

Bacterial collections are important resources of microorganisms, however, the potential that genomics has to offer remains to be realised as it is still virtually absent in any study involving strain collections. This feature thus framed the experimental objectives for this study, whose aim was to define the most comprehensive way to apply genomic based methods (sequencing and bioinformatics) to a strain collection in order to solve the critical problem of microbial identification and classification. The study selected the Coryneform group of organisms, as it constituted a heterogeneous bacterial population, posing a unique technical challenge, containing bacteria which are normally difficult to classify using traditional approaches. Initially a preliminary analysis was performed on the Corynebacterium genus. A total of 207 bacteria was studied. Strategies used included 16S rRNA sequencing of all isolates together with multilocus sequence typing for strains of the same species. The 16S rRNA gene sequencing strategies developed were applied to surface cheese samples in an attempt to identify any coryneform bacteria present.

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