

1 **Appendix/Dryad**

2 **Is MHC diversity a better marker for conservation than neutral genetic diversity? A case**
3 **study of two contrasting dolphin populations**

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49	Variant:	1		10		20		30		40		50		60		70		79										
50	Tu-DQB-1	C	ACG	GAG	CGG	GTG	CGG	GTC	GTG	GAC	AGA	TCC	ATC	TAT	AAC	CGG	GAG	GAG	TTA	GTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG
51	Tu-DQB-2	•	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••
52	Tu-DQB-3	•	•••	•••	•••	•••	•••	•A•	•••	A••	•••	•A•	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••
53	Tu-DQB-4	•	•••	•••	•••	•••	•••	•••	A••	A••	•••	•A•	•••	•••	•••	•••	•••	•••	•••	•A•	A••	•••	•••	•••	•••	•••	•••	•••
54	Variant:	80		90		100		110		120		130		140		150		157										
55	Tu-DQB-1	TTC	CGG	GCG	GTG	ACC	GAG	CTG	GGC	CGG	CCG	GAC	GCC	GAG	TAC	TGG	AAC	AGC	CAG	AAG	GAC	ATC	CTG	GAG	CGG	AAA	CGG	
56	Tu-DQB-2	•••	•••	••C	•••	•••	•••	•••	•••	•••	TG	AT	•••	•••	•••	•••	•••	•••	•••	•••	•••	T	•••	•••	•••	•••	•••	
57	Tu-DQB-3	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	GA	G	•••
58	Tu-DQB-4	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•A	G	•••
59	Variant:	160		172																								
60	Tu-DQB-1	GCC	GAG	CTG	GAC	ACG																						
61	Tu-DQB-2	•••	•••	•••	•••	•••																						
62	Tu-DQB-3	•••	••C	G	••	••	G																					
63	Tu-DQB-4	•••	••C	G	••	••	••																					

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65 **Fig. A1** Alignment of MHC II DQB sequence variants detected as homozygous. Numbers above sequence alignment (first row)
66 indicate the number of basepairs (i.e. position). The most prevalent sequence variant (Tu-DQB-1), which was found homozygous in
67 individuals of the two *Tursiops* populations is listed first as reference. A dot (•) indicates an identical basepair with reference to Tu-
68 DQB-1. Following Heimeier *et al.*, 2009, MHC II DQB codons that encode peptide binding sites are indicated according to: Murray *et*
69 *al.*, 1995; Hoelzel *et al.*, 1999; Seddon & Ellegren, 2002; Hayashi *et al.*, 2003 and Baker *et al.*, 2006. The peptide binding sites are
70 highlighted in turquoise color. Primer sequences are not included in this alignment or the analysis.

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77 **Table A1** Microsatellite loci and primer sequences for Shark Bay and Bunbury population

Locus	Primer sequences		Multiplex	Label	Allele size range (bp)	No. of Alleles	References
	Forward (5'-3')	Reverse (5'-3')					
D22	ACATTCCCAATAAAAAGTTAAAGT	CTCTTTGACATGCCCTCACC	2	NED	110-124	5	(a)
KWM12*	CTGGGCACTGTCTCTGAACATC	AGGAACGGCACATAAAGCACTGA	3	VIC	156-190	15	(b)
MK3	TGCATTCATGTAAAGGTGCG	CTGCAACTAGAGAAAGCC CG	3	NED	147-171	10	(c)
MK5	CTCAGAGGGAAATGAGGCTG	TGTCTAGAGGTCAAAGCCTTCC	3	6-FAM	205-219	6	(c)
MK6	GTCCTCTTTCCAGGTGTAGCC	GCCCACTAAGTATGTTGCAGC	1	PET	152-190	16	(c)
MK8	TCCTGGAGCATCTTATAGTGGC	CTCTTTGACATGCCCTCACC	3	PET	87-117	11	(c)
MK9	CATAACAAAGTGGGATGACTCC	TTATCCTGTTGGCTGCAGTG	3	6-FAM	168-178	6	(c)
Tur4_E12	CTGGGCACTGTCTCTGAACATC	AGGAACGGCACATAAAGCACTGA	1	PET	256-280	6	(d)
Tur4_F10	TCTTGATGGCTCAGAGGATGATTTTAC	AGCCAAACTGAAGATGCAACTGACTAC	2	6-FAM	374-398	7	(d)
Tur4_66	GAGGGTGAATGGGGACAAAAT	TGAAGCCAGGAGACTAGGACAGGTT	1	VIC	185-205	6	(d)
Tur4_80	AGCCAATGTCAGGGTGCTGGAT	GGGGCTTCTTGGCCTCTGTAA	3	NED	287-331	9	(d)
Tur4_87	CCCCATATGATGCCTTTGTAAGTCC	AATTCCTTGTAACAAACCTCTTTATCT	2	VIC	178-194	5	(d)
Tur4_91	GTTGGCTCTCCAGCTCTCAGGT	CAGTGGCTCCCATCTGTATTAGTCA	2	PET	207-235	8	(d)
Tur4_98*	GTCCCAGAACTTAGCACACTGTC	CAACTGGGGTCCAAAGAAAGAAG	1	NED	192-196	2	(d)
Tur4_105	CCCCGGCCTGCTTACCTCTG	CCGCCCCCTCCCCAAGTC	1	6-FAM	367-403	9	(d)
Tur4_108	ACAGGGACCTGAGTGGGTGTAAG	CTCCCTGGGTCTCTAGGCTACC	1	6-FAM	258-270	2	(d)
Tur4_111	CTCTGTAAGCACCCGTCCTGTGTA	TTCCCGCAGAATTCTGTGAACC	1	VIC	287-307	5	(d)
Tur4_117	TTGCAGTCAGCGTTTTCCAGAGA	GCCAGCCCATCCTTCAGATTTT	1	6-FAM	175-191	5	(d)
Tur4_128	ACGTGCGCATGTCTTTGTCTTAT	CTTTGGACGGGAGTAGAACCTA	1	NED	295-311	5	(d)
Tur4_132	CTTCCATGCGCCAGACAACCT	TGGCAAGATGAGAGGGAAAGAGG	3	VIC	326-334	3	(d)
Tur4_138	GTGGCTTACCATGGTGGATTCAG	GCATGGCCATAAAGGGAGGAG	2	6-FAM	207-231	7	(d)
Tur4_141	CACAAGCCTCAACCCTGGTGT	CTAGTCTGCCAATCTGCCCTACAG	2	NED	218-286	13	(d)

Tur4_142	GGCCCCCTTTTCCATCCTCA	CCAGCCCCCAAATCACGAGT	3	PET	330-346	5	(d)
Tur4_153	TGAGTAACCCCAATCTCGGTCTCT	CCAGCCCCCAAATCACGAGT	3	PET	215-219	2	(d)
Tur4_162	GCCAACCTCCAGGCAAACACTC	TGCAGTCAACCTGAGGCAAGTCTC	3	6-FAM	365-419	6	(d)

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79 Primer sequences for 25 microsatellite loci used for genotyping Shark Bay and Bunbury bottlenose dolphins. *Loci KWM12 and
80 Tur4_98 were removed from final analysis because they departed from Hardy-Weinberg-Equilibrium expectations. Annealing
81 temperature for polymerase chain reaction was 60 °C for all three multiplex PCR reactions. Fluorescent labels for forward primers are
82 listed in the column “Labels”. The range of allele sizes and the total number of alleles (‘No. Alleles’) for each locus of all individuals
83 sampled in Shark Bay and Bunbury are listed. References for the primer sequences are (a): Shinohara et al. 1997; (b): Hoelzel et al.,
84 1998; (c): Krützen et al., 2001; (d): Nater et al., 2009. This table is modified from supplementary Table S1, Manlik et al. (2018):
85 Manlik, O., Chabanne, D., Daniel, C., Bejder, L., Allen, S.J., Sherwin, W.B. 2018. Demography and genetics suggest reversal of dolphin
86 source-sink dynamics, with implications for conservation. *Mar. Mammal Sci.*, doi:10.1111/mms.12555.

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97 **Table A2** Conservative sampling of individuals with MHC and microsatellite data, which
 98 included equal numbers of males, females, calves (calf), juveniles (juv.) and adults (adu.) for
 99 each of the two populations. Age classes, i.e. calves, juveniles and adults are defined as in
 100 Manlik *et al.* (2016).

Cons. Sampling	calf	juv.	adu.	males	females	Total
BB cons.	2	15	38	32	23	55
SB sample 1	2	15	38	32	23	55
SB sample 2	2	15	38	32	23	55
SB sample 3	2	15	38	32	23	55

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120 **Table A3** Microsatellite and MHC II DQB diversity measures of the two sampling locations
 121 of Shark Bay. Measures of microsatellite diversity (A_e = effective number of alleles; 1H =
 122 Shannon index; F_{IS} = fixation index) and MHC II DQB nucleotide diversity (π) are listed for
 123 the two sampling locations in Shark Bay: East Shark Bay (ESB) and West Shark Bay (WSB).
 124 Subpopulation fixation index (F_{ST}) indicates the degree of differentiation between ESB and
 125 WSB.

Location	Microsatellite diversity					MHC II DQB nucleotide diversity		
	<i>n</i>	A_e	1H	F_{IS}	F_{ST}	<i>n</i>	π	
ESB	Mean	409	3.131	1.205	0.030	Mean	231	0.06548
	SE		0.365	0.102	0.009			SD
ESB vs WSB					0.006			
WSB	Mean	258	3.180	1.225	0.026	Mean	45	0.06197
	SE		0.334	0.099	0.010			SD

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141 **Table A4** MHC II DQB variants* and BLASTN hits. Names of MHC II DQB sequence
 142 variants found in the Shark Bay and Bunbury *Tursiops aduncus* populations are listed in
 143 order from Tu-DQB-1 to Tu-DQB-3. Only the four sequence variants of thirty-nine
 144 individuals that are homozygous for all 172 nucleotide sites are listed here. Sequence
 145 identities to alleles that closely match these sequence variants and are published on GenBank
 146 are shown along with allele names and species in which they were found. Note that Tu-DQB-
 147 4 is identical (100% identity at 100% coverage) to the MHC II DQB exon 2 allele *Dede-a*,
 148 which was reported in the common dolphin (*Delphinus delphis*). Additional sequence
 149 variants, i.e. haplotypes, which were inferred by haplotype reconstruction, are not shown here
 150 (see main text).

Variant	Identity	Allele	Species
Tuad-DQB*1	99%	Tutr-DQB*27	<i>Tursiops truncatus</i>
	100%	Tutr-DQB*06 (Note: 98% coverage)	<i>Tursiops truncatus</i>
	98%	Stco-DQB*04	<i>Stenella coeruleoalba</i>
	98%	Orbr-a	<i>Orcaella brevirostris</i>
	97%	Cehe-DQB*02	<i>Cephalorhynchus hectori</i>
	97%	Tutr-DQB*25	<i>Tursiops truncatus</i>
Tuad-DQB*2	100%	Tutr-DQB*03 (Note: 98% coverage)	<i>Tursiops truncatus</i>
	98%	Stco-DQB*04	<i>Stenella coeruleoalba</i>
	98%	Cehe-DQB*02	<i>Cephalorhynchus hectori</i>
	97%	Tutr-DQB*01; Tutr-DQB*15	<i>Tursiops truncatus</i>
Tuad-DQB*3	99%	Stco-DQB*06	<i>Stenella coeruleoalba</i>
	99%	Tutr-DQB*24 (Note: 98% coverage)	<i>Tursiops truncatus</i>
	99%	Tutr-DQB*13 (Note: 98% coverage)	<i>Tursiops truncatus</i>
	98%	Stco-DQB*05	<i>Stenella coeruleoalba</i>
Tuad-DQB*4	100%	Dede-a	<i>Delphinus delphis</i>
	99%	Tutr-DQB*01	<i>Tursiops truncatus</i>
	98%	DQB*0101 (LOC101278540)	<i>Orcinus orca</i>
	98%	Tutr-DQB*02	<i>Tursiops truncatus</i>

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159 **Table A5** Comparison of microsatellite measures within three SB subsamples.
 160 Mean values for microsatellite observed heterozygosity (H_o), expected heterozygosity relative
 161 to Hardy-Weinberg Equilibrium expectations (H_e), effective number of alleles (A_e) and
 162 Shannon indices (1H) are shown for each of the subsamples (SB sample 1-3). F and p -values
 163 for analysis of variance (ANOVA) test are tabulated comparing the three subsamples.
 164 *ANOVA test on A_e was based on log-transformed values because the original values were
 165 not normally distributed.

	SB sample 1	SB sample 2	SB sample 3	F	p	Sig.
H_o	0.551	0.566	0.576	0.0919	0.9124	ns
H_e	0.561	0.587	0.585	0.130	0.8793	ns
A_e	2.931	3.094	3.051	0.0788*	0.9243*	ns*
1H	1.141	1.194	1.185	2.886	0.0655	ns

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