CORRIGENDUM

Population genetics of *Schistosoma haematobium*: development of novel microsatellite markers and their application to schistosomiasis control in Mali – CORRIGENDUM

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Further sequence analysis has revealed that a number of the 16 novel primer sequences reported in Table 1 are the same or reverse complements of each other, 2 of which were used in the multiplex PCR used to analyse the samples. Re-analyses of the dataset reveal that whilst this does not impact the results and conclusions drawn in the Gower *et al*. (2011) paper, it is nevertheless important that researchers intending to use this multiplex PCR remove loci C2. Researchers should also be aware of the additional primer duplications if designing their own further multiplexes. All authors on the Gower *et al*. paper apologise for these issues.

Precise details are thus:

(1) C2 (EF60044), C111 (HM856649) and C112 (HM856650) are the same loci with C112 being the reverse sequence of C2 and C111. The forward primer designed for C111 and the reverse primer designed for C112 are the same primer but the reverse complement of each other and the reverse primers for both C2 and C111 are identical.
(2) C120 (HM856654) and C119 (HM856653) are the same loci but the sequences are the reverse of each other.
(3) D105 (HM856647) and D3 (EF608047) are the same sequence but the reverse of each other and the forward primer of D105 and the reverse primer of D3 are the reverse complement of each other.

REFERENCE

Gower, C. M., Gabrielli, A. F., Sacko, M., Dembele, R., Golan, R., Emery, A. M., Rollinson, D. and Webster, J. P. (2011). Population genetics of *Schistosoma haematobium*: development of novel microsatellite markers and their application to schistosomiasis control in Mali. *Parasitology* **138**, 978–994.

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