S1 File: **Microsatellite amplification protocols**

Nine neutral microsatellite loci (from Lagardier et al (1999) and Peichel et al (2001) were amplified in two multiplex reactions (Multiplex A: Gac1097, Gac 1125, Gac4170, Gac5196, Gac7033; Multiplex B: STN18, STN32, STN75, STN84) after Kalbe *et al*. (2009). PCR amplification was carried out using Top-Bio PPP mastermix (Top Bio, Czech Republic); total reaction volume was 3.5 *μ*l with 1.5 *μ*l mastermix, 1 *μ*l template DNA (1-5 ng), and 0.035 *μ*l (10 pM) of each primer with the remainder volume made up with ddH20. Identical thermocycler conditions were used for both multiplexes, 110°C heated lid, denaturation at 95°C for 15 min and then 20 cycles of 95°C for 30 s, 57°C for 1.5 min and 72°C for 1.5 min, with a final extension of 60°C for 30 min. QTL-linked markers (STN380, STN381, STN382, STN211 AND STN 219) were amplified separately (i.e. not multiplexed) using an identical amplification mix and the following thermocycler conditions: 93°C for 3 min. 59°C for 30 s, 72°C for 30s; five cycles of 94°C for 30s, 59°C for 30 s, 72°C for 30 s; 35 cycles of 90°C for 30 s, 60°C for 30 s, 72°C for 30 s and 72°C for 10 minutes following Marchinko (2009). Fragment analysis was then performed on a 96 capillary 3730xl DNA Analyzer (Applied Biosystems Inc). Raw fragment profiles for each individual were then manually genotyped using GENEMAPPER v4.1 (Applied Biosystems Inc).

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