2 – 4 June 2010
Braga, PORTUGAL
BOOK OF ABSTRACTS

16.15 - 16.45	Coffee break
16.45 – 17.45	**S3. Plant barcoding session / Chair Peter Hollingsworth**
16.45 - 17.15	S3O1. Peter Hollingsworth - Choosing and using a plant barcode.
17.15 - 17.30	S3O2. Sofia Caetano - Do plants' life cycles influence assignment success in DNA barcoding? An answer based on seven genera of trees, shrubs and herbs.
17.30 - 17.45	HS3O3. Harald Meimberg - Multiple origins as potencial error source for barcoding in polyploids. Patterns of chloroplast haplotypes shared between polyploid and diploid representatives of the genus *Aegilops* (Poaceae).

Thursday, 3 June

9.00 – 10.30	**S4. Fungi barcoding session / Chair Ursula Eberhardt**
9.00 - 9.15	S4O1. Johannes Groenewald - Barcoding fungi of quarantine importance to Europe – WP2 of QBOL.
9.15 - 9.30	S4O2. Pedro Crous - DNA barcoding the genus Calonectria.
9.30 – 9.45	S4O3. Seena Sahadevan - DNA barcoding of fungi: a case study using ITS sequences for identifying aquatic hyphomycete species.
9.45 - 10.00	S4O4. Jozsef Geml - The use of DNA-barcodes in biodiversity assessments of ectomycorrhizal fungi in arctic and boreal ecosystems.
10.00 – 10.15	S4O5. Nelson Lima – Portuguese isolates of *Aspergillus* section *flavi* unravelled by the calmodulin gene
10.30 - 11.00	Coffee Break
11.00 - 12.30	**S5. Protist barcoding / Chair Jan Pawlowski**
11.00 - 11.15	S5O1. Mónica Moniz - Barcoding Diatoms with ITS – evaluation and case study.
11.15 - 11.30	S5O2. El Mahdi Bendif - A morphogenetic assessment of micro-evolution in extant *Noelaerhabdacean coccolithophorids*.
11.30 - 11.45	S5O3. Edward Mitchell - COI phylogenies reveal unsuspected, pseudo-cyptic diversity in testate amoebae (Rhizaria: Euglyphida & Amoebozoa: Arcellinida).
11.45 - 12.00	S5O4. Jan Rueness - DNA barcoding of selected freshwater and marine red algae (Rhodophyta).
12.00 - 12.15	S5O5. Jonas Zimmermann - Diatom barcoding: Water monitoring using molecular tools.
12.30 - 14.00	Lunch
14.00 - 16.00	**S6. Data management and analyses session / Chair Mehrdad Hajibabaei**
14.00 - 14.15	S6O1. Robert Vaughan - Services for the BARCODE community at the European Nucleotide Archive.
14.15 - 14.30	S6O2. Vincent Robert - QBOL and ECBOL data management and analyses system.
14.30 - 14.45	S6O3. Karl Larsson - The UNITE database for molecular identification of fungi.
14.45 - 15.15	S6O4. Discussion Panel with session speakers open to audience. Methods for data analyses and management for DNA barcoding data.
15.30 - 17.00	Poster sessions with coffee break
17.15 - 20.00	**Visit to the city of Guimarães - bus leaves at 17.30h.**
20.00	**Dinner at the HOTEL DE GUIMARÃES**

S4O5.

Portuguese isolates of *Aspergillus* section *Flavi* unraveled by the calmodulin gene

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Aspergillus is a large genus, with a complex and ever evolving taxonomy. Section *Flavi* is one of the most significant sections in the genus. Taxonomy and species identification is subject of great interest for scientists aiming to clarify the species concept and limits within the section. Furthermore, this section comprises both toxigenic and non-toxigenic species/strains, with great interest to biotechnology and food industry. Various genes, namely the rRNA (ITS region), calmodulin and ß-tubulin genes, have been widely reported as good markers for *Aspergillus* species identification, because they are rapid and cost-effective. In the present study, we evaluated the discriminatory power of the ITS region and the calmodulin gene to distinguish closely related taxa within *Aspergillus* section *Flavi*. For this purpose, 26 isolates of *Aspergillus* section *Flavi* obtained from Portuguese almonds were characterized at various levels: i) phenotypic, regarding various aspects of morphology and physiology; ii) spectral, using MALDI-TOF ICMS to obtain protein fingerprinting; and iii) genotypic, by sequence analysis of a 730 bp segment of the calmodulin gene and a 908 bp segment of the ITS region. For the various methods, dendrograms were created and results were compared. Both genotypic and spectral analyses divided the isolates in 3 groups corresponding to closely related taxa of *A. flavus*, *A. parasiticus* and *A. tamarii*. Except for the ITS region, all sets of analysis positioned 5 of the 26 isolates in two unidentified clades close to *A. parasiticus,* and divided the *A. flavus* group in two distinct clades. The phylogenetic analysis of the calmodulin sequences resulted in very similar dendrograms when using various methods of analysis (Neighbor-Joining, Maximum Likelihood, Bayesian Inference), and altering the analytical parameters did not result in significant changes. Furthermore, the genetic dendrograms were strongly supported by the phenotypic and spectral analyses. These results confirm the calmodulin gene as a robust and reliable genomic marker for this group of fungi. The unsolved isolate identifications are currently under further analysis.