

Table S1: The distribution of the 97 haplotypes observed among the 169 ninespine sticklebacks CR sequences.

Haplotype Name	Population of origin (n = number of individuals)
Attu Island	
AI_1	AI (8)
AI_2	AI (1)
Alaska	
<i>Nome</i>	
NO_1	NO (4)
NO_2	NO (1)
NO_3	NO (1)
NO_4	NO(2)
NO_5	NO (1)
<i>Matanuska-Susitna Valley</i>	
AK_1	CH (10), GH (2), ML (2), PT (2)
AK_2	GH (1)
AK_3	GH (1)
AK_4	GH (1)
AK_5	GH (1)
AK_6	ML (2)
AK_7	ML (1)
AK_8	ML (1)
AK_9	ML (1)
AK_10	PT (1)
AK_11	PT (5)
Manitoba	
DM_1	DM (1)
DM_2	DM (2)
Prince Edward Island	
PEI_1	GF (6), OK (2)
PEI_2	GF (1)
PEI_3	GF (1)
PEI_4	GF (1)
PEI_5	GF (1)
PEI_6	OK (1)
PEI_7	OK (1)
PEI_8	OK (1)
PEI_9	OK (1)
PEI_10	OK (1)
Massachusetts	
NB_1	NB (1)
NB_2	NB (1)
NB_3	NB (1)
NB_4	NB (2)
NB_5	NB (1)
NB_6	NB (1)
Great Lakes	
GL_1	LH (1), LS (1)
GL_2	LH (1)

GL_3	LH (1), MR (1), RM (1)
GL_4	LH (1)
GL_5	MR (1)
Ireland	
LE_1	LE (1)
LE_2	LE (1)
LE_3	LE (1)
LE_4	LE (1)
RB_1	RB (4)
Kuril Islands	
KI_1	PM (2)
KI_2	PS (3), SK (3)
KI_3	SK (1)
KI_4	SK (1)
KI_5	SK (1)
KI_6	TF (1)
KI_7	TF (1)
KI_8	TF (1)
KI_9	UR (1)
KI_10	UR (1)
St Lawrence River	
ST_1	ST (2)
ST_2	ST (2)
ST_3	ST(1)
Northwest Territories	
NWT_1	AE (1)
NWT_2	AE (1)
NWT_3	CT (1)
NWT_4	CT (1)
NWT_5	CT (1), DL (1)
NWT_6	CT (1), DL (1), SL (2)
NWT_7	DL (1)
NWT_8	DL (1), SN (1)
NWT_9	DL (1)
NWT_10	FH (4)
NWT_11	FH(1)
NWT_12	FH(1)
NWT_13	FH(1)
NWT_14	PL (1)
NWT_15	PL (4)
NWT_16	PL (1)
NWT_17	PL (1)
NWT_18	SL (1)
NWT_19	SL (1)
NWT_20	SL (1)
NWT_21	SL (1)
NWT_22	SL (1)
NWT_23	SL (1)
NWT_24	SL (1)
NWT_25	SR (5)

NWT_26	SR (1)
NWT_27	SR (1)
NWT_28	SR (1)
NWT_29	SR (2)
NWT_30	SN (1)
Sweden	
SW1_1	AS (1)
SW1_2	AS (1)
SW1_3	AS (1)
SW2_1	OS (1)
SW2_2	OS (1)
SW2_3	OS (1)
SW2_4	OS (1)
SW2_5	OS (1)

Table S2: Pair-wise population F_{ST} values. A Bonferroni correction was applied to the data with $\alpha=0.0001$. Significant F_{ST} values are in italics.

Table S3: Hierarchical analysis (AMOVA) of genetic divergence in ninespine stickleback geographical regions/lineages and habitats.

Group	Among groups			Among sites			Within sites		
	%	F _{CT}	P value	%	F _{ST}	P value	%	F _{SC}	P value
Geographic regions/ Lineages (all)	28.25	0.283	***	20.45	0.285	***	51.30	0.515	***
Alaska				26.32	0.263	***	73.68	0.296	*
NWT + Manitoba				25.91	0.259	***	74.09	0.317	*
East Coast				17.75	0.177	***	82.25	0.220	***
Great Lakes				11.56	0.115	NS	88.44	0.035	NS
NE Asia				57.37	0.574	***	42.63	0.578	NS
Ireland				20.04	0.200	***	79.96	0.317	*
Sweden				12.32	0.123	***	87.68	0.204	*
Habitat type (all)	3.02	0.030	NS	44.16	0.455	***	52.82	0.472	***
Marine				44.97	0.449	***	55.03	0.477	*
Freshwater				45.81	0.458	***	54.19	0.488	***

P values: NS = not significant, * P < 0.05, *** P < 0.001

Table S4: Isolation by distance analysis (Mantel test) between geographic regions and F_{ST} . A Bonferroni correction was applied to the data with $\alpha=0.01$. No significant correlations were found after correction.

Region/ Lineage	Correlation coefficient	P - value
Alaska	0.227	0.397
NWT + Manitoba	-0.205	0.881
East Coast	0.991	0.042
Great Lakes	-0.137	0.658
NE Asia	0.541	0.124
Ireland	-	-
Sweden	-	-