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# Author Correction: Population genomics of virulence genes of *Plasmodium falciparum* in clinical isolates from Uganda

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This Article contains errors.

The primers and conditions reported for the PCR amplification of the *var* gene DBLα domains are incorrect. PCR products of ~ 477 bp were generated in this study using the method previously described in Rask et al., 2016[57] with modifications.

In the Methods section, "*Var* DBLα PCR and sequencing"

"The *P. falciparum var* genes from genomic DNA were amplified using the DBLα domain as previously described with modifications[12,13.] From each isolate of genomic DNA, a ~550–700 bp region of the DBLα domain was amplified using a degenerate primer set (*F: 5′-CMTGYGCDCCRTWYMGAMG, R: 5′-TCKGCCCATTCYTCRAACCA*) designed against the semi-conserved blocks B and H of DBLα[8]. Each of the DBLα primers were designed by adding a GS FLX Titanium primer sequence 10 bp multiplex identifiers (MID) published by Roche[53]. These MID primers were used to 'barcode' and distinguish the DBLα sequences amplified from a unique isolate once all isolates were pooled and sequenced together[54]. The PCR conditions for the DBLα amplification were as follows: 2 µl of isolate genomic DNA, dNTPs at a final concentration of 0.07 mM, each primer (forward and reverse with same MID combination) at a final concentration of 0.375 µM, $MgCl_2$ at a final concentration of 2 mM, 1x reaction buffer, and 3 units GoTaq Flexi polymerase (Promega) in a 40 µL total reaction volume. PCR cycling was carried out on an Eppendorf thermal cycler and involved an initial denaturation step of 95 °C for 2 min, 30 cycles of 95 °C × 40 sec, 49 °C × 90 sec, and 65 °C × 90 sec, followed by a final extension step of 65 °C for 10 min. Finally the isolate amplicons were pooled and sequenced using next generation 454 sequencing (Roche) performed at NYU School of Medicine at the Center for Health Informatics and Bioinformatics and the Memorial Sloan-Kettering Cancer Center Genomics Core Laboratory. The 454 sequencing provides average read lengths of 400 bp, therefore lending itself to the assembly of the individual var DBLα amplicons of 550–700 bp lengths using the forward and reverse sequence reads from each direction."

should read:

"From the genomic DNA we performed PCR amplification of the DBLα domain of the *var* genes using fusion primers for multiplexed 454 Titanium amplicon sequencing as previously described with modifications[57]. We coupled template-specific degenerated primer sequences targeting homology block 2 and 3 (*DBLαAF, 5′-GCACGMAGTTTYGC-3′ and DBLαBR, 5′-GCCCATTCSTCGAACCA-3′*)[11,46]. Each of the DBLα primers were designed by adding a GS FLX Titanium primer sequence 10 bp multiplex identifiers (MID) published by Roche[53]. These MID primers were used to 'barcode' and distinguish the DBLα sequences amplified from a unique isolate once all isolates were pooled and sequenced together[54].The PCR conditions for the DBLα amplification were as follows: 2 µl of isolate genomic DNA, dNTPs at a final concentration of 0.07 mM, each primer (forward and reverse with same MID combination) at a final concentration of 0.375 µM, MgCl2 at a final concentration of 2 mM, reaction buffer at a final concentration of 0.5x, and 3 units GoTaq Flexi polymerase (Promega) in a 40 µL total reaction volume. PCR cycling was carried out on an Eppendorf thermal cycler and involved an initial denaturation step of 95 °C for 2 min, 30 cycles of 95 °C × 40 sec, 49 °C × 90 sec, and 65 °C × 90 sec, followed by a final extension step of 65 °C for 10 min. Finally, the isolate amplicons of ~477 bp were pooled and sequenced

using next generation 454 sequencing (Roche) performed at NYU School of Medicine at the Center for Health Informatics and Bioinformatics and the Memorial Sloan-Kettering Cancer Center Genomics Core Laboratory."

References

8. Smith, J. D., Subramanian, G., Gamain, B., Baruch, D. I. & Miller, L. H. Classification of adhesive domains in the *Plasmodium falciparum* Erythrocyte Membrane Protein 1 family. *Mol. Biochem. Parasitol.* **110**, 293–310 (2000).

11. Rask, T. S., Hansen, D. A., Theander, T. G., Pedersen, A. G. & Lavstsen, T. *Plasmodium falciparum* erythrocyte membrane protein 1 diversity in seven genomes—divide and conquer. *PLoS Comput. Biol.* **6** (2010).

12. Barry, A. E. et al. Population genomics of the immune evasion (var) genes of *Plasmodium falciparum*. *PLoS Pathog.* **3**, e34 (2007).

13. Chen, D. S. et al. A molecular epidemiological study of var gene diversity to characterize the reservoir of *Plasmodium falciparum* in humans in Africa. *PLoS ONE* **6**, e16629 (2011).

46. Bull, P. C. et al. *Plasmodium falciparum* variant surface antigen expression patterns during malaria. *PLoS Pathog.* **1**, 0202–0213 (2005).

53. Roche. Using multiplex identifier (MID) adaptors for the GS FLX titanium chemistry–extended MID set. Tech Bull Genome Seq FLX Syst TCB No 005–2009 (2009).

54. Hamady, M., Walker, J. J., Harris, J. K., Gold, N. J. & Knight, R. Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. *Nat. Methods* **5**, 235–237 (2008).

57. Rask, T. S., Petersen, B., Chen, D. S., Day, K. P. & Pedersen, A. G. Using expected sequence features to improve basecalling accuracy of amplicon pyrosequencing data. *BMC Bioinform.* **17**, 176 (2016).