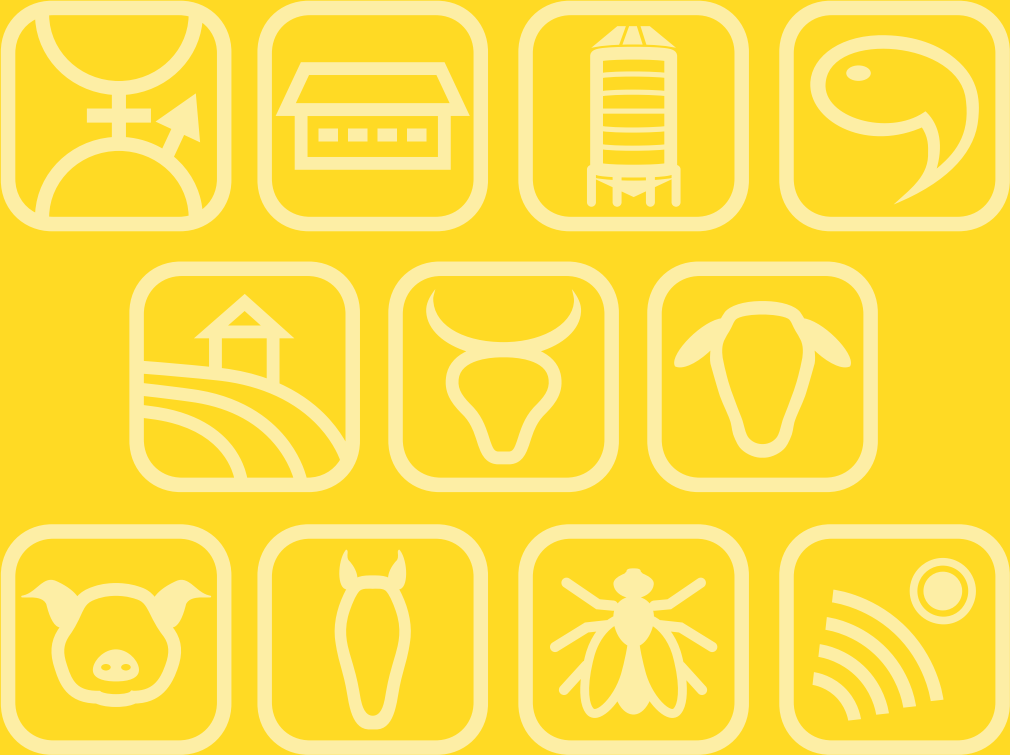
Book of Abstracts
of the 75th Annual Meeting of the European Federation of Animal Science



Book of Abstracts No. 34 (2024)
Florence, Italy
1-5 September, 2024

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EAAP

European Federation of Animal Science

The European Federation of Animal Science wishes to express its appreciation to the
Ministero dell'agricoltura, della sovranità alimentare e delle foreste (Italy) and the
Associazione Italiana Allevatori (Italy)
for their valuable support of its activities.

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ISBN: 979-12-210-6769-9

First published, 2024

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Evaluation of Shiga toxin-producing Escherichia Coli (STEC) in Traditional Dairy farms in Trentino

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Shiga toxin-producing Escherichia coli (STEC) are foodborne pathogens that pose a global public health and food safety challenge. The aims were to evaluate the presence of STEC in Trentino province (North Eastern Italy) dairy farms and possible correlations between STEC presence and milk quality parameters. The pathogen's presence was screened monthly in 15 farms delivering the milk to the local dairy factory for raw milk cheese production. We collected bulk milk samples, milking filters and environmental samples by overboots swabs. Milk samples were homogenized, decimally diluted in sterile peptone water and plated for the research of total bacterial count, lactococci, lactobacilli, coliforms, hemolytic streptococci and Prototheca spp. Milking filters and environmental samples were enriched with selective different antibiotics. All filters and environmental samples were tested by multiplex-PCR for the detection of the genes. Positive enrichments were subcultured on SMAC; positive colonies were isolated as putative STEC and tested by multiplex-PCR analysis. Preliminary results showed no positive correlation between the presence of Shiga toxin-producing genes and coliform count (mean 1.48 log UFC/mL, range 0.97 to 2.63 log UFC/mL). Moreover, despite having a positive presence in filters, many of the environmental samples were negative. Further investigations are scheduled to perform Whole Genome Sequencing (WGS) on more than 300 isolates. This study was carried out within the ONFoods2 and received funding from the European Union Next-GenerationEU (PNRR-MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.3–D.D. 1550 11/10/2022, PE00000003).

Identification of apathogenic bacteria as a reservoir for antibiotic resistance genes in bulk tank milk samples and in-line milk filters

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The intramammary use of antimicrobial agents in dairy farming is a controversial issue in the context of increasing antimicrobial resistance (AMR) in dairy farming. The widespread generalised use of antibiotic drying-off agents can lead to selection pressure on the bacteria, which promotes resistance. Particular attention is being paid here to the occurrence of methicillin-resistant Staphylococcus (S.) aureus (MRSA). The methicillin resistance of MRSA is mainly encoded by the mecA gene, which is located on a mobile element called SCCmec that enables transmission to other Staphylococcus species. Recent studies suggest that the element has been transferred from coagulase-negative staphylococci (CoNS) to S. aureus. One way to test for the presence of certain antibiotic-resistant genes on dairy farms is to analyse tank and raw milk as well as the milk filters used. Studies have shown that the microbiome and AMR-determinants detected on milk filters can be considered representative of the microbiome and resistome of milk and its production environment. Milk filter and tank milk samples as well as rinse samples were taken. Samples were then cultivated on culture media and the presence of mecA was then analysed by PCR. The mecA gene was detected in the tank milk, in the rinse sample and in the five milk filters analysed. In addition, S. sciuri was identified as a reservoir for mecA in the rinse sample and in the four milk filters and S. aureus in one milk filter. The detection of mecA in analysed milk filter samples does not initially allow any direct conclusions to be drawn about the resistance situation of important udder pathogens, as the CoNS species S. sciuri does not necessarily have to originate from the udder. This is to be determined retrospectively using the individual animal milk samples, which were taken in parallel with the milk filter sampling. Regardless of the source of entry, S. sciuri-isolates in combination with the mecA gene were identified not only in the milk filter but also in the tank milk itself, which makes the hygiene measures on the farm under investigation even more important.