In-silico analyses for the discovery of drug and vaccine targets in *Corynebacterium camporealensis*: A Novel Hierarchical Approach

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The genus Corynebacterium contains some bacterial species having clinical and biotechnological importance. In the last 2 decades, the taxonomy characterization of this noteworthy bacterial group has improved a lot. Pathogen genome sequencing and comparative genomics have resulted in identification of large number of effector genes shown to be responsible for promoting pathogenesis in human, animal and plants. We are reporting here *Corynebacterium camporealensis* strain CIP105508. It is a gram positive, non-spore forming, non-motile and pleomorphic rod shaped bacterium that occurs singly or are arranged in palisades or v-shaped forms. The bacterium was isolated from sheep milk affected by subclinical mastitis. Furthermore, we identify effector genes clustered in pathogenicity islands (PAIs) by scanning the genome regions for atypical GC content, codon usage biased approaches and other nucleotides statistical analysis. The present study aims at identification and qualitative characterization of promising drug targets in *C. camporealensis* using a novel hierarchical *in silico* approach, encompassing three phases of analyses. In phase I, four sets of proteins were mined through chokepoint, pathway, virulence factors, and resistance genes and protein network analysis. These were filtered in phase II, in order to find out promising drug target candidates through subtractive channel of analysis. The analysis resulted in therapeutic candidates, which are likely to be essential for the survival of the pathogen and non-homologous to host. Finally, in phase III, the candidate targets were qualitatively characterized through cellular localization, broad spectrum, interactome, functionality, and druggability analysis. The study explained their subcellular location identifying drug/vaccine targets, possibility of being broad spectrum target candidate, functional association with metabolically interacting proteins, cellular function (if hypothetical), and finally, druggable property. Outcome of this study could facilitate the identification of novel antibacterial agents for better treatment of *C. camporealensis* infections.