Erratum

Short communication

Erratum to: Isolation and sequencing of a new glucoamylase gene from an *Aspergillus niger* aggregate strain (DSM 823) molecularly classified as *Aspergillus tubingensis*

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Published in *Antonie van Leeuwenhoek*, Volume 88, Nos. 3-4, pp. 267–275, 2005,
DOI 10.1007/s10482-005-3989-5.

Due to an unfortunate turn of events the sentences indicated below in the second column on page 272 were typeset erroneous. The correct version displayed below in the right hand column should however be treated as definitive by the reader.

The predicted molecular mass is 68.013 kDa, a value comparable with other *Aspergillus* glucoamylases, e.g., from *A. shirousami* with 68.126 kDa (Acc. no. D10460) and *A. kawachii* with 68.267 kDa (Acc. no. D00427), which are taxa belonging to the *A. niger* aggregate (Raper and Fennell 1965), and *A. niger* glucoamylase G1 with 65.424 kDa (Acc. no. X00712). The amino acid sequence offers 8 asparagine linked glycosylation sites allowing an increase of the protein molecular mass by about 9 kDa to approximately 77 kDa (Ftouhi-Paquin et al. 1997). A similar increase in molecular weight is known from glucoamylase G1 from *A. niger*, which amounts after glycosylation to 82 kDa (Svensson et al. 1983). Comparing sequence similarities among glucoamylases from several *Aspergilli*, that from *A. tubingensis* did show 92% similarity to *A. niger* G1 glucoamylase at the nucleotide level 99% and 94% at the amino acid levels. Its similarity with glucoamylases from *A. shirousami* and *A. kawachii* was at the nucleotide level. Converting these results into a phylogram (Figure 2) the data demonstrate that *A. tubingensis* glucoamylase belongs to the monophyletic group of *A. kawachii*, *A. shirousami* and *A. awamori* glucoamylases, which is distinctly different from the *A. niger* glucoamylase.

Within the five conserved regions identified in fungal glucoamylases, several amino acids were

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