## CHARACTERIZATION OF STAPHYLOCOCCUS AUREUS ISOLATES RECOVERED FROM MILK SAMPLES

\*Ferenc Peles<sup>1</sup>, Martin Wagner<sup>2</sup>, Ingeborg Hein<sup>2</sup>, Petra Rieck<sup>2</sup>, Klaus Gutser<sup>2</sup>, Péter Keresztúri<sup>1</sup>, Béla Béri<sup>3</sup>, András Szabó<sup>1</sup>

*Staphylococcus aureus* is known worldwide as a frequent cause of mastitis in dairy cattle and also as a principal contaminant of raw milk. Bacterial contamination can originate from multiple sources, such as mastitic cows, dirty udders and poorly cleaned milking equipment.

The aim of our research was to examine the genetic diversity and the antimicrobial drug susceptibility of sixty-nine *S. aureus* strains which derived from bulk tank milk (n=54) and udder quarter milk (n=15) of mastitic cows from dairy farms of different size.

Sixty-nine *S. aureus* isolates recovered from bulk tank milk of fourteen dairy farms and mastitic cows milk of two farms in Hajdú-Bihar county were compared genotypically. Macrorestriction analysis of SmaI-digested chromosomal DNA, using pulsed-field gel electrophoresis (PFGE) was performed to typing and estimate genetic relationships among the isolates. Antimicrobial drug susceptibility testing was performed on Mueller-Hinton agar by disk diffusion method according to National Committee for Clinical Laboratory Standards guidelines (NCCLS) by using antibiotic disks.

The sixty-nine strains were classified into eighteen pulsotypes (A-R) and three subtypes (D1, F1, K1). Isolates from bulk milk (n = 54), were divided into sixteen pulsotypes (A-D, F-R) and two subtypes (F1, K1). The mastitis (n = 15) isolates belonged to three different pulsotypes (D, E, F) and one subtype (D1). Only one or two PFGE related patterns were recovered from milk, showing a lack of genetic diversity within each farm. On the contrary the genetic diversity of the strains were great between the herds. In most instances we found different strains in each herd. The same types were found in bulk milk and in udder quarter milk samples. This indicates that *S. aureus* from infected udders may contaminate bulk milk. The results of the present investigation showed that pulsotypes D, E, F and subtype D1 seemed to be responsible for most cases of bovine mastitis in two examined farms and partly responsible for contamination of bulk tank milk.

All strains were susceptible to methicillin, cefoxitin, lincomycin, tetracycline, erythromycin and sulfamethoxazole/trimethoprim. Fourty-four of the sixty-nine isolates (63.8%) were susceptible to all antibiotics tested and twenty-five strains (36.2%) were resistant to penicillin. Resistant strains comprised of eleven (44.0%) from bulk tank milk and fourteen (56.0%) from mastitic cows milk. Fourteen out of the fifteen isolates (93.3%) derived from udder quarter milk of mastitic cows were penicillin-resistant.

The twenty-five penicillin-resistant isolates belonged to six pulsotypes (D, E, F, J, L, N) and two subtypes (D1, F1). Isolates from the same herd mostly had the same antibiotic resistance profile.

Department of Agricultural Microbiology, Centre of Agricultural Sciences, University of Debrecen, Böszörményi út 138, H-4032 Debrecen, Hungary

<sup>&</sup>lt;sup>2</sup> Institute of Milk Hygiene, Milk Technology and Food Science, University of Veterinary Medicine Vienna, Veterinärplatz 1, A-1210 Vienna, Austria

<sup>&</sup>lt;sup>3</sup> Department of Animal Husbandry, Breeding and Nutrition, Centre of Agricultural Sciences, University of Debrecen, Böszörményi út 138, H-4032 Debrecen, Hungary