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Bioinformatics and protein modelling of the GS element of *Mycobacterium avium subsp. paratuberculosis* (MAP) and GS-encoded proteins as drug targets and vaccine components

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Abstract

AIM: To determine the function and cellular localization of GS encoded proteins and to assess their potential as drug targets and vaccine components.

METHODS: Bioinformatics software was used to predict the function of GS-encoded proteins and their location within MAP. Protein modelling software was used to build protein structures.

RESULTS: The gene *gsa* is a truncated glycosyl transferase and probably nonfunctional. *gsbA* and *gsbB* produce GDP fucose which is methylated by *gsc* and acetylated by *mpa*. *gsd* is a fucosyl transferase which attaches fucose to subterminal rhamnose on cell surface glycopeptidolipid. *gsa*, *gsbA* and *gsbB*- and *gsc* are located within the cytoplasm. *mpa* is embedded in the plasma membrane with 10 transmembrane regions and a conspicuous extracellular loop. *gsd* is lipid linked and predicted to localize to the microbial cell surface.

CONCLUSION: GS encodes the biosynthetic machinery to give -MAP a surface coat of methylated and acetylated fucose which may contribute to its protease-resistant nature and ability to minimize immune recognition. The *gsbA*/*gsbB*-operon and *gsd* are promising drug targets and *gsd* is a good candidate component of a new class of anti-MAP vaccines.

Key words: *Mycobacterium avium*; Paratuberculosis; Glycosyltransferase; Vaccines; Genes; Protease inhibitors

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