**S1 Materials and Methods**. **PCR reactions and thermocycling conditions for multiplex 1 – 3.**

We used 14 highly polymorphic microsatellite loci (1-3) and two DNA markers associated with the Y sex chromosome carried by males (Zn, Zn-finger; Amel, Amelogenin), but not by females (4), labeled with fluorescent dyes and arranged in three PCR multiplex reactions (multiplex 1 - F124-PET, FCA391-NED, FCA043-NED, FCA275-VIC, FCA096-6-FAM, FCA126-PET, FCA090-6-FAM, Zn-6-FAM; multiplex 2 - F85-VIC, F98-6-FAM, FCA741-PET, FCA225-PET, FCA008-6-FAM, Amel-6-FAM; multiplex 3 - F53-NED, FCA441-6-FAM) to enhance performance and efficiency. The three multiplexes each contained 5.2 µL PCR mixture and 1.8 µL of DNA. Multiplex 1 included 3.5 µL 1 x concentrated Qiagen Master Mix (Qiagen, Inc.), 0.7 µL of 0.5 x concentrated Qiagen Q solution (Qiagen, Inc.), 0.98 µL of primers (0.10µM F124, 0.34µM FCA391, 0.07µM FCA043, 0.13µM FCA275, 0.21µM FCA096, 0.20µM FCA126, 0.20µM FCA090, 0.14µM Zn), 0.02 µL H2O, and 1.8 µL DNA extract. Multiplex 2 consisted of 3.5 µL 1 x concentrated Qiagen Master Mix, 0.7 µL of 0.5 x concentrated Qiagen Q solution, 0.85 µL of primers (0.20µM for F85, 0.09µM for F98, 0.11µM for FCA741, 0.43µM for FCA225, 0.10µM for FCA008, 0.29µM for Amel), 0.15 µL H2O, and 1.8 µL DNA extract. Multiplex 3 only differed in the amount of water (0.76 µL) and primers (0.24 µL; 0.20µM for F53, 0.14µM for FCA441) added. Microsatellite PCR amplifications were conducted using a DNA Engine Tetrad 2 Peltier Thermal Cycler (Bio-Rad Laboratories, Inc.) starting with an initial denaturation step of 15 min at 95 °C; followed by 13 cycles of 30 s at 94 °C for denaturation, 1.5 min at 60 °C with a decrease in annealing temperature of 0.8 °C in each cycle, and 1 min elongation at 72 °C; followed by 30 cycles of 30 s at 94 °C for denaturation, 1.5 min at 50 °C for annealing, and 1 min elongation at 72 °C; and 30 min at 60 °C for final elongation. A polymerase chain reaction negative was included in each group of PCR reactions to indicate the presence/absence of contamination. We visualized PCR products using an ABI PRISM® 377 automated DNA sequencer (Applied Biosystems™), and genotypes were identified using the software GENEMAPPER, version 3.7 (Applied Biosystems™).

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