

Characterization of *Staphylococcus aureus* strains isolated from mastitis bovine milk in Argentina.

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Abstract

The study reported in this Research Communication was conducted to characterize *Staphylococcus aureus* isolates recovered from mastitis bovine milk from dairy herds in Argentina. A total of 229 *S. aureus* isolates were recovered from 829 mastitis bovine milk samples obtained from 21 farms giving a prevalence of isolation of 28.1%. These isolates were tested for antimicrobial susceptibility to penicillin, erythromycin and clindamycin. Out of the 229 isolates, 53 (23.1%) were resistant to penicillin, 31 (13.5%) to erythromycin and 28 (12.2%) to clindamycin. All isolates were negative for *mecA*, *mecC* and *pvl* genes by PCR. Southernblot hybridization revealed that the *ermC* gene was located on plasmid bands. Eighty isolates were randomly selected from the 229 for further characterization. Restriction analysis of chromosomal DNA with Cf9I followed by PFGE of the 80 isolates revealed 23 distinct pulsotypes at 80% similarity. Seven major types (A, B, N, P, S, T, U and V) accounted for 68.7 % of these isolates and 12 pulsotypes (A, B, F, G, J, K, M, N, P, S, T and U) occurred on more than one farm indicating genetic diversity within the farms. MLST of a representative isolate from dominant types identified the STs 97,705, 746, 2102 and 2187 with ST97 being the most predominant. Antimicrobial susceptibility testing showed that 53.7% of the 80 randomly selected isolates were resistant to at least one antimicrobial. To our knowledge, this study represents the first large scale molecular studies on *S. aureus* isolates from dairy farms in Argentina.