	100

Table S5. Summary of reef area and total population sizes of adult *Chaetodon vagabundus* in 2009 and 2011. Details include total reef area (Reef area), estimated population size (Pop size), 95% confidence intervals on population size estimate (95% CI), number of adults sampled (Adults sampled), and percentage of adults sampled (% sampled).

Sites	Reef area (km ²)	Pop size	95% CI	Adults sampled	% sampled
<i>2009</i>					
Lolobau Islands	1.04	793	193	358	45
Cape Huessner	0.44	765	203	336	44
Kimbe Island	0.43	1563	358	409	26
Restoff/ Schumann Islands	0.42	n/a	n/a	3	n/a
Malu Malu Islands	0.47	849	228	147	17
Tarobi	0.47	1678	542	486	29
Wulai Islands	1.36	2394	664	282	12
Walindi reefs	0.59	n/a	n/a	n/a	n/a
<i>2011</i>					
Lolobau Islands	1.04	2100	371	713	34
Cape Huessner	0.44	807	185	442	55
Kimbe Island	0.43	766	130	367	48
Restoff/ Schumann Islands	0.42	n/a	n/a	0	n/a
Malu Malu Islands	0.47	1045	263	336	32
Tarobi	0.47	1509	319	1078	71
Wulai Islands	1.36	2604	476	2012	77
Walindi reefs	0.59	n/a	n/a	n/a	n/a

Table S6. Best-fit dispersal kernels for *Amphiprion percula* and *Chaetodon vagabundus* in 2009 and 2011. Bolded values indicate the dispersal kernel model with the highest Akaike Information Criterion (AIC) value, indicating the best fit of the three models used.

Dispersal kernel	<i>A. percula</i> , 2009	<i>A. percula</i> , 2011	<i>C. vagabundus</i> , 2009	<i>C. vagabundus</i> , 2011
Laplacian	670.6	632.6	n/a	8940
Gaussian	847.1	886.9	n/a	8935
Ribbens	903.8	978.4	n/a	8931

Fig. S1. Fitted potential larval dispersal kernels for *A. percula* (a) and *C. vagabundus* (b), based on results collected in 2009 and 2011. Solid lines indicate the expected relative strength of larval dispersal at a given distance from the natal reef. Dashed lines indicate 95% bootstrap confidence intervals. Shaded area indicates the area within which 90% of the larvae are expected to settle. Inset boxes in panels show bi-plots of predicted versus observed dispersal distances, along with line of equality (solid grey line).

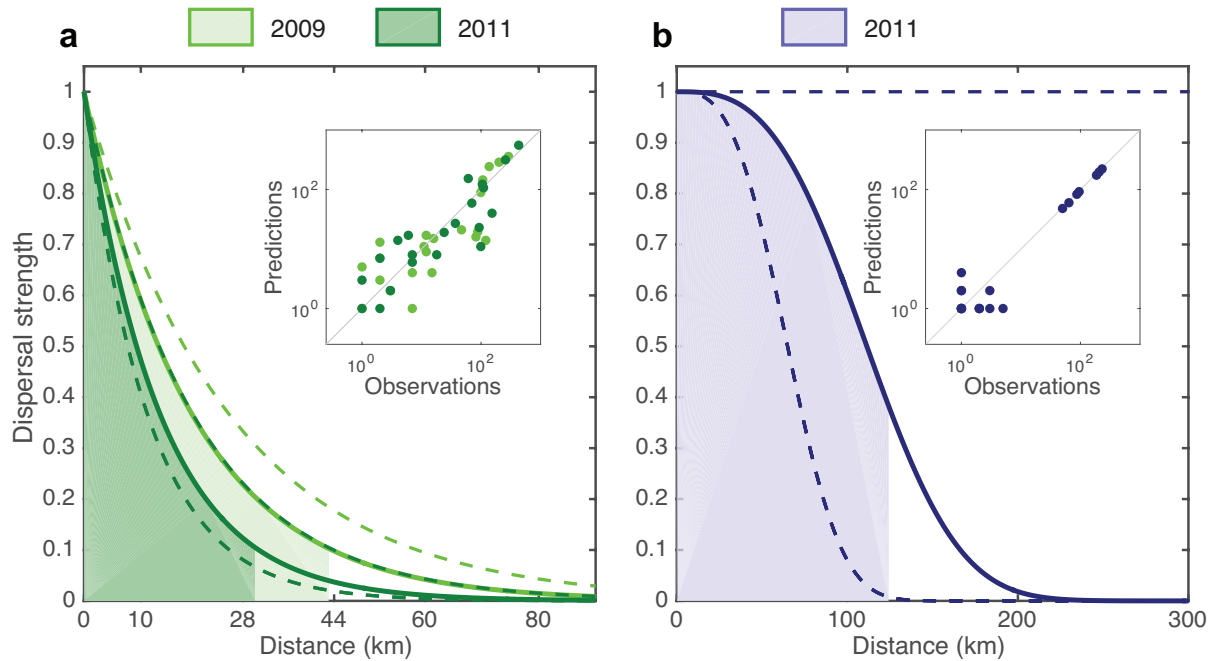
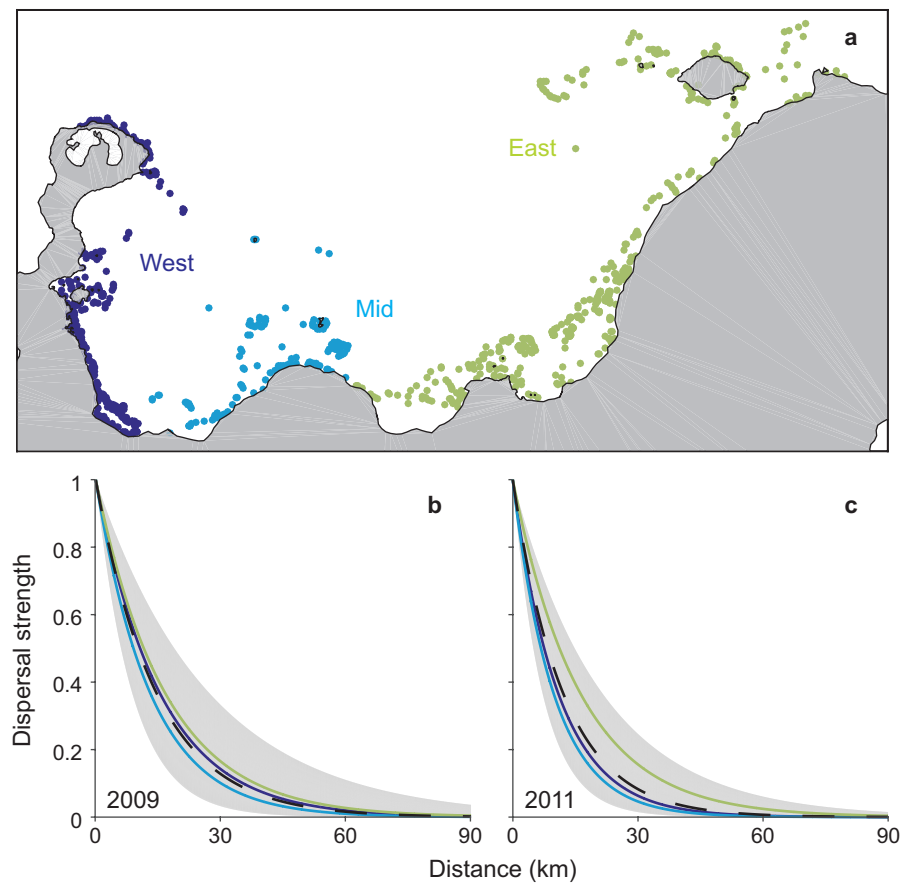


Fig. S2. Fitted potential larval dispersal kernels for *A. percula* from each of three zones (a) within Kimbe Bay based on results collected in 2009 (b) and 2011 (c). Locations of each anemone are identified by a colored dot indicating its assigned zone in panel A. Solid lines indicate the expected relative strength of larval dispersal at a given distance from the natal reef for each of the three zones, while the dashed line represents the pooled dispersal kernel across zones. Shaded area indicates pooled 95% confidence intervals among the three dispersal kernels for each zone.



Extra References

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