



Contribution ID: 57

Type: Oral presentation

Genomic and virulence insights of Western European *Aeromonas salmonicida* subsp. *salmonicida* and development of *Galleria mellonella* infection assay

Friday 12 September 2025 15:15 (15 minutes)

Aeromonas salmonicida subsp. *salmonicida* is the etiological agent of furunculosis, a fish disease highly aggressive for salmonids and responsible for significant economic losses in aquaculture worldwide. This study aimed to explore genomic and antimicrobial resistance traits of Western European *A. salmonicida* subsp. *salmonicida* strains and to develop an adapted *Galleria mellonella* infection model to assess the pathogenic potential of this psychrophilic subspecies. Three strains isolated from salmonids displaying symptoms of furunculosis were tested against a panel of antibiotics and sequenced to characterize their genome. Virulence was evaluated in *G. mellonella* larvae using bacterial doses ranging from 101 to 106 CFU/larva. Two isolates exhibited multidrug resistance to antibiotics commonly used against furunculosis. Although closely related to the reference strain A449, genomic analyses revealed multiple plasmids known to encode antibiotic resistance genes. Virulence assays demonstrated that this subspecies is lethal at doses as low as 101 CFU/larva, and that a fully functional Type III Secretion System (T3SS) is not essential for the infection of *G. mellonella*, likely due to the presence of other virulence factors in T3SS-deficient strains. These findings enhance the genomic characterization of European *A. salmonicida* subsp. *salmonicida* and validate the use of *Galleria mellonella* larvae as a relevant alternative infection model for studying this psychrophilic subspecies.

Keywords

European *Aeromonas salmonicida*; virulence; *Galleria mellonella*; antimicrobial resistance; mobile genetic elements

Registration ID

ECVM25-47

Professional Status of the submitter, who is also the speaker

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Session Classification: Omics techniques

Track Classification: Veterinary Bacteriology, Mycology and Virology