



| | |
|----------------|---|
| Title | Erratum to: Development of novel multiplex microsatellite polymerase chain reactions to enable high-throughput population genetic studies of <i>Schistosoma haematobium</i> |
| Authors | Webster, BL; Rabone, M; Pennance, T; Emery, AM; Allan, F; Gouvras, A; Knopp, S; Garba, A; Hamidou, AA; Mohammed, KA; Ame, SM; Rollinson, D; Webster, JP |
| Description | © Webster et al. 2015. Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated. |
| Date Submitted | 2018-01-31 |

ERRATUM

Open Access



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

B. L. Webster^{1,2*}, M. Rabone¹, T. Pennance^{1,3}, A. M. Emery¹, F. Allan¹, A. Gouvras¹, S. Knopp^{1,4,5}, A. Garba⁶, A. A. Hamidou⁶, K. A. Mohammed⁷, S. M. Ame⁷, D. Rollinson¹ and J. P. Webster^{2,3}

* Correspondence: b.webster@nhm.ac.uk

¹Wolfson Wellcome Biomedical Laboratories, Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK

²Department of Infectious Disease Epidemiology, Imperial College Faculty of Medicine (St Mary's Campus), Norfolk Place, London W2 1PG, UK
Full list of author information is available at the end of the article

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 GCTGAGCTTGAGATTG CTTCTGTCCCATCGATACC they should have been Sh6 Forward Primer GGTGGATTACGCAATAG, Sh6 Reverse Primer TTTAATCAACCGGGTGTC and Sh9 Forward Primer GGGATGTATGCAGACTTG, Sh9 Reverse Primer TTGTTTGGCTGCAGTAAC respectively.

A corrected version of Table 1 is included below.

Author details

¹Wolfson Wellcome Biomedical Laboratories, Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK. ²Department of Infectious Disease Epidemiology, Imperial College Faculty of Medicine (St Mary's Campus), Norfolk Place, London W2 1PG, UK. ³RVC Department of Pathology and Pathogen Biology, Centre for Emerging, Endemic and Exotic Diseases (CEEED), Royal Veterinary College, University of London, Hertsfordshire AL97TA, UK. ⁴Department of Epidemiology and Public Health, Swiss Tropical and Public Health Institute, Socinstrasse 57, Basel 4002, Switzerland. ⁵University of Basel, Petersplatz 1, Basel 4003, Switzerland. ⁶Réseau International Schistosomoses, Environnement, Aménagement et Lutte (RISEAL-Niger), 333, Avenue des Zarmakoye, Niamey B.P. 13724 Niger. ⁷Public Health Laboratory - Ivo de Carneri (PHL-IdC), Wawi, Chake Chake, Pemba, United Republic of Tanzania.

Received: 1 October 2015 Accepted: 1 October 2015

Published online: 09 October 2015

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 **Ho** = 0.596, **He** = 0.609, for Pemba **Ho** = 0.599, **He** = 0.638. The overall **Ho** = 0.597, **He** = 0.623

| Panel | Marker | Forward Primer 5'-3' | Reverse Primer 5'-3' | Dye | Size Range (bp) | Repeat | A | Niger | | Zanzibar | |
|---------|--------|------------------------|-----------------------------|-------|-----------------|--------|----|-------|------|----------|-------|
| | | | | | | | | Ho | He | Ho | He |
| Panel 1 | C102 | TGTCTCTGTAATGACCGAAT | TTAGATGAATAATAATGTTGAAACCAC | VIC | 184-199 | ATT | 6 | 0.42 | 0.37 | 0.02 | 0.02 |
| | Sh1 | GCATCCAATTCGTACAC | CCACATTAGGCCAACAAG | VIC | 245-284 | AAT | 13 | 0.76 | 0.72 | 0.84 | 0.80 |
| | Sh14 | GTCCTCCTCCCTCTTTG | CACATTGTCCTAGATATCG | NED | 184-240 | ACTC | 15 | 0.94 | 0.85 | 0.86 | 0.88 |
| | C131 | CTTGTCATTTGGGCATTGTG | CATGGTGAGGTTCAAACGTG | NED | 253-265 | AAT | 4 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Sh6 | GGTGGATTACGCAATAG | TTAATCAACCGGGTGTG | NED | 309-321 | AAT | 7 | 0.48 | 0.44 | 0.84 | 0.76 |
| | Sh9 | GGGATGTATGCAGACTTG | TTGTTTGGCTGCAGTAAC | 6-FAM | 197-227 | AAT | 11 | 0.46 | 0.76 | 0.46 | 0.86 |
| | Sh3 | GCTGAGCTTGAGATTG | CTTCTGTCCCATCGATAAC | 6-FAM | 270-366 | AAT | 30 | 0.76 | 0.86 | 0.94 | 0.86 |
| | C111 | CCCTTGCTTCAATGCGGTTA | GAACGTCTAACTGGCGATCA | PET | 201-225 | ATT | 9 | 0.74 | 0.67 | 0.76 | 0.68 |
| | Sh7 | TCCAAGCACCATTATCAAG | ACGGAACCTGTTGAAATG | PET | 293-311 | AAT | 7 | 0.46 | 0.62 | 0.42 | 0.48 |
| Panel 2 | Sh2 | TTAGTGTGTTTGGCTTCAAC | CCTCGAATGAAATCCTGAC | NED | 155-218 | AAT | 21 | 0.84 | 0.90 | 0.56 | 0.89 |
| | Sh5 | TGTGCACAAGAAAGATTAATG | ACGACAATGTTGCAAGTTC | NED | 263-314 | AAT | 16 | 0.78 | 0.81 | 0.36 | 0.48 |
| | Sh13 | GAGCAGCTATTTTCGTATCG | ACCGTGGACAGTTCATCAG | 6-FAM | 163-211 | AAT | 17 | 0.78 | 0.72 | 0.68 | 0.64 |
| | Sh4 | CCCATCGCTGATATTAAG | TCTAGTCGCTTGGGATCC | 6-FAM | 268-313 | AAT | 13 | 0.84 | 0.78 | 0.72 | 0.79 |
| | Sh10 | CGCATGCATACCTATCTCC | GCTTATCAGGCCTATCTCC | PET | 183-207 | AAT | 9 | 0.18 | 0.34 | 0.74 | 0.70 |
| | Sh12 | CGTCTTAGTGAGCCAGATG | CTCGTGGACATCATCAG | PET | 245-278 | AAC | 11 | 0.06 | 0.06 | 0.56 | 0.65 |
| | Sh8 | CTAAACTGGCAAGATTTTC | CAACGTGCCTTTATTTTC | PET | 282-321 | AAT | 14 | 0.76 | 0.81 | 0.84 | 0.83 |
| | Sh11 | TTGGTTTAGAAATTACATCACC | CCAACAATATTAATGGACAGC | VIC | 183-213 | ATC | 9 | 0.68 | 0.58 | 0.68 | 0.69 |
| | Sh15 | CTTTCAGTAGGATTTGTTG | CGACGTCAAGCACTGTAC | VIC | 274-301 | ATC | 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). **Ho** = observed heterozygosity, **He** = expected heterozygosity