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New insights concerning the distribution of *Salmonella* virulence factor Rck

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Salmonella are facultative intracellular bacteria able to infect a broad range of hosts using several virulence factors, including the Rck outer membrane protein. This protein is responsible for (i) resistance to complement, in particular through membrane attack complex formation inhibition, (ii) bacterial adhesion, through laminin binding, and (iii) host-cell invasion, through a Zipper-like mechanism following interaction with the EGF-R. The *rck* ORF belongs to the *pefI-srgC* operon, carried on the virulence plasmid of *Salmonella*. Currently, *rck* has only been characterized on the virulence plasmid of three serovars, i.e. Enteritidis, Typhimurium and Bovismorbificans. As the literature suggested a larger distribution, our aim was to study the prevalence of the *rck* ORF in the genus *Salmonella* taking advantage of the large online database Enterobase and of its experimental data associated (e.g. *in silico* serovars prediction, wgMLST sequence type). 188,233 genomes belonging to more than 471 *Salmonella* serovars were analyzed. Our results revealed the presence of the *rck* gene in 39 serovars and a predominance of some alleles for some serovars. They also suggest that the gene might not be exclusively carried on plasmids. Finally, despite a relatively high number of haplotypes, amino acid sequences comparison revealed a strong conservation of the protein sequences, as the majority of the identified variants showed only minor sequence variations with the three currently described Rck proteins. In conclusion, Rck is more widely distributed in *Salmonella* serovars than previously expected and consequently could play a role in the virulence of all these serovars.