Supplememtary information 2.

Microsatellite allele length ranges, number of alleles found (A) and genetic diversity (H_E) in each genome, number of incongruent cases for each country (and number of ponds with >2 cases, where incongruent loci were not excluded but corrected) and the correction for incongruence.

Primer	L alleles	R alleles	A L	A R	H_E L	H_E R	DK**	SE**	D**	Bal**	Incongruence correction
Ca1b6*	74-90	83-96	5	10	0.109	0.476	1	1	23(3)	4(1)	L -> R (four different alleles)
Res16*	121+125	123+127	4	2	0.015	0.174	21(0)	7(0)	24(5)	1	R -> L (two different alleles)
RlCA1b5*	119+145	132+134	2	2	0.001	0.288	2	3(0)	2		
Ga1a19red.*	195+230	199-243	2	8	0.009	0.535	2	1	1		
Re1CAGA10	90-98	95-185	4	28	0.041	0.797	2	1	3(1)		L -> null
Rrid059Ared.	278	300-337	1	13	0.000	0.590			2		
RlCA2a34	113-156	106+109	17	3	0.666	0.033	9(1)		3(0)	17(2)	L -> null (DK), R -> null (Bal)
Rrid013A	290-302	281+287	5	2	0.158	0.068		1	14(2)		L -> null
Res20	85-151		22		0.549					2	
RlCA5	233-264		11		0.510		1	2	12(1)		L -> R
ReGA1a23	98-139		17		0.786		1				
RlCA1a27	95-141		15		0.717		1		1		
RlCA18	171-196		12		0.259						
Re2CAGA3		169-236		13		0.784	1		1	5(1)	R -> L
Rrid064A		211-235		6		0.649	256(9)		2		R -> null in all Jutland ponds
Res22		82-124		14		0.721			5(0)		
Rrid169A		176-203		11		0.567		6(1)	23(3)	12(2)	R -> null
Rrid135A		107-207		9		0.520					

* Dosage effect when the L and R alleles are not too different in length. Dosage effects were clearer with Ga1a19redesigned and Res16 than with Ca1b6 and, especially, RlCA1b5.

** Total sample sizes: DK (Denmark) 1562 individuals (54 ponds), SE (Sweden, first sample only) 409 (12), Bal (Baltic states) 224 (12) and D (Germany) 312 (13).