

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. *acidum* 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
ICIFE isolates	-----GGGTIENNDLAAYCQP						
ARSEF 7524	-----NVVYWGQNGGGTIENNDLAAYCQP						
E6	MHHLRALVGVGLAGLAAGVPLTDKISVKPRQAPGAQN VVYWGQNGGGTIENNDLAAYCQP						
M34412	-----NVVYWGQNGGGTIENNDLAAYCQP						
CQMa 102	MHHLRALAGVGLVGLASGVPTDNISIKPRQAPGAQNI VYWGQNGGGTIENNDLAAYCQP						
ARSEF 23	MHHLRALVGVGLAGLAAGVPLTDKISVKPRQAPGAQN VVYWGQNGGGTIENNDLAAYCQP						
ICIFE isolates	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIIL						
ARSEF 7524	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIIL						
E6	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIVL						
M34412	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIIL						
CQMa 102	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIIL						
ARSEF 23	NSGIDVLVLAFLYQFGNGGNIPSGTIGQSCYISTSGQGQNC EALTAAIHTCQSAGVKIIL						
ICIFE isolates	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSSFVNGFDFDIEVNGGSSQ						
ARSEF 7524	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSSFVNGFDFDIEVNGGSSQ						
E6	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSNFVNGFDFDIEVNGGSSQ						
M34412	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSNFVNGFDFDIEVNGGSSQ						
CQMa 102	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSNFVNGFDFDIEVNGGSSQ						
ARSEF 23	SLGGATSSYSLQTQAQAEQIGQYLWDSYGNSGNKTVQRPF GSNFVNGFDFDIEVNGGSSQ						
ICIFE isolates	YYQYMIAKLRANFASDKSNTYELITGAPQCP IPEPNMGVI ISNAVFDHLYVQFYNNNNYTV						
ARSEF 7524	YYQYMIAKLRNSNFASDKSNTYELITGAPQCP IPEPNMGVI ISNAVFDHLYVQFYNNNNYTV						
E6	YYQYMIAKLRANFASDKSNTYELITGAPQCP IPEPNMGVI ISNSVFDHLYVQFYNNNNYTV						
M34412	YYQYMIAKLRANFASDKSNTYELITGAPQCP IPEPNMGVI ISNSVFDHLYVQFYNNNNYTV						
CQMa 102	YYQYMIAKLRNSNFGSDEANTYYITGAPQCP IPEPNMGVI ISNSVFDHLYVQFYNNNNYTV						
ARSEF 23	YYQYMIAKLRNSNFASDKSNTYELITGAPQCP IPEPNMGVI ISNSVFDHLYVQFYNNNNYTV						
ICIFE isolates	PCALGINGNAPFNYNWTSFIADTPSAGAKVFIGVPASPLAST GTPSGAQYYAAPEQLAA						
ARSEF 7524	PCALGINGNAPFNYNWTSFIADTPSAGAKVFIGVPASPLAST GTPSGAQYYAAPEELAA						
E6	PCALGINGNAPFNYNWTSFIADTPSAGAKVFIGVPASPLAST GTPSGAQYYAAPEQLAA						
M34412	PCALGINGNAPFNYNWTSFIADTPSAGAKVFIGVPASPLAST GTPSGAQYYAAPEQLAA						
CQMa 102	PCALGINGNAPFNYNWTSFISNTPSANAKVFIGVPASPLAST GTPSGAQYYATPDQLAA						
ARSEF 23	PCALGINGNAPFNYNWTSFIADTPSAGAKVFIGVPASPLAST GTPSGAQYYAAPDQLAA						
ICIFE isolates	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILV S G A P C P S S G P P S S T P A T A P						
ARSEF 7524	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILV S G A P C A S S G P P S S T P A T A P						
E6	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILV N G A P C P S S G P P S S T P A T A P						
M34412	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTYAQQAKSILV N G A P C P S S G P P S S T P A T P P						
CQMa 102	IVGEYKGD AHFGGIMMWSAGFSDANVNDGCTYAQQAKN I L V N G A A C G S S G P P I P T P T T P						
ARSEF 23	IVGEYRSDAHFGGIMMWSAGFSDANVNDGCTSGPDRDHD A I F D F G V - L S G S V A Y R R H S S P						
ICIFE isolates	APTATTMPSSSTSVSSPAASPTGGTVPQWGQCGGEGY-----						
ARSEF 7524	APTATTMPSLT--SSPAASPTGGTVPQWGQCGGEGYSGPTQ CVPP-----						
E6	APTATTMPSSSTSVSSPTASPTGGTVPQWGQCGGEGYSGPT QCVPPYQCVKQGDWSSCR-						
M34412	GPTATTMPSSSTSVSSPTASPTGGTVPQWGQCGGEGYSGPT QCVPP-----						
CQMa 102	ATTTPTTASST--FSPTASPTGGTVPQWGQVSLTPKSR L C S W R K K K K L A R -----						
ARSEF 23	VGSAHTVAMSS--AAARAIPVLPALPLTNVSSKAIGGRHAGE VGHRAPTIYKTGFIVES						
ICIFE isolates	-----						
ARSEF 7524	-----						
E6	-----						
M34412	-----						
CQMa 102	-----						
ARSEF 23	GSIHFIFA						

FIGURE 2: The multiple sequence alignment (MAFFT; geneious 6.1.6 software) showing the relationship between the ICIFE *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.

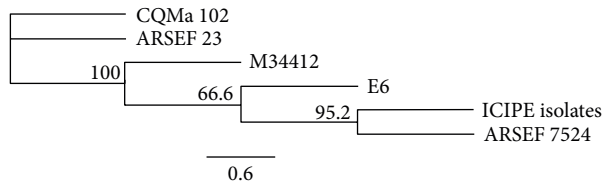


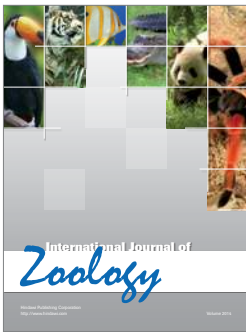
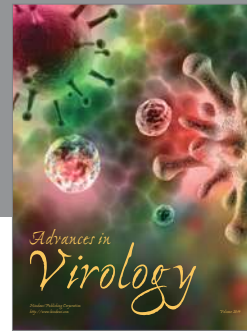
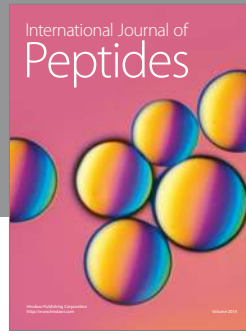
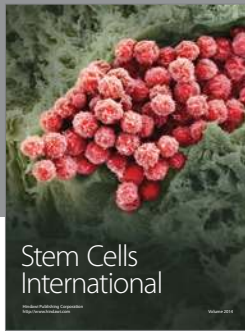
FIGURE 3: A dendrogram showing the relationships between the *chi2* gene of *icipe* isolates and the related sequences of the outgroup isolates.



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	GAKNGVHPLGWIPIDARIRQHGYNVISAAFPVILPDGTALWEDGMDANVKVATPAEMC						
ARSEF 7524	GAKNGVHPLGWIPIDARIRQHGYNVISAAFPVILPDGTALWEDGMDANVKVATPAEMC						
IMI 330189	-----YNVISAAFPVILPDGTALWEDGMDVNVKVATPAEMC						
ICipe strains	QAKAAGATMIMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
M34412	QAKAAGATMIMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
ARSEF 7524	QAKAAGATMVMSIGGAAAIDLSSSSVADKVFSTIVPILKRYNFDGVDIDIEAGLSGSGT						
IMI 330189	QAKAAGATILMSIGGAAAIDLSSSTVADKFI STIVPILKRYNFDGVDIDIEAGLSGSGS						
ICipe strains	IGTLSASQANLVRIIDGILAQMPNSFGLTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
M34412	IGTLSASQANLVRIIDGILAQMPNSFGLTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
ARSEF 7524	FGTLSASQANLVRIIDGILAQMPNSFGLTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
IMI 330189	INTLSASQANLIRIIDGILAQMPNSFGLTMAPETAYVTGGSVTYGSIWGAYLPIIKKYAD						
ICipe strains	NGRLWNLNMQYYNGAMYGCSGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVVPYDKQVPG						
M34412	NGRLWNLNMQYYNGAMYGCSGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVVPYDKQVPG						
ARSEF 7524	NGRLWNLNMQYYNGAMYGCSGDSYEAGTVKGFVAQTDCLDKGLVIQGTTRVVPYDKQVPG						
IMI 330189	NGRLWNLNMQYYNGAMYGCSGDSYEAGTVKGFIAQTDCLNKGLVIQGTTRVLPYSMQVPG						
ICipe strains	LPAQSGAGGGYMSPSLVGQAWDHYNGSLK-----						
M34412	LPAQSGAGGGYMSPSLVGQAWDHYNGSLKGLMTWSINWDGSK						
ARSEF 7524	LPAQSGAGGGYMSPSLVGQAWDHYNGSLKGLMTWSINWDGSK						
IMI 330189	LPAQPGAGGGYMSPSLVGQALDHYHNSLK-----						

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).



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