P1751
Paper Poster Session
Microbial pathogenesis and virulence

Characterization of four clinical isolates of Streptococcus pyogenes recovered from different sites of infection under human plasma supplementation

Gustavo Sambrano[1], Camilla Thorn[2], Thiago Paim[3], Renata Soares*[3], Adriana Rossato[3], Neidimar Tolfo[3], Pedro Alves D'azevedo[4], Florence Abram[1]

[1]*National University of Ireland Galway, Galway, Ireland*

[2]*National University of Ireland Galway , Galway, Ireland*

[3]*Federal University of Health Sciences of Porto Alegre , Porto Alegre, Brazil*

[4]*Federal University of Health Sciences of Porto Alegre , Department of Science Basic of Health, Porto Alegre, Brazil*

Background: *Streptococcus pyogenes* is a human-specific pathogen, highly prevalent worldwide and causing approximately 750 million infections per year. Throat and skin epithelia are the primary ecological niches of *S. pyogenes*. Invasive disease is a relatively rare outcome of *Streptococcus pyogenes* infection but results in high mortality rates. The aim of this study is to investigate the response of *Streptococcus pyogenes* isolated from different body sites to the presence of different concentrations of human plasma.

Material/methods: Four isolates identified as *Streptococcus pyogenes* were recovered from four different sites of infection: blood, skin lesion, oropharynx and vaginal secretion. The *emm* gene of the four isolates was sequenced according to CDC protocols and the presence or absence of 32 genes encoding virulence factors was also assessed. For phenotypic characterisation, the isolates were grown for 24 hours at 37°C in Todd-Hewitt broth with and without human plasma supplementation at the following concentrations: 1%, 5%, 10% and 20%.

Results: The *emm* types and clusters were defined by BLAST search within the CDC *Streptococcus* Laboratory database and classified as follows: blood strain (emm227.0, emm-cluster A-C3), skin lesion strain (emm169.3, emm-cluster E4), oropharynx strain (emm8.0, emm-cluster E4) and vaginal secretion strain (emm1.87, cluster A-C3). Investigation of 32 virulence factors, including superantigens, DNases, streptolysins and proteases, revealed that only 14 of these virulence factors were common to all four isolates' genomes. The skin lesion strain presented 28/32 of the virulence genes while the oropharynx, blood and vaginal secretion were found to harbour 27/32, 23/32 and 20/32, respectively. Maximum growth rate for the blood isolate was obtained upon human plasma supplementation. The skin lesion isolate was unaffected by plasma supplementation while the isolates recovered from oropharynx and vaginal secretion displayed maximum growth rate in the presence of 10% and 1% plasma, respectively.

Conclusions: Human plasma supplementation has been described as an important factor to trigger the expression of different proteins in isolates of *S. pyogenes*. The analysis of virulence genes and their relationships with growth rates demonstrates that a trade-off between virulence and fitness might exist, which requires further investigation. In order to address this question, whole genome sequencing, proteomic and transcriptomic analyses of the four isolates are currently under way.
Financial Support: Capes, CNPq