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ERRATUM

Erratum to: Purification and characterization of a nitrilase from *Aspergillus niger* K10

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The previous article reported on the biochemical characterization of a nitrilase purified from Aspergillus niger K10. The amino acid sequence of this enzyme was recently analyzed by mass spectroscopy which revealed that the N-terminal sequence reported in Fig. 3A (by KB) in the previous article was incorrect. This N-terminal sequence (XAPVLKKYKAAXVNXE), which was highly homologous to those of a number of hypothetical proteins in genus Aspergillus (Aspergillus fumigatus Af29, Aspergillus oryzae, Aspergillus nidulans FGSC A4) did not belong to the enzyme purified and characterized in the previous article. Mass spectrum analyses of this enzyme were recently performed as follows. Briefly, the peptides were extracted after in gel digestion of the enzyme with trypsin and analyzed by MALDI-ToF MS using Bruker Biflex IV (Bruker Daltonics, Germany). Alternatively, the peptides were analyzed by using UHPLC Dionex Ultimate3000 RSLC nano (Dionex, Germany) equipped with a ESI-Q-ToF Maxis Impact (Bruker Daltonics, Germany) mass spectrometer. Spectra were interpreted using Mascot software (Matrix Science, UK). These analyses (Fig. S1) suggested a 42.5-58.1 % sequence coverage of the enzyme with a putative nitrilase from Aspergillus kawachii IFO 4308 (gi|358373570) having N-terminal sequence MSHDGPKTIRVAAVQA (Fig. 1).

The N-terminal amino acid sequence reported in the previous article belonged to another enzyme encoded in the same strain (gb|ABX75546). This enzyme was later expressed in E. coli, purified and characterized, and its substrate specificity was found to be different from that of the nitrilase purified in A. niger K10 (Kaplan et al. 2011). This was hypothesized to be caused by a misfolding or by a posttranslational modification (Kaplan et al. 2011) but this hypothesis has been corrected according to the new MS analyses (Kaplan et al., Corrigendum to: Heterologous expression, purification and characterization of nitrilase from Aspergillus niger K10 (BMC Biotechnol (2011) 11:2). BMC Biotechnol, submitted manuscript). The aforementioned enzyme from A. nidulans FGSC A4 was later characterized as a cyanide hydratase (Basile et al. 2008). In

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  1 MSHDGPKTIR VAAVQAEPEW NNLQKGVEKT IRLIIEAGKN GANVMGFPEV
 51 WIPGYPWSIW NQSVVDNVEF MDEYFRNSLE RDSEEMNRIR CAVKEAGIFC
101 VLGYSERYQG SLYISQSFID ENGDIVHHRR KIKPTHVERG FWGEGQADSL
151 KSVVKSSFGN IGGLNCWEHT QTLLRYYEYA QNVDIHIASW PLIFGACAEM
201 QYHISSEMCG KLTQVMSMEG ACFTLICSQV MSAENCERNK VDKWSFVKAP
251 GGGFSMIYGP AGEPLVEAPD AGEEVILYAD VKLAEKWRAK QNLDVVGHYS
301 RPDLLSLKVT NNAASQVHFA
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Fig. 1 Amino acid sequence of a hypothetical nitrilase from Aspergillus kawachii IFO 4308 (gi|358373570). The peptides identified in the purified nitrilase from Aspergillus niger K10 are marked in bold

accordance with this finding, the same activity was found in the protein gb|ABX75546 expressed in E. coli. A detailed investigation of this activity is in progress.

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