Erratum to: Development of novel multiplex microsatellite polymerase chain reactions to enable high-throughput population genetic studies of Schistosoma haematobium

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Unfortunately, the original version of this article [1], contained a mistake. In Table 1, the primers for Sh6 and Sh9 were included incorrectly. Instead of GGGATGTATGCAGACTTG TTGTTTGGCTGCAGTAAC and GCTGAGCTTGAGATTGCTTCTGTCCCATCGATACC they should have been Sh6 Forward Primer GGTGGATTACGCAATAG, Sh6 Reverse Primer TTTAATCAACCGGGTGTC and Sh9 Forward Primer GGGATGTATGCAGACTTG, Sh9 Reverse Primer TTGTGATGGCTACGTAAC respectively.

A corrected version of Table 1 is included below.

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Reference

1. Webster BL, Rabone M, Pennance T, Emery AM, Allan F, Gouvras S, et al. Development of novel multiplex microsatellite polymerase chain reactions to enable high-throughput population genetic studies of Schistosoma haematobium. Parasit and Vectors. 2015;8:432.
Table 1: Details of the 18 selected microsatellite loci and the characteristics of the two multiplex microsatellite PCR assays. Loci Sh1-15 are from Travis et al., 2013 and Loci C102, C111 and C131 are from Gower et al., 2011. For Niger $H_o = 0.596$, $H_e = 0.609$, for Pemba $H_o = 0.599$, $H_e = 0.638$. The overall $H_o = 0.597$, $H_e = 0.623$.

| Panel 1 | Marker | Forward Primer 5'- 3' | Reverse Primer 5'- 3' | Dye | Size Range (bp) | Repeat | A     | Niger $H_o$ | Niger $H_e$ | Zanzibar $H_o$ | Zanzibar $H_e$ |
|---------|--------|------------------------|------------------------|-----|----------------|--------|-------|------------|------------|--------------|--------------|
| Panel 1 | C102   | TTGCTCTGTGAATGACCGAAT | TTAGATGAATAATAATGTTGAAACCAC | VIC | 184-199 | ATT    | 6     | 0.42      | 0.37       | 0.02         | 0.02         |
|         | Sh1    | GCATCCAATTTCGTACAC     | CCACATTAGGGCCAACAGAAG  | VIC | 245-284 | AAT    | 13    | 0.76      | 0.72       | 0.84         | 0.80         |
|         | Sh4    | GTCCCTCCTCTCCCTTTTG    | CACATTGCTCTAGATATCG    | NED | 184-240 | ACTC   | 15    | 0.94      | 0.85       | 0.86         | 0.88         |
|         | C131   | CTGTGCTTGGGCGATTTG     | CATGTGGAGGTCAACGTCG    | NED | 253-265 | AAT    | 4     | 0.00      | 0.00       | 0.00         | 0.00         |
|         | Sh6    | GGGAGATTACGCAATAG      | TTAGATGAATAATAATGTTGAAACCAC | VIC | 309-321 | AAT    | 7     | 0.48      | 0.44       | 0.84         | 0.76         |
|         | Sh9    | GGGATGTAGCGACGTTLG     | TTAGATGAATAATAATGTTGAAACCAC | VIC | 484-524 | AAT    | 11    | 0.46      | 0.76       | 0.46         | 0.86         |
|         | Sh3    | GGGAGGCTTTGGGATTTG     | CACGTTGGAGGTCAACGTCG    | NED | 270-366 | AAT    | 30    | 0.76      | 0.86       | 0.94         | 0.86         |
|         | C111   | GCACTTCTTCTAATCG       | GACCGTTGAGGTCAACGTCG    | NED | 201-225 | AAT    | 9     | 0.74      | 0.67       | 0.76         | 0.68         |
|         | Sh7    | TCCGAACCTTCACTCAATG    | CACCGTTGAGGTCAACGTCG    | PET | 293-311 | AAT    | 7     | 0.46      | 0.62       | 0.42         | 0.48         |
| Panel 2 | Sh2    | TTAGTGTTGGGTTCCTGCAAC | CACCGTTGAGGTCAACGTCG    | NED | 155-218 | AAT    | 21    | 0.84      | 0.90       | 0.56         | 0.89         |
|         | Sh5    | TGGGCTCAAGGAAGATTTAATT | ACCGTTGAGGTCAACGTCG    | NED | 263-314 | AAT    | 16    | 0.78      | 0.81       | 0.36         | 0.48         |
|         | Sh13   | GAGGCACTCTAATCG        | ACCGTTGAGGTCAACGTCG    | NED | 163-211 | AAT    | 17    | 0.78      | 0.72       | 0.68         | 0.64         |
|         | Sh4    | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 268-313 | AAT    | 13    | 0.84      | 0.78       | 0.72         | 0.79         |
|         | Sh10   | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 183-207 | AAT    | 9     | 0.18      | 0.34       | 0.74         | 0.70         |
|         | Sh12   | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 245-278 | AAT    | 11    | 0.06      | 0.06       | 0.56         | 0.65         |
|         | Sh8    | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 282-321 | AAT    | 14    | 0.76      | 0.81       | 0.84         | 0.83         |
|         | Sh11   | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 183-213 | AAT    | 9     | 0.68      | 0.58       | 0.68         | 0.69         |
|         | Sh15   | GGGAGGCTTTGACATAG      | ACCGTTGAGGTCAACGTCG    | NED | 274-301 | AAT    | 10    | 0.78      | 0.65       | 0.50         | 0.466        |

Panel = single multiplex PCR. A = observed number of alleles. Dye = the fluorescent dye label of the forward primer (VIC = green, NED = yellow, 6-FAM = Blue, PET = red). $H_o$ = observed heterozygosity, $H_e$ = expected heterozygosity.