

Characterisation of Bifidobacterium species—a review

ABSTRACT

Identification of Bifidobacterium species are a difficult task because of phenotypic and genetic heterogeneities. Various DNA-based techniques to rapidly characterise Bifidobacterium species and to support the conventional biochemical and morphological classification methods have been described. Sequencing of the 16S rRNA gene and 16S to 23S internally transcribed spacer region and comparing with the sequences data present in GenBank are the most popular techniques in identifying Bifidobacterium species. Conserved sequences other than the 16S rRNA gene such as *ldh*, *recA* and *hsp60* genes have become worthy tools for the elucidation of various taxonomic features such as genera, species and strains of Bifidobacterium. However, as an alternative to sequencing which is both time consuming and technically demanding, genus- or species-specific primers or probes were successfully designed to rapidly identify Bifidobacterium species. In this review, amplified ribosomal DNA restriction analysis (ARDRA) method derived from the 16S rRNA gene is also discussed because of its rapid, reproducible and easy to handle characteristics. Furthermore, randomly amplified polymorphic DNA (RAPD), Pulsed-Field Gel Electrophoresis (PFGE) and repetitive elements fingerprinting (Rep) were the popular methods to study the genetic diversity among Bifidobacterium species due to its versatility.

Keyword: Biochemical; F6PPK; 16S rRNA; RAPD; REP