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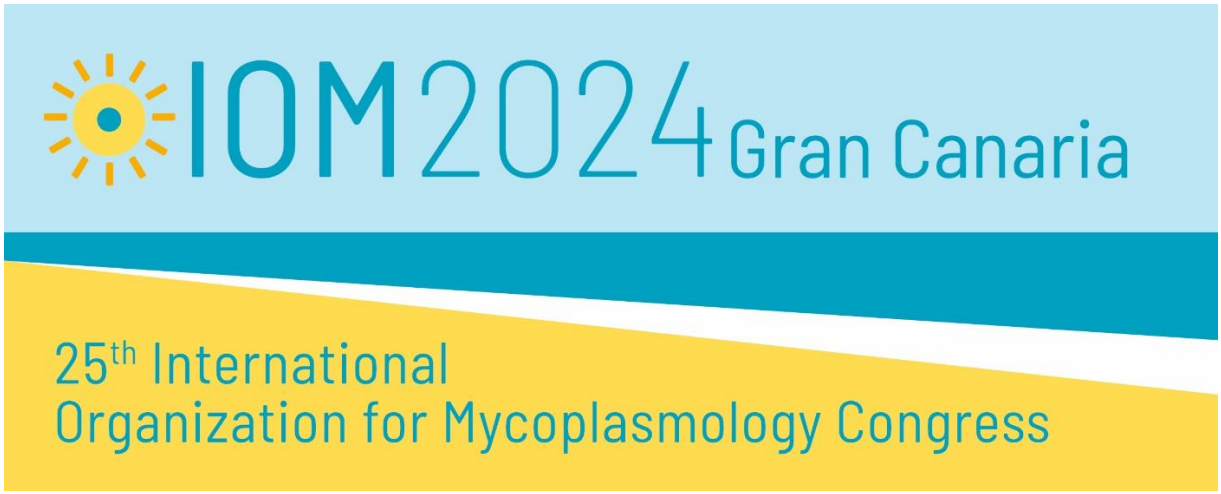
IOM 2024 Gran Canaria

25th International Organization for Mycoplasmology Congress

25th Congress of the International Organization for Mycoplasmology

July 7th–11th, 2024, Gran Canaria, Spain

Program and abstracts



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Immunology and Vaccines

P-43

Deep sequencing and variant frequency analysis for the quality control of T1 vaccine against contagious bovine pleuropneumonia

François Thiaucourt (1, 2), Antoni Exbrayat (1, 2), Etienne Loire (1, 2), Anne Boissière (1, 2), Nick Nwankpa (3, 4), Lucía Manso-Silván (1, 2)

(1) CIRAD, UMR ASTRE, Montpellier, France
(2) ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France
(3) Pan-African Veterinary Vaccine Centre of the African Union (AU -PANVAC), Bishoftu, Ethiopia
(4) National Veterinary Research Institute (NVRI), Vom, Nigeria

Vaccination is the most cost-effective tool to control contagious bovine pleuropneumonia. The vaccines currently used in Africa are derived from a live strain called T1, which was attenuated by passage in embryonated eggs and broth culture. The number of passages is directly correlated to the degree of attenuation of the vaccinal strains and inversely correlated to their immunogenicity in cattle. Current quality control protocols applied to vaccine batches allow the assessment of identity, purity, and titers, but cannot assess the level of genetic drift form the parental vaccine strains. Deep sequencing was used to assess the genetic drift generated over controlled in vitro passages of the parental strain, as well as on commercial vaccine batches. Signatures of cloning procedures were detected in some batches, which imply a deviation from the standard production protocol. Deep sequencing is proposed as a new tool for the identity and stability control of T1 vaccines.