

**Comparative assessment of probiotic attributes of *Lactobacillus Plantarum* strains of Ireland and Pakistan**Asma Manzoor<sup>1</sup>, Javed Iqbal Qazi<sup>1</sup>, Paul Ross<sup>2,3</sup>, Johar Ali<sup>4</sup> and Catherine Stanton<sup>2,3</sup><sup>1</sup>University of the Punjab, Pakistan<sup>2</sup>Teagasc Food Research Center, Ireland<sup>3</sup>University College Cork, Ireland<sup>4</sup>Rehman Medical Institute Peshawar, Pakistan

Fourteen *Lactobacillus plantarum* strains isolated from various food sources and two different climatic regions (Ireland and Pakistan) were genetically characterized at sub-species level with *recA* gene based multiplex PCR amplifications and pulsed-field gel electrophoresis. All the strains were tested in vitro for functional probiotic properties, which included the production of bacteriocin against the major food borne pathogens (*L.innocua* and *L. monocytogenes*), acid tolerance, survival in simulated gastric juice, NaCl tolerance, bile salt hydrolase activity and antibiotic resistance. The genes encoding bacteriocin (plantaracin 423) were identified from *L. plantarum* strains, and enzymes sensitivity assays to protinase K and pepsin were tested. Results of genomic fingerprinting following ApaI digestion revealed 10 distinctly different strains of PFGE patterns. Anti-microbial screening revealed, *L. plantarum* AS-4, AS-6, AS-8, AS-13 and AS-14 strains as the potential producers of bacteriocin. The culture supernatants of these strains expressed GIZ up to 12, 12, 14, 11 and 13 mm, respectively against *L. innocua* and the 3932 Da molecular mass was determined by using MALDI-TOF mass spectrometry along with control (*L. plantarum* LMGP-26358) The positive control, previously characterized plantaracin producer strain LMGP-26358, also showed GIZ of 12 mm. On the other hand, all the *L. plantarum* strains were active against a broad range of microorganisms including *L. monocytogenes* DPC 6179, *Enterococcus faecalis* 5055 (LMG9737), *E. coli* DPC EC101, *Bacillus subtilis* LMG 8198, *Clostridium perfringens* LMG 10468, *Clostridium difficile* ATCC 42593 and *Staphylococcus aureus* DPC 6867. Molecular characterization of these isolates was performed by amplification of previously known bacteriocin genes. Polymerase chain reaction analyses revealed that plantaracin genes were present in the genome of *L. plantarum* strains AS-4, AS-6, AS-7, AS-13 and AS-14 along with *L. plantarum* LMGP-26358 and for these bacteria almost similar growth pattern of bacteriocin production was observed. The loss of activity of 13 out of 15 strains confirmed that the antimicrobial substance produced by *L. plantarum* strains was indeed proteinaceous. All the strains showed good in vitro functional potential and a significant relationship was found between source of isolation and functional score with promising probiotic potential. Some of the desired characteristics were even better than those of probiotic referenced strains. This study confirmed a high heterogeneity in functional properties of the *L. plantarum* strains and provides insight into optimal screening strategies

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