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Paper Poster Session
Microbial pathogenesis and virulence

Inactivation of st313-td in Salmonella Dublin increases virulence in the mouse infection model

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Background: *Salmonella enterica* (*S. enterica*) serovar Dublin is a host-restricted serovar associated with typhoidal disease in cattle which can occasionally infect humans causing invasive disease. In previous studies a new virulent gene discovered in the pathogenic and multidrug-resistant lineage *S.* Typhimurium ST313, *st313-td*, of unknown function, was found to be conserved in the *S.* Dublin genomes. In ST313, the gene is harbored is a new potential pathogenicity island (ST313-GI of ca. 17,7 kb) while in Dublin, it is contained in a region of ca. 6.8 kb matching a part of ST313-GI (99% identity) (Figure).

Material/methods: In order to analyze the role of *st313-td* in the virulence of *S.* Dublin, several mutants, including the knocked-out and the complemented strains (ΔSD*st313-td* and SD3246-C) were constructed by using mutagenesis techniques. The wild type *S.* Dublin 3246 and isogenic strains were tested in different experiments, including; infection of cultured cell lines (human gut epithelial, murine and cattle macrophages), mice mixed infections, as well as growth competition in LB and cattle blood.

Results: In contrast to the results obtained for *S.* Typhimrium ST313, the lack of *st313-td* is associated to an increase in virulence in *S.* Dublin; the inactivation of the gene leads to an increased uptake by macrophages and the mutant strain (ΔSD*st313-td*) outcompetes the wild type isolate in the mouse model of infection.

Conclusions: *st313-td* also affects pathogenicity of this serovar and since it plays opposite roles in both S. Typhimurium ST313 and *S.* Dublin, it may act in a serovar specific-manner and might mediate regulatory functions. This study also contributes to better understand the relevance of a particular gene on host-pathogen interactions allowing the increase of knowledge about serovar differences on host adaptation.

Figure. Genetic structure of ST313-GI and region of the island present in the publicly available *S.* Dublin genomes (Herrero et al., 2014 modified). A region of ca. 6,8 kb out of the ca. 17.7 kb corresponding to the whole ST313-GI is present in the chromosome of *S.* Dublin (indicated with a discontinued line in green). The sequence data have been extracted from the sequenced genome of the strains *S.* Typhimurium D23580 and S. Dublin CT_02021853, accession no. FN424405.1 and CP001144, respectively. The location of the common region of ca. 6,8 kb within the *S.* Dublin genome is 624458_631264.