

Supplemental table S2. Description of primers used in the study

Primer	Sequence	Size range (bp)	Number of amplified alleles	Number of specific alleles
<i>Pul01*</i>	F: CAC CTT GTC CAC GGT TCT G R: ACC AGG TCA GAG AGC TCA AC	161-176	15	3
<i>Pul02*</i>	F: TGA GTT CTT GCA CTT CAG GG R: AAT CCC ACG AGT TAG TGC C	326-334	8	1
<i>Pul04*</i>	F: ACC GTT ACT GTC CAA CGG G R: CCTGTA TGA ATG CAA CTT GAC G	219-234	15	1
<i>Pul05*</i>	F: GAT TAA TGG CGG GCG ACA G R: TGG GTG CGC TAA TCG AGG	238-251	10	1
<i>Pul06*</i>	F: TGG CAT TCC TAG TTG ACG ATG G R: GCT AGA CAA ACA AGA ATG CCT GC	161-170	8	0
<i>Pul07*</i>	F: ATC CCG AGG GAG AAT GCA C R: AAG CAT GAG GTG TCT TGG C	328-338	10	2
<i>Pul10*</i>	F: TTT CCA AGC TCC GGC CAC R: ACC GGT TGA GAC ACC CAA G	94-103	8	0
<i>Pul11*</i>	F: TCA ATC AAC CGC ATG TAG AGC R: CAC GTG TAT TCG GCA GTC AG	296-337	18	0
Total			92	8

  

Primer	Sequence	Number of amplified bands	Number of specific bands
ISJ 4	5' GTC GGC GGA CAG GTA AGT 3'	27	2
ISJ 5	5' CAG GGT CCC ACC TGC A 3'	23	0
ISJ 11	5' TGC AGG TCA AAC GTC G 3'	25	4
Total		75	6

\*Szczecińska et al. (2013)