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Genetic diversity of common toads (*Bufo bufo*) along the Norwegian coast: disjunct distribution of locally dominant haplotypes

Table 1. Pairwise F_{st} values between 20 sampling localities in Norway. *: $p < 0.05$; **: $p < 0.001$ after Bonferroni corrections. Negative F_{st} values arise when the variance of genetic variation among individuals within populations is greater than the variance among populations, and in our case are linked to partially very low sample sizes per locality (see Table 2). They should be regarded as zero.

	KRF	MAS	TIK	SAH	EGE	VI	MOR	BØA	STL	STV	BØE	TYH	AUH	NEV	BES	ØY	BRM	VOU	HI
MAS	0.09	-																	
TIK	0.23	0.73	-																
SAH	0.82**	1.00**	0.65*	-															
EGE	0.84**	1.00**	0.70*	0.00	-														
VI	-0.84	0.00	-0.33	1.00	1.00	-													
MOR	-0.84	0.00	-0.33	1.00	1.00	0.00	-												
BØA	-0.13	0.00	0.25	1.00**	1.00*	0.00	0.00	-											
STL	-0.13	0.00	0.25	1.00**	1.00**	0.00	0.00	0.00	-										
STV	0.31**	0.78*	0.02	0.83**	0.86*	-0.50	-0.50	0.25	0.25	-									
BØE	-0.26	0.00	0.11	1.00	1.00*	0.00	0.00	0.00	0.00	0.08	-								
TYH	0.03	0.62	0.00	0.90**	0.92**	-1.00	-1.00	0.00	0.00	-0.07	-0.20	-							
AUH	0.67	1.00	-0.33	0.00	0.00	1.00	1.00	1.00	1.00	0.00	1.00	0.33	-						
NEV	0.03	0.62	0.00	0.90**	0.92**	-1.00	-1.00	0.00	0.00	-0.07	-0.20	-0.20	0.33	-	-				
BES	0.67	1.00	-0.33	0.00	0.00	1.00	1.00	1.00	1.00	0.00	1.00	0.33	0.00	0.33	-0.40				
ØY	0.40**	0.70**	-0.16	0.34*	0.39	0.20	0.20	0.43	0.43	0.24	0.37	0.26	-0.40	0.26	0.00	-			
BRM	0.77**	1.00**	0.44	0.00	0.00	1.00	1.00	1.00*	1.00*	0.68*	1.00*	0.79*	0.00	0.79**	0.00	0.21	-		
VOU	0.78**	1.00**	0.52	0.00	0.00	1.00	1.00	1.00*	1.00*	0.74*	1.00*	0.83**	0.00	0.83*	-0.29	0.25	0.00	-	
HI	0.58**	0.78**	0.19	0.35*	0.39*	0.48	0.49	0.60**	0.60**	0.35*	0.57*	0.45**	-0.29	0.45**	0.00	0.17*	0.23	0.27*	-
DØ	0.84**	1.00**	0.70	0.00	0.00	1.00*	1.00	1.00**	1.00**	0.86**	1.00*	0.92**	0.00	0.92**		0.39*	0.00	0.00	0.39*

Table 2. Geographic distribution of cytb region haplotypes across different countries in Europe. N, Sample size; H, Haplotype; h, haplotype numbers; Current study: Nor, Norway. Recuero et.al. 2012: Swe, Sweden; UK, United Kingdom; Net, The Netherlands; Bel, Belgium; Fra, France; Ger, Germany; Pol, Poland; Hun, Hungary; Slo, Slovakia; Ita, Italy; Cro, Croatia; Ser, Serbia; Mac, Macedonia; Alb, Albania; Mon, Montenegro; Gre, Greece; Rom, Romania; Tur, Turkey; Ukr, Ukraine; Rus, Russia.

	Nor	Swe	UK	Net	Bel	Fra	Ger	Pol	Hun	Slo	Ita	Cro	Ser	Mac	Alb	Mon	Gre	Rom	Tur	Ukr	Rus	H, combined 16S+cytb Recuero et.al. 2012
N	154	8	1	1	2	9	3	4	12	3	58	2	21	1	1	4	7	11	5	7	11	
H_1	85						1	2	7	2		1	6			1		7		6	7	1,9,16,17,21, 31,84,85,88 28
H_2	57	1																				
H_3	1																					-
H_4	1																					-
H_5	1																					-
H_6	1																					-
H_7	2																					-
H_8	6	2																				26,81
H_9			1	1	2	5	2		1													2,4
H_10													5									10,15
H_11													1									11
H_12													1									12
H_13													2					1				13
H_14													2			1		1				14,18
H_15													1									19
H_16													1									24
H_17													2	1	1	1	2					25,55,59
H_18										1												92
H_19		1																				27
H_20		1																				79
H_21		1																				29
H_22		1																				30
H_23		1																				80
H_24																				1		45
H_25																					1	38
H_26																					3	39
H_27																	1					54
H_28																	1					56
H_29																	1					20
H_30																	1					57
H_31																	1					58
H_32						1																71
H_33						2			1													23
H_34						1																106
H_35												1										77
H_36								1														82
H_37								1														83
H_38																1						22
H_39									1													89
H_40									1													90
H_41									1													91
H_42																		1				96
H_43																		1				64

	Nor	Swe	UK	Net	Bel	Fra	Ger	Pol	Hun	Slo	Ita	Cro	Ser	Mac	Alb	Mon	Gre	Rom	Tur	Ukr	Rus	H, combined 16S+cytb
H_44																			1			97
H_45																			3			36,37,99
H_46																			1			98
H_47											9											100
H_48											5											101
H_49											1											102
H_50											5											103
H_51											3											104,121
H_52											23											107,110,113, 114,117,118 108,109
H_53											2											
H_54											1											111
H_55											1											112
H_56											1											115
H_57											1											116
H_58											2											119
H_59											1											120
H_60											2											122
H_61											1											123
h	8	7	1	1	1	4	2	3	6	2	15	2	9	1	1	4	6	5	3	2	3	