Evaluation of the Diversity in Two Species of the Genus Propionibacterium: Mass Spectrometry Versus Triple-Locus Sequence Analysis for 40 Strains of Propionibacterium acnes and Propionibacterium freudenreichii.

Author(s) Valence-Bertel Florence[1], Bouvet Philippe[3], Jardin Julien[4], Dalmasso Marion[4], Nicolas Cabanel[2], Chantal Bizet[2], Clermont Dominique[2]

Institution(s) 1. CIRM-BIA, INRA, CIRM-BIA, French National Institut for Agricultural Research, UMR 1253 Science et Technologie du Lait et de l'Œuf, F-35042 Rennes, France 2. CRBIP, Pasteur Institut, Collection de l'Institut Pasteur, F-75724 Paris Cedex 15, France 3. CNR botulisme, Pasteur Institut, Institut Pasteur, F-75724 Paris Cedex 15, France 4. UMR 1253 STLO, INRA, UMR 1253 Science et Technologie du Lait et de l'Œuf, INRA, UMR 1253 Science et Technologie du Lait et de l'Œuf, F-35042 Rennes, Franc

Abstract:

A preliminary study was performed on two species of *Propionibacterium coming from very different biotope. The first specie, Propionibacterium acnes, is a commensal of the human skin. As an opportunistic pathogen, Propionibacterium acnes is involved in the pathogenesis of acne and may cause severe infections. The second specie, Propionibacterium freudenreichii belongs to the dairy group of propionic acid bacteria and is the main species involved in the holes and flavor formations in Swiss-type cheeses. The partial sequencing of genes coding for proteins (RpoB and RecA) and for 16S rRNA in addition to a mass spectrometric analysis of proteins (MALDI-TOF, MS) were applied to 20 strains of Propionibacterium acnes (15 from the collection of the National Reference Center for anaerobic bacteria and botulism from the Institut Pasteur and 5 strains from the Collection de l'Institut Pasteur) and to 20 strains of Propionibacterium freudenreichii from International Center of Microbial Ressources of Bacteria of Food Interest (CIRM-BIA, INRA). Main objective of this study is dual. Firstly, to determine the degree of molecular diversity of the strains at two levels, species level and clonal diversity level, taking into account that strains were selected in order to offer the largest diversity as possible in terms of biotopes and geographic origin for both species. Secondly, to compare the ranking of the strains according to the methodology applied: triple-locus sequence analysis or mass spectrometry. For mass spectrometry two equipments, an Applied Biosystems instrument and a Bruker Daltonics autoflex, were used to obtain mass spectra in order to evaluate and guarantee the reproducibility of the method. Results should also help to compare triple-locus sequence analysis to the MLST analysis which incorporates a greater number of genes (usually 6 to 7).*

Key words: *Propionibacterium freudenreichii, Propionibacterium acnes, Mass Spectrometry, Triple-Locus Sequence Analysis, Diversity*