Erratum

Erratum to “Use of *Metarhizium anisopliae* Chitinase Genes for Genotyping and Virulence Characterization”

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Errors occurred during the uploading of the reviewed article and the authors would like to add some additional information. The following changes are to be considered to improve the quality of the paper.

**Main Text.** Page 4, Section 3.4 should be changed to “Comparison of the chi2 nucleotide sequences from all selected *M. anisopliae* (GenBank Accession (GBA): KF445078-85) isolates originating from three different parts of Africa showed no differences in the open reading frames composed of 229 amino acid residues. However, when compared with the similar chitinase sequences retrieved from NCBI database, there were differences in amino acid composition (Figure 2).”

Page 4, Section 3.4 should be changed to “The phylogenetic analysis showed over 95% amino acid identity of chitinase chi2 sequence. *Metarhizium anisopliae* var. *acridum* strain CQMa 102 (GBA: EFY85519) and *M. robertsii* ARSEF 23 (GBA: EFY95562) were genetically different from other *M. anisopliae* including the icipe chi2 consensus and the other three outgroups M34412 (GBA: ACU30524), E6 (GBA: AAY34347), and ARSEF 7524 (GBA: ACU30523) (Figure 3).”

Page 4, Section 3.6. should be changed to “All *M. anisopliae* var. *anisopliae* ICIPE isolates had identical chi4 nucleotide sequences (JX898505-12). After the editing process to remove the ambiguous base calls a BLAST analysis using chi4 sequence on NCBI GenBank database revealed the highest amino acid identities to *M. anisopliae* var. *anisopliae*M34412 (GBA: ACU30522) and ARSEF7524 (GBA: ACU30521) (Figure 5).”

**Figure and Legands.** The legends of Figures 2–5 were changed as shown below.
Figure 2: The multiple sequence alignment (MAFFT; geneious 6.1.6 software) showing the relationship between the ICIPE *Metarhizium anisopliae* isolates’ Chitinase 2 sequences and similar sequences obtained from NCBI. The highlighted residues in red (VI and YR) show the conserved residues of CID.
Figure 3: A dendrogram showing the relationships between the $\chi_2$ gene of *icipe* isolates and the related sequences of the outgroup isolates.

Figure 4: Chitinase2 ($\chi_2$) model as predicted using the Swiss-Pdb Viewer. The residues highlighted (Val238 and Ile239; Tyr325 and Arg326) represent conserved residues in the Carbohydrate Insertion Domain (CID) of chitinases.

Figure 5: The multiple sequence alignment (MAFFT; Geneious 6.1.6 software) showing the relationship between the ICIPE *Metarhizium anisopliae* isolates’ Chitinase4 sequences and similar sequences obtained from NCBI as well as IMI330189 (GBA: JX898513).