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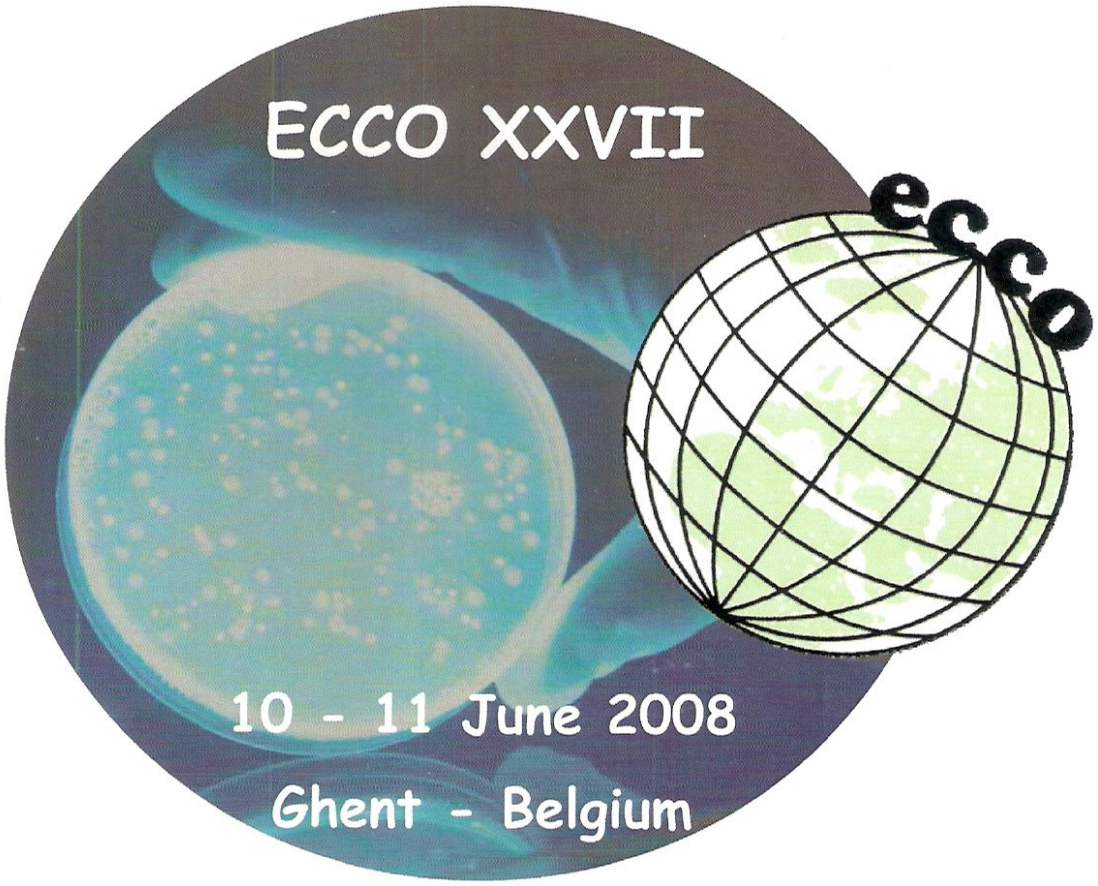

HARMONISATION & VALIDATION OF METHODS

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INTEGRATION OF MALDI-TOF MS DATA IN THE QUALITY CONTROL OF MICROBIAL CULTURE COLLECTIONS

C. Santos[1], R. R. M. Paterson[2,3], A. Venâncio[2] and N. Lima[2,4]

[1]Fundamental Chemistry Department, Federal University of Pernambuco, Recife-PE, Brazil
cledirs@hotmail.com
[2]Micoteca da Universidade do Minho, IBB-Institute for Biotechnology and Bioengineering, Biological Engineering Centre, University of Minho, 4710-057 Braga, Portugal
[3]IOI Professorial Chair, Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor Darul Ehsan, Malaysia
[4]Biochemistry Department, Federal University of Pernambuco, Recife-PE, Brazil

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The ultimate goal for microbial culture collections (CC) quality control (QC) systems is that they maintain and extend knowledge about the biological resources and processes. This will enable CC to pass this knowledge on to their customers and as a result, improve the guidance and good services that they provide. On one hand, great emphasis is placed on this and with it CC demonstrate to users of their strains that they are delivering the quality that they promise. On the other hand, the users benefit from conformity of quality and authenticity of biological material, and access to the related processes and procedures. These key elements underpin the changes to the paradigm which the traditional CC have undergone in relation to the new one of certificated/accredited biological resources centres (BRCs). OECD best practices guidelines for BRCs emphasise the importance of QC for the biological material. Each strain that arrives at a CC undergoes a battery of morphological, physiological and molecular tests for characterisation. These characteristics are comparing with the description of the species in order to determine the identity of the strains as an authentication process. The two approaches form the basis for the operation of the BRCs when linked to the conformity criteria and documentation specifying the quality management system. To perform a reliable strain authentication CC normally follow the polyphasic approach. This means that they combine the more traditional phenotypic and physiological approaches with modern techniques (*e.g.* molecular biology). Recently, microbial mass spectral analysis has been incorporated. Matrix Assisted Laser Desorption Ionization Time of Flight (MALDI-TOF) mass spectroscopy microbial analysis uses a nitrogen laser to irradiated fresh bacterial cells or freeze dried fungal mycelia mixed with a matrix (an aromatic compound such as 2,5-dihydroxy benzoic acid acidified with trifluoroacetic acid) that gentle ionizes the cellular proteic components. The spectrum of protein masses in a range of 2000 to 20000 Da are used as *taxon* specific fingerprints, after archiving in a database. The advantages of this novel approach as a microbial authentication method are the (a) simple sample preparation procedure, (b) short time for analysis and (c) reliability of the data. This technique has the potential to be used as part of a QC process in CC. The present work will report attempts to implement this technique in our CC and integrate these data into QC systems.

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