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PROTEOMICS EVALUATION OF MOLECULAR MECHANISMS INVOLVED IN PATHOGENESIS OF SALMONELLA SPP.

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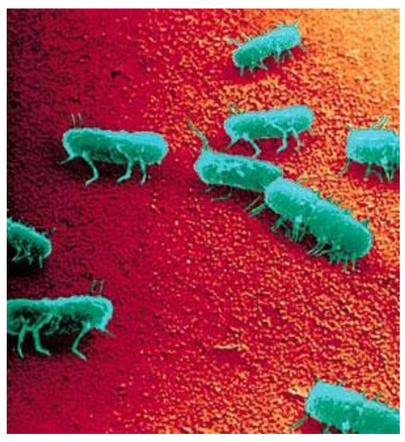

Salmonella enterica spp. include several closely related *serovars*, which differ in host ranges and pathogenic activities. Most cases of food related diseases are caused by *S. enterica*, which often infects cattle and poultry and also may occur in the food processing through cross contamination from raw food or infected food handlers. The molecular basis for the diversity in host range and pathogenic potential of *serovars* is not well understood and it is not known what factors are lost or acquired during adaptation to a specific environment. Therefore, the need to find valid strategies to control diffusion and decreasing incidence of these pathologies has currently a high priority.

!! PRIORITY: NEW MOLECULAR TARGET SITES TO IMPROVE DIAGNOSIS AND TO DRAW NEW THERAPEUTIC STRATEGIES

HOW?: 2D electrophoresis to compare *serovars* Typhimurium and Enteritidis isolated from food

COMPARATIVE PROTEOMICS: Typhimurium VS Enteritidis

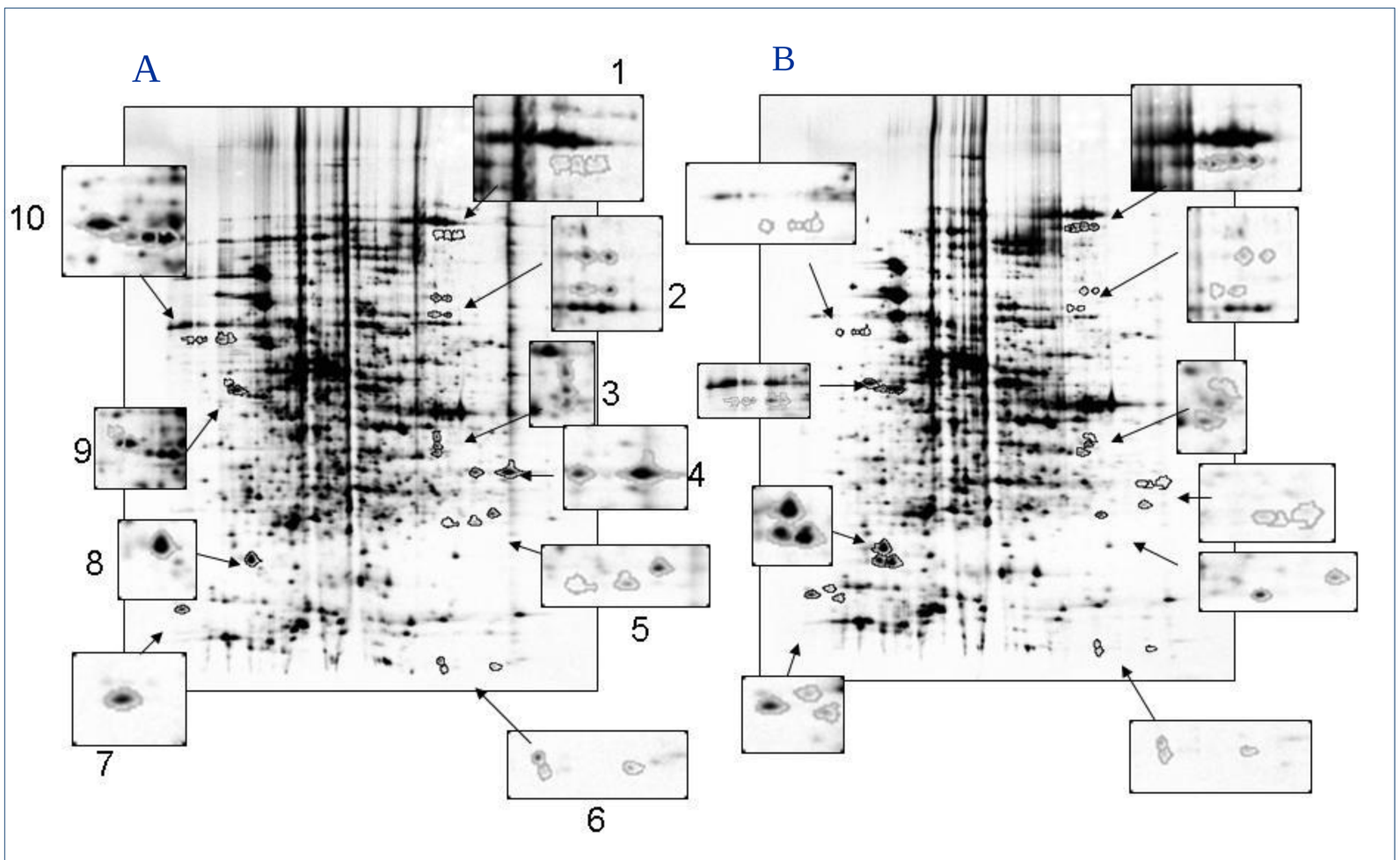

Fig.1: serovars Typhimurium (A) VS Enteritidis (B)

METHODS

IEF was performed using home made IPG strips with a linear pH range of 4-8. The amount of 200 µg of protein sample was loaded into IPG strips via cathodic cup loading. SDS-PAGE was performed on 10% polyacrylamide gels. Gels were stained with blue colloidal Coomassie G-250. The raw images were processed and altered spots were compared on their volume percentages in the total spot volume over the whole gel image.

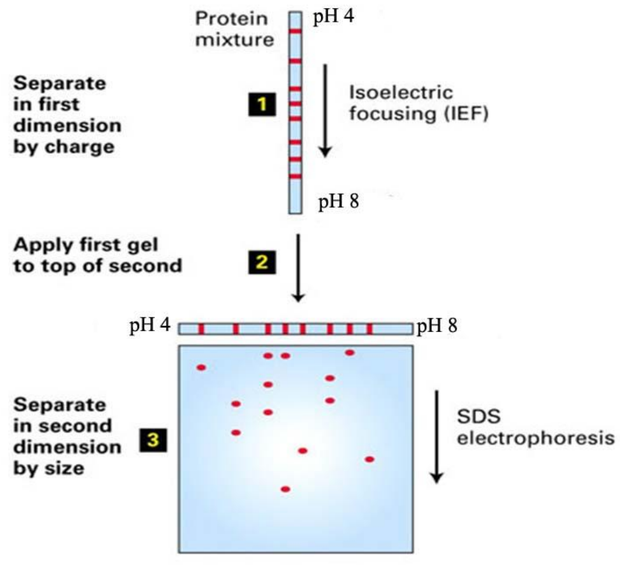

Fig.2: experiment workflow

RESULTS

Quantitative image analysis highlighted several differences between serovars Enteritidis and Typhimurium. 2D maps have been compared with S.enterica subspecies thyphimurium for a preliminary identification of proteins (Encheva V. et al, 2005).In particular, major changes are related to proteins involved in lipid metabolism (3-oxoacyl[ACP] sinthase, spot 10), transport of small molecules (PTS-Hpr, spot 6) and DNA duplication (protein chain elongation factor, spot 2). Regarding sugar metabolism, it have not been observed drammatic changes.

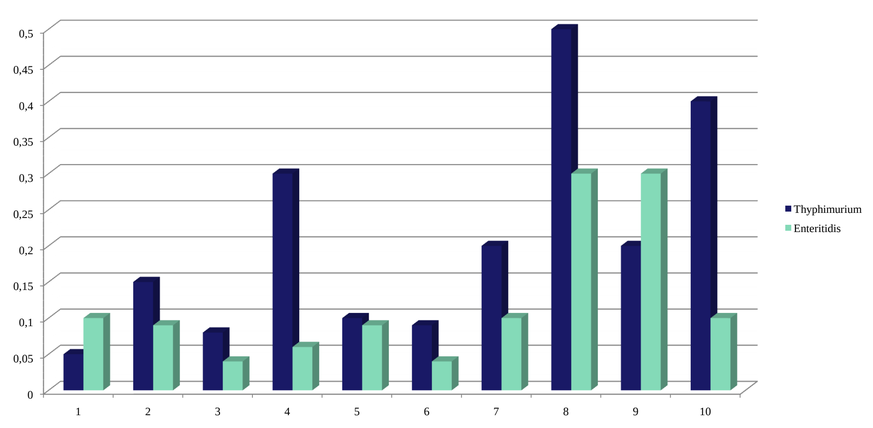

Fig.3: quantitative expression of changed spots.

CONCLUSION

This study has shown the importance of incorporating a large number of strains of a species, as the diversity of the proteome in the microbial population appears to be significantly greater than expected. The characterisation of a diverse selection of strains revealed parts of the proteome of *S. enterica* that alter their expression while others remain stable and allowed for the identification of serovar-specific factors that have so far remained undetected by other methods.

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