Molecular analyses identifies new domains and structural differences among Streptococcus pneumoniae immune evasion proteins PspC and Hic.

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Immune evasion of *Streptococcus pneumoniae* in patients with kidney disease
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Abstract

The PspC and Hic proteins of Streptococcus pneumoniae are some of the most variable microbial immune evasion proteins identified to date. Due to structural similarities and conserved binding profiles, it was assumed for a long time that these pneumococcal surface proteins represent a protein family comprised of eleven subgroups. Recently, however, the evaluation of more proteins revealed a greater diversity of individual proteins. In contrast to previous assumptions a pattern evaluation of six PspC and five Hic variants, each representing one of the previously defined subgroups, revealed distinct structural and likely functionally regions of the proteins, and identified nine new domains and new domain alternates. Several domains are unique to PspC and Hic variants, while other domains are also present in other virulence factors encoded by pneumococci and other bacterial pathogens. This knowledge improved pattern evaluation at the level of full-length proteins, allowed a sequence comparison at the domain level and identified domains with a modular composition. This novel strategy increased understanding of individual proteins variability and modular domain composition, enabled a structural and functional characterization at the domain level and furthermore revealed substantial structural differences between PspC and Hic proteins. Given the exceptional genomic diversity of the multifunctional PspC and Hic proteins a detailed structural and functional evaluation need to be performed at the strain level. Such knowledge will also be useful for molecular strain typing and characterizing PspC and Hic proteins from new clinical S. pneumoniae strains.

Identifier

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