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Research Article

MODELING OF ompC PROTEIN OF *SALMONELLA GALLINARUM*

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ABSTRACT

ompC protein of *Salmonella gallinarum* was subjected to modelling at SWISS-MODEL software online using different modelling tools. The ompC protein appeared compact globe. The model revealed antigenic sites, different groups and structures.

KEY WORDS: *Salmonella gallinarum*, ompC protein, modelling, SWISS-MODEL

INTRODUCTION

Salmonella gallinarum (SG) is non-motile host-adapted salmonella that causes fowl typhoid, a severe systemic disease responsible for heavy economic losses to the commercial poultry industry through morbidity, mortality and reduced egg production (Pomeroy and Nagaraja, 1991). Fowl typhoid has been controlled and eradicated from Australia, North America and most of the European countries, however, it still remains endemic in many countries of Africa, the Middle East, Central and South America and Asia (Shivaprasad, 2000). Shah *et al* (2005) described the application of a PCR-based signature-tagged mutagenesis system to identify in vivo-essential genes of SG. Ninety-six pools representing 1152 SG mutants were screened in a natural-host chicken infection model. Twenty presumptive attenuated mutants were identified and examined further. The identity of the disrupted gene in each mutant was determined by cloning of the DNA sequences adjacent to the transposon, followed by sequencing and comparison with the bacterial genome database. In vitro and in vivo competition indices were determined for each identified mutant and a total of 18 unique, attenuating gene disruptions were identified. These mutations represented six broad genomic classes: Salmonella pathogenicity island-1 (SPI-1), SPI-2, SPI-10, SPI-13, SPI-14 and non-SPI-encoded virulence genes. SPI-13 and SPI-14 were newly identified and designated in this study. Most of the genes identified in this study were not previously believed or known to play a role in the pathogenesis of SG infection in chickens. Each STM identified mutant showed competitiveness and/or virulence defects, confirmed by in vitro and in vivo assays, and challenge tests.

Cho *et al* (2014) investigated SG outer membrane proteins (OMP) as potential vaccine candidate proteins and established a proteomic map and database of antigenic SG-OMP. A total of 174 spots were detected by 2DE. Twenty-two antigen-reactive spots were identified as nine specific proteins using PMF. OmpA was the most abundant protein among all of the identified OMP, and it exhibited seven protein species. OmpA was considered to be an antigenic cross-reactive protein among the three serovars. This study shed new light on our understanding of cross-protection among *Salmonella* serovars. Schroll *et al* (2014) showed that Serovars of *Salmonella enterica* exhibit different host-specificities where some have broad host-ranges and others, like *S. gallinarum* and *S. typhi*, are host-specific for poultry and humans, respectively.

In the present study, we did modelling of ompC protein of *Salmonella gallinarum* to understand its structural and antigenic details.

MATERIALS AND METHODS

ompC protein of *Salmonella gallinarum*

The base sequence of the ompC gene was converted to amino acid sequence using DNAstar/lasergene Editseq software.

Mkvkvlsllvpallvagaanaaeiynkdgnkldlfgkvd
glhyfsddkgsdgdqtymrig
fkgetqvndqltgygqweyqiqgnqtegsndswtrvafa
glkfadagsfdygrnygvtyd
vtswtdvlpefggdtygadnfmqqrgngyatyrntdffgl
vdgpdfalqyqgqngsvsge
ntngrsllnqngdgyggsltyaigegfsvggaittskrtadq
nntadehlygngdratvy
tgglkydanniylaaqysqtynatrfgtsngnnkstsygfa
nkaqnfevvaqyqfdfglr
psvaylqskgkdistgygasygdqdivkyvdvgatyyfn
knmstyvdykinlldkndftr
dgintddivalglvyqf

Fig.1. ompC protein of *Salmonella gallinarum* used for modeling at SWISS-MODEL

Modeling

Modeling was done at swiss-model software online. Different modeling parameters were used: SCRATCH (SSpro) (Pollastri *et al*, 2002a), CONpro and ACCpro (Pollastri *et al* (2002b),CMapPro and CMap23Dpro (Pollastri and Baldi, 2002), **PredictProtein (**Rost, 1996), **ProSite** (Hofmann *et al*, 1999), **ProDom (**Corpet *et al*, 2000), **MaxHom** (Sander and Schneider, 1991), **MView** (Brown *et al*, 1998), **PHD (**Rost, 1996), **PHDhtm** (Rost *et al*,1996), **PROF, PROFsec, GLOBE** (Rost *et al*, 2004), **ASP** (Young *et al*, 1999)**.**

RESULTS AND DISCUSSION

The results are shown in Table1 and Fig 2-5. The ompC protein appeared as compact, as a globular domain. GLOBE: prediction of protein globularity: nexp = 195 (number of predicted exposed residues), nfit = 152 (number of expected exposed residues, diff = 43.00 (difference nexp-nfit).

Table1. Residue composition of *S. gallinarum* ompC protein.

%A: 7.7	**%C: 0.0**	**%D: 9.0**	**%E: 2.4**	**%F: 5.3**
%G: 13.3	**%H: 0.5**	**%I: 2.9**	**%K: 4.8**	**%L: 6.6**
%M: 1.1	**%N: 8.2**	**%P: 1.1**	**%Q: 5.8**	**%R: 2.9**
%S: 5.8	**%T: 7.4**	**%V: 6.1**	**%W: 0.8**	**%Y: 8.2**

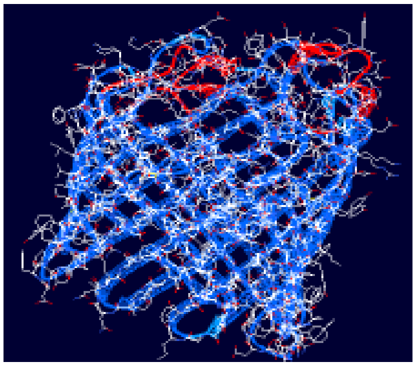

Fig.2. ompC protein of *Salmonella gallinarum* modeled at SWISS-MODEL and viewed in spdbv

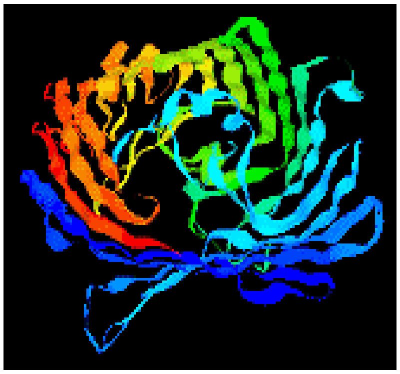

Fig.3. ompC protein of *Salmonella gallinarum* modeled at SWISS-MODEL and viewed in

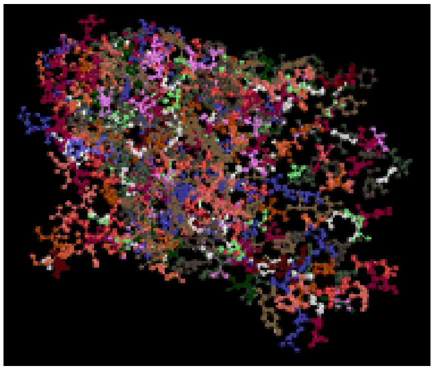

Fig.4. ompC protein of *Salmonella gallinarum* modeled at SWISS-MODEL and viewed in Rasmol as ball & stick color group.

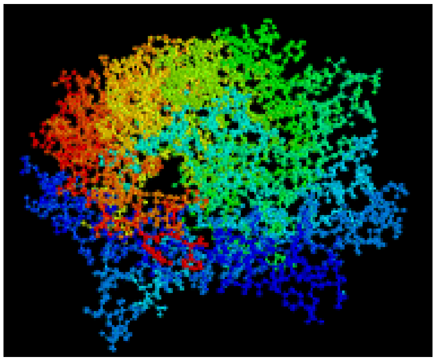

Fig.5. ompC protein of *Salmonella gallinarum* modeled at SWISS-MODEL and viewed in Rasmol as ball & stick color shapely.

CONCLUSION

Modeling of ompC protein of *Salmonella gallinarum* revealed that it is a compact globular protein.

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