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S2-3 Next-generation of omics for microbial identification and characterisation: what is needed?

Nelson Lima and Cleidir Santos

Micoteca da Universidade do Minho, Centre of Biological Engineering, Braga, Portugal

Post-Graduate Programme in Agricultural Microbiology, Federal University of Lavras, Lavras, MG, Brazil

The rapid development in technologies (e.g., DNA sequencing and mass spectrometry) allows very high-definition and quantity of data concerning DNA sequences, and transcriptome, proteome and metabolome profiles. These will, undoubtedly, significantly increase our knowledge about microorganisms. All these data only will have utility if endowed with bioinformatics tools to improve structural and functional annotation mechanisms to correctly assign the data. For microbial identification and characterisation, the next-generation of omics, with integrated data systems, will give an unprecedented opportunity to go beyond the current boundaries of (a) species identification, (b) the strain level with specific profiles, such as multiple-drug resistance, different expressions to environmental stimuli (epigenetics), (c) complex multi-operon pathways and, (d) genome level modifications. Besides these achievements, the concept of some microbial species remains ambiguous and the delineation of new species, such as in some filamentous fungi, can be controversial. Our workable fungal species definition incorporates the phylogenetic species concepts of population, lineage, and phenotype, assuming that the genotype of the

species is only an indirect indication of phenotype and ecological adaptation. Taking this into consideration, the current authors use the polyphasic approach for identification and characterisation of filamentous fungal strains (Simões et al., 2013). Integrated and sound information about each fungus (e.g., morphological and molecular descriptions, including modern spectral data from MALDI-TOF mass spectrometry, physiological and biochemical features, ecological roles, and societal risks or benefits) are the key elements in fungal identifications. To enrich our knowledge of microbial diversity, and to solve the problems encountered in fungal identification and characterisation, the next-generation of omic technologies will be presented and discussed.

Reference

Simões, M.F., Pereira, L., Santos, C. and Lima, N. 2013. Polyphasic identification and preservation of fungal diversity: Concepts and applications. In: Management of Microbial Resources in the Environment (Malik, A., Grohmann, E. & Alves, M., Eds), Chap. 5, pp. 91-117. Springer, Dordrecht. ISBN 978-94-007-5930-5.