

Graphical Abstract

Staphylococcus sciuri are anaerobic facultative and non-motile bacteria that causes *significant human pathogenesis such as* endocarditis, wound infections, peritonitis, UTI and septic shock. Some methicillin-resistant *S. sciuri* (MRSS) also infects animals that include healthy broilers, cattle, dogs and pigs. The emergence of MRSS strains thereby poses a serious health threat and thrives the scientific community towards novel treatment options. Herein, we investigated the druggable genome of *S. sciuri* by employing subtractive genomics strategy whose different steps and tools employed for mining druggable targets in *S. sciuri* and identification of novel TCM inhibitors are represented in a schematic block diagram.

