

Molecular signatures to define members of the actinobacterial family Streptosporangiaceae

**Dr P. Meyers, University of Cape Town
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Higher order taxonomic assignments (family level and above) in the phylum Actinobacteria are currently based only on 16S-rRNA gene phylogenetic analysis and 16S-rRNA gene signature nucleotides. There is a need for additional molecular markers to be identified to increase the number of reference points that can be used to define actinobacterial families and other higher taxa. Furthermore, since most novel actinobacterial taxa are defined at the level of species and genera, it is necessary to define molecular signatures at the genus level to enhance the robustness of genus descriptions. The current use of chemotaxonomic markers to define genera could be improved by the identification of genus-specific amino acid insertions and deletions and/or signature sequences. The actinobacterial suborder Streptosporangineae (order Actinomycetales) contains the families Nocardioseae, Streptosporangiaceae and Thermomonosporaceae. The family Streptosporangiaceae contains 13 genera, the largest of which are Nonomurea and Streptosporangium. Our preliminary work in the family Streptosporangiaceae based on the gyrase B subunit gene (*gyrB*) has shown that there are genusdefining insertions for the genera *Herbidospira* and *Microbispora*. Furthermore, there are *GyrB* amino acid signatures which distinguish the family Streptosporangiaceae from the family Nocardioseae. We propose expanding this analysis of the family Streptosporangiaceae to the *recA*, *rpoB* and *relA* genes to establish the first set of molecular signatures for all the genera within an actinobacterial family. This will improve the taxonomy of the family Streptosporangiaceae and increase the robustness of genus definitions. Furthermore, these data will also help those wishing to conduct biodiversity and/or bioprospecting surveys of members of the family Streptosporangiaceae. The long-term aim is to extend the molecular-signature analyses to other actinobacterial families.