

Population genetics of the common whelk (*Buccinum undatum* L.) in Iceland and the Faroe Islands

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Introduction

A subtidal gastropod, the common whelk *Buccinum undatum* is widely distributed in the North Atlantic as well as the Greenland and Norwegian seas (1). The morphology of the common whelk shows regional differences which have been observed in whelk from Breiðafjörður among other places. The regional variability in shell morphology indicates that migration of whelks between areas might be limited enough to form genetically distinct subpopulations. The aim of this study was to test the hypothesis that different populations of the common whelk are present within Iceland and that the populations are different between Iceland and the Faroe Islands. The hypotheses was tested by analyses of partial nucleotide sequences of two mitochondrial genes, 16S rRNA and COI from whelks collected at five locations, four in Iceland and one in the Faeroe Island.

Methods

Whelks were collected from four locations in Iceland; Faxaflói, Breiðafjörður (two sites) and Húnaflói as well as from Nólsoyarfjarður in the Faroe Islands. DNA was extracted from the mantle of the whelk with phenol free CTAB/chloroform extraction. Fragments of two mitochondrial genes, 16S rRNA and COI, were successfully amplified by PCR. Approximately 463 bp fragment of the 16S rRNA gene and a 530 bp fragment of the COI gene were amplified with primer pairs from Iguchi *et al.* (2,3). The PCR product was sequenced using ABI PRISM 3100 Genetic Analyser. The DNA sequencing reactions on PCR products were run on an ABI PRISM 3100 Genetic Analyser. Data was analyzed with Arlequin 3.1 and R 2.6.2.

Results

The mitochondrial 16S rRNA gene fragment (360 bp) was sequenced from 373 individuals and contained three polymorphic sites (Table 1). The individuals could be classified into six different haplotypes (Table 1, Figure 1). Additionally, the mitochondrial COI gene fragment (437bp) was sequenced from 346 whelk and three polymorphic sites were revealed, which gave rise to four haplotypes (Table 2, Figure 2). According to pairwise tests of differentiation, genetic differentiation was significant for 16S rRNA between the Faroe Islands and all locations in Iceland, as well as between Húnaflói and Breiðafjörður (Table 3). Pairwise tests of differentiation revealed that the genetic differentiation was significantly different for COI between Húnaflói and Breiðafjörður as well as between Faxaflói and Hemptill, but not between the Faroe Islands and other locations (Table 3). The superhaplotype contained six polymorphic sites and 13 haplotypes (Table 4) but the haplotypes showed no geographical pattern in distribution.

Table 1. Nucleotide polymorphisms and haplotype frequency in a 360 bp part of the 16S rRNA gene sequence of *B. undatum*. Identity with the topmost sequence is indicated with an asterisk (*). Position of the polymorphic site is numbered with respect to the 3' end of the

Haplotype	Position			Frequency	Location					
	157	176	324		Hemptill	Oddbjarnarsker	Húnaflói	Faxaflói	Faroe Islands	
BUusr1	C	-	C	163	43	53	36	9	22	
BUusr2	T	*	*	109	30	18	3	2	56	
BUusr3	T	*	T	69	11	11	37	9	1	
BUusr4	T	A	T	28	1	1	14	0	12	
BUusr5	*	*	T	3	0	1	2	0	0	
BUusr6	*		T	1	0	0	0	0	1	
Total				373	85	84	92	20	92	

Table 2. Nucleotide polymorphisms and haplotype frequency in a 437 bp part of the COI gene sequence of *B. undatum*. Identity with the topmost sequence is indicated with an asterisk (*). Position of the polymorphic site is numbered with respect to the 3' end of the

Haplotype	Position			Frequency	Location					
	77	117	435		Hemptill	Oddbjarnarsker	Húnaflói	Faxaflói	Faroe Islands	
BUcoi1	G	G	A	166	35	50	31	8	42	
BUcoi2	*	A	*	119	33	21	18	2	45	
BUcoi3	*	A	G	59	7	12	32	8	0	
BUcoi4	A	*	*	2	0	2	0	0	0	
Total				346	75	85	81	18	87	

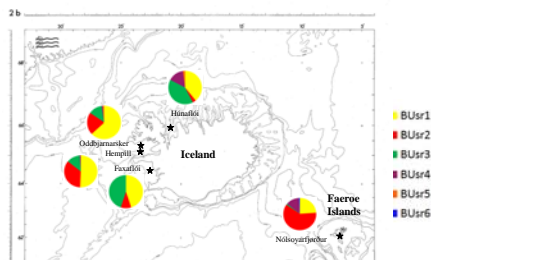


Figure 1. 16S rRNA haplotype frequency (%) at four locations in Iceland and one in the Faeroe Islands. See Table 1 for additional information on haplotypes.

Table 3. Pairwise genetic differentiation between populations based on the analysis of 16S rRNA (A) and COI (B) sequences. Number of permutations:1023. Above diagonal (*italics*): FST values, the fixation index. Below diagonal: P-value. Level of significance was P<0.005 (according to the Bonferroni procedure).

A					
Location	Hemptill	Oddbjarnarsker	Húnaflói	Faxaflói	Faroe Islands
Hemptill	x	0.018	0.137	0.098	0.115
Oddbjarnarsker	0.0693±0.0085	x	0.122	0.092	0.227
Húnaflói	<0.001	<0.001	x	-0.005	0.288
Faxaflói	0.0117±0.0033	0.0225±0.0042	0.4092±0.0159	x	0.295
Faroe Islands	<0.001	<0.001	<0.001	<0.001	x

B					
Location	Hemptill	Oddbjarnarsker	Húnaflói	Faxaflói	Faroe Islands
Hemptill	x	0.033	0.094	0.138	0.001
Oddbjarnarsker	0.0361±0.0059	x	0.070	0.072	0.227
Húnaflói	<0.001	0.0019±0.0014	x	-0.020	0.172
Faxaflói	0.0049±0.0025	0.0381±0.0061	0.6689±0.0158	x	0.238
Faroe Islands	0.2803±0.0162	0.0019±0.0014	<0.001	0.0010±0.0010	x

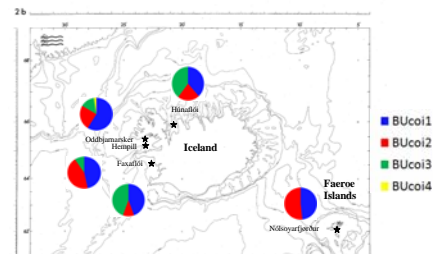


Figure 2. COI haplotype frequency (%) at four locations in Iceland and one in the Faeroe Islands. See Table 2 for additional information on haplotypes.

Table 4. Haplotype frequency of the combined sequences of the COI and the 16S rRNA gene sequence of the common whelk at the five sample locations.

Haplotype	Location					Frequency
	Hemptill	Oddbjarnarsker	Húnaflói	Faxaflói	Faroe Islands	
BU1	34	49	28	8	20	141
BU2	25	18	2	2	34	81
BU3	6	11	30	8		55
BU4	1	1	12		10	24
BU5	1				19	20
BU6	2	2	4			8
BU7	3					3
BU8		1	2			3
BU9			1		1	2
BU10			1			2
BU11		2				2
BU12					1	1
BU13	1					1
Total	73	84	80	18	85	343

Discussion

Life history characteristics of the common whelk, such as direct development and limited adult movement, suggest that individuals may become adapted locally as a result of limited mixing between adjacent populations. Our mitochondrial genetic results are in line with this hypothesis; they showed significant genetic differentiation between Iceland and the Faeroe Islands, and moderate or little genetic differentiation within Icelandic waters. Interestingly, the haplotype distribution of the superhaplotype (16S rRNA and COI) revealed no geographical clusters, based on neighbour-joining tree analysis.

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