

**ERRATUM**

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# 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 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.

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**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