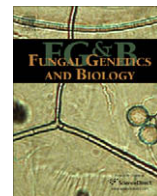




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Introduction

Preface

The idea to publish a special issue on “*Aspergillus* Genomics and Beyond” was born in the summer of 2006. It arose during one of the day-long sessions between Herman Pel, Hein Stam and myself at a quiet conference centre in the city of Amersfoort. The three of us were writing the final version of the Nature Biotechnology paper about the sequencing and analysis of the enzyme-producing *Aspergillus niger* CBS 513.88 strain (Nature Biotech. 25, 221–231, 2007), presently known as the “DSM sequence”. The final result, 10 pages of text and a long list of Supplementary material, was based on an extensive analysis of the *A. niger* genome sequence carried out by a consortium of about 30 expert groups. We felt that the huge amount of data generated deserved more detailed exposure to avoid it being hidden or lost. This seemed particularly timely as the DOE Joint Genome Institute had just made the sequence available of a second *A. niger* strain, the citric acid-producing strain ATCC 1015 (<http://www.jgi.doe.gov/aspergillus>).

In September 2006, another major community annotation initiative was launched through Eurofungbase, a coordination action programme funded by the European Commission. Steve Oliver, Dave Ussery, Cees van den Hondel and myself met in Leiden with Jennifer Wortman to organize an Annotation Jamboree with the purpose of re-annotating the *Aspergillus nidulans* genome. Besides mobilizing the *Aspergillus* community this also required a careful preparation of the infrastructure to enable the expert annotation effort of the community to be effective. The close collaboration between TIGR/ JCVI (Jennifer Wortman, Vinita Joardar) and Manchester University (Jane Mabey Gilsenan, Mike Cornell) and some further input of Jennifer Deegan (EBI) supported by the infrastructure of the CBS at DTU made the Copenhagen Jamboree later that year a stimulating and successful event.

At that stage I revived the idea of a special issue with a broader scope. Both DSM and Eurofung supported that concept and, with representatives of the *A. niger* and *A. nidulans* consortia, the editor in chief of Fungal Genetics and Biology, Neil Gow was approached.

He liked the idea which led to the outcome that I could make an arrangement with Elsevier and a team of guest editors was proposed. It was decided to focus on *A. nidulans*, *A. niger* and comparative genomic aspects by including other aspergilli which were sequenced. Quite some time has elapsed between that moment

and the appearance of this volume and that is largely due to the transfer for various reasons of data from one database to another. All this has become irrelevant now and hopefully this volume will turn out to be a useful resource not just for the *Aspergillus* community but for the entire fungal community as well.

This is also the place to acknowledge those who have been important in realizing this special issue. In the first place the support of Hein Stam and Herman Pel, both from DSM, and of Cees van den Hondel (Eurofungbase) has to be mentioned. The re-annotation of the *A. nidulans* genome has really been a community effort but could only succeed due to the inspiring guidance of the three J's at the Copenhagen Annotation Jamboree and the dedicated effort by the team leaders covering the various topics in their reports. The finishing touch turned out to be hard work done by the writing team consisting of Jennifer Wortman, John Clutterbuck, Steve Oliver and Geoff Turner in particular.

The productive and pleasant collaboration with Jim Kronstad, the review editor of FGB, and with the Elsevier staff certainly needs to be mentioned here as well. The collaboration with JCVI was essential to improve the *A. nidulans* annotation for which we are grateful.

Last but not least the financial support of the European Commission (LSSG-CT–2005–018964) and of DSM, Delft, The Netherlands, which enabled publication of this issue, is highly appreciated.

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