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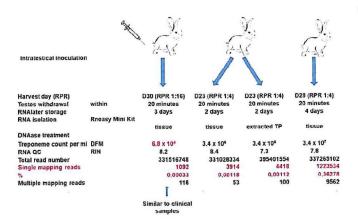
Introduction

MUNT

Treponema pallidum subspecies pallidum (TPA), causative agent of venereal syphilis, has a genome of size 1.14 Mbp comprising 1039 open reading frames out of which 55% are proteins of unknown function [1]. Research of syphilis has lagged behind other bacterial diseases due to the long-term absence of robust *in vitro* cultivation system and our knowledge of physiology and pathogenesis was mostly based on *in silico* analysis of genome sequences. Recently published cocultivation of *T. pallidum* with rabbit epithelial cells [2] enables genetic manipulations leading to functional analysis of proteins and proteomic analyses. Finding immunogenic proteins leading to protective immunity is a key to select candidates for future vaccine against syphilis. Hundred of genomic sequences were obtained from contemporary clinical samples but transcriptomic studies are scarce [3].

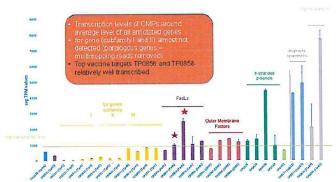
Methodology

RNA isolation protocol from treponemes harvested from rabbit testes was optimized to achieve a high quality RNA from a mixture of treponemal and rabbit cells from experimental intratesticular infection.



Results

Transcriptomes of laboratory strains Nichols and Haiti B were assessed using Illumina sequencing with the aim to discover which genes are expressed during experimental rabbit infection. Expression levels of all annotated genes were assessed with the aim to confirm expression of outer membrane protein vaccine candidates.



Conclusions

- Transcription levels of outer membrane proteins around average level of all annotated genes.
- tpr gene (subfamily I and II) almost not detected (paralogous genes multimapping reads removed).
- Top vaccine targets TP0856 and TP0858 relatively well transcribed.

References

- 1.Fraser CM, Norris SJ, Weinstock GM, et al. Complete genome sequence of Treponema pallidum, the syphilis spirochete. Science., 281:375-88 (1998).
- 2.Edmondson DG, Norris SJ. In Vitro Cultivation of the Syphilis Spirochete Treponema pallidum. Curr Protoc. 1:e44. (2021).
- 3. Smajs D, McKevitt M, Howell JK, Norris SJ, Cai WW, Palzkill T, Weinstock GM. Transcriptome of *Treponema pallidum*: gene expression profile during experimental rabbit infection. J Bacteriol., 187:1866-74 (2005).

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