In silico Identification of common putative vaccine candidates against *Treponema pallidum*: A reverse vaccinology based approach

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Sexually transmitted infections (STIs) are caused by a wide variety of bacteria, viruses, and parasites that are communicated from one human being to another primarily by vaginal, anal, or oral sexual contact. Syphilis is also a serious disease of sexually transmitted infection. Syphilis is caused by the bacterium *Treponema pallidum* subspecies pallidum. *Treponema pallidum* is a motile, gram-negative spirochaete bacterium, it can be transmitted both sexually and from mother to child, and it can invade virtually any organ or structure in the human body. The current worldwide prevalence of syphilis emphasizes the need for continued preventive measures and strategies. Unfortunately, effective measures are limited. In this study, we mainly focus on identification of vaccine targets and putative drug against Syphilis disease using reverse vaccinology and subtractive genomics. We compared 13 strains of *Treponema pallidum* keeping *Treponema pallidum* Nichols as reference genome. Furthermore, the orthoMCL software was used to predict the cluster of orthologous genes. CDSs shared by all species were considered to be part of the core genome. Considering human as a host, a set of 565 conserved non-hosts homologous proteins were identified. These conserved non-host homologous proteins were analysed using reverse vaccinology for antigenic properties of candidate vaccine, subtractive proteomics and modelomics approaches for drug target identification. Based on this analysis, we have classified 207 gene products as secreted proteins, putative surface-exposed proteins or membrane protein. A set of 26 cytoplasmic proteins constituting distinct quality model were selected as drug target for the bacteria. These proteins were considered as essential and non-host homologs, and have been subjected to virtual screening using two different compound libraries (extracted from the ZINC database and plant-derived natural compounds). The proposed drug molecules show favourable interactions, lowered energy values and high complementarity with the predicted targets.