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 Legends. The legends of Figures 2–5 were changed as shown below.

	1	10	20	30	40	50	60
ICIPE isolates							
ARSEF 7524	-----	-----	-----	-----	-----	GGGTIENNDLAAYCQP	
E6	-----	-----	-----	-----	NVYVWGQNGGGTIENNDLAAYCQP		
M34412	-----	-----	-----	-----	NVYVWGQNGGGTIENNDLAAYCQP		
CQMa 102	-----	-----	-----	-----	-----	GGGTIENNDLAAYCQP	
ARSEF 23	-----	-----	-----	-----	-----	GGGTIENNDLAAYCQP	
ICIPE isolates	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
ARSEF 7524	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
E6	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
M34412	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
CQMa 102	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
ARSEF 23	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC	ALTA	IHTC	QSAGVKIIL			
ICIPE isolates	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
ARSEF 7524	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
E6	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
M34412	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
CQMa 102	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
ARSEF 23	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPFGSSFVNGFDLDIEVNGGSSQ						
ICIPE isolates	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
ARSEF 7524	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
E6	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
M34412	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
CQMa 102	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
ARSEF 23	YYQYMIAKLRANFASDKSNTYLITGAPQCP	PEPNMG	VI	ISNA	VFDHLYVQFYNNNYT	YAV	
ICIPE isolates	PCALGINGNAPFNYNWTSF	IADTPSAGAK	VFIGVPASPLASTGTPSGAQY	YAAPEQLAA			
ARSEF 7524	PCALGINGNAPFNYNWTSF	IADTPSAGAK	VFIGVPASPLASTGTPSGAQY	YAAPEQLAA			
E6	PCALGINGNAPFNYNWTSF	IADTPSAGAK	VFIGVPASPLASTGTPSGAQY	YAAPEQLAA			
M34412	PCALGINGNAPFNYNWTSF	IADTPSAGAK	VFIGVPASPLASTGTPSGAQY	YAAPEQLAA			
CQMa 102	PCALGINGNAPFNYNWTSF	ISNTPSANAK	VFIGVPASPLASTGTPSGAQY	YATPDQLAA			
ARSEF 23	PCALGINGNAPFNYNWTSF	IADTPSAGAK	VFIGVPASPLASTGTPSGAQY	YAAPEQLAA			
ICIPE isolates	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILVSGAPCPSSGPPSPSTPATAP						
ARSEF 7524	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILVSGAPCPSSGPPSPSTPATAP						
E6	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILVSGAPCPSSGPPSPSTPATAP						
M34412	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILVSGAPCPSSGPPSPSTPATAP						
CQMa 102	IVGEYKSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILVSGAACGSSGPPPIPTPTTP						
ARSEF 23	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTSGPDRDHAIFDFGV-LSGSVAYRRHSSP						
ICIPE isolates	APTATTMPSSSTSVSSPAASPTGGTVPQWGQCGGEGY	-----					
ARSEF 7524	APTATTMPSLT--SSPAASPTGGTVPQWGQCGGEGYSGPTQCVPP	-----					
E6	APTATTMPSSSTSVSSPTASPTGGTVPQWGQCGGEGYSGPTQCVPPYQCVKQGDWSSCR	-----					
M34412	GPTATTMPSSSTSVSSPTASPTGGTVPQWGQCGGEGYSGPTQCVPP	-----					
CQMa 102	ATTTPTTASST--FSPTASPTGGTVPQWGQVSLTPKSRKCSWRKKKKKLAR	-----					
ARSEF 23	VGSHTVAMSS--AAARAIPVLPSALPLTNVSSKAIGGRHAGEVGHRAPTIYKTGFIVES						
ICIPE isolates	-----						
ARSEF 7524	-----						
E6	-----						
M34412	-----						
CQMa 102	-----						
ARSEF 23	GSIHFI						

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 *chi2* gene of *icipe* isolates and the related sequences of the outgroup isolates.

FIGURE 4: Chitinase2 (*chi2*) 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.

	1	10	20	30	40	50	60
ICipe strains	-----YNVISAAFPVILPDGTALWEDGMDANVKVATPADMC						
M34412	GAKNGVHPPLGWIPIDARIRQHGYNVISAAFPVILPDGTALWEDGMDANVKVATPAEMC						
ARSEF 7524	GAKNGVHPPLGWIPIDARIRQHGYNVISAAFPVILPDGTALWEDGMDANVKVATPAEMC						
IMI 330189	-----YNVISAAFPVILPDGTALWEDGMDVNVKVATPAEMC						
ICipe strains	QAKAAGATMIMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
M34412	QAKAAGATMIMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
ARSEF 7524	QAKAAGATMIMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
IMI 330189	QAKAAGATILMSIGGAAAIDLSSSTVADKFISTIVPILKRYNFDGVDIDIEAGLSGSGS						
ICipe strains	IGTLSASQANLVRIIDGILAQMPNSNFGTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
M34412	IGTLSASQANLVRIIDGILAQMPNSNFGTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
ARSEF 7524	FGTLSASQANLVRIIDGILAQMPNSNFGTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
IMI 330189	INTLSASQANLIRIIDGILAQMPNSNFGTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
ICipe strains	NGRLWWLNMQYYNGAMYGCLGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVPYDKQVPG						
M34412	NGRLWWLNMQYYNGAMYGCSGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVPYDKQVPG						
ARSEF 7524	NGRLWWLNMQYYNGAMYGCSGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVPYDKQVPG						
IMI 330189	NGRLWWLNMQYYNGAMYGCSGDSYEAGTVKGFIAQTDCLNKGGLVIQGTTRLPYSMQVPG						
ICipe strains	LPAQSGAGGGYMSPSLVGQAWDHYNGSLK-----						
M34412	LPAQSGAGGGYMSPSLVGQAWDHYNGSLKGLMTWSINWDGSK						
ARSEF 7524	LPAQSGAGGGYMSPSLVGQAWDHYNGSLKGLMTWSINWDGSK						
IMI 330189	LPAQPGAGGGYMSPSLVGQALDHYHGSGLK-----						

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).