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Abstract (poster session)

**Whole genome sequencing of *Neisseria meningitidis* serogroup C isolates reveals subtle genetic difference in the capsule locus of an outbreak strain**

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Objective: Comparative analysis of the genomes of *N. meningitidis* serogroup C isolates in order to detect cues associated with a highly virulent phenotype. Methods: Whole genome sequencing by using the standard shotgun and the 3-Kb paired-end protocols provided by Roche 454 next generation platform. Results: We sequenced the whole genome of two isolates of *N. meningitidis* serogroup C, which were isolated from patients with invasive disease in northern Italy during the 2007-2008 winter and belonged to the same ST-11/ET-37 clonal complex. One of the two strains was responsible of an outbreak with seven cases of meningitis, including three fatal cases, while the other strain was isolated from a sporadic case of meningitis in the same area and period. Whole-genome comparative analysis revealed local and remarkable differences between the genomes of the two isolates and in comparison with the reference genome of strain FAM18. Since these differences between the two *N. meningitidis* isolates could be the result of genetic variations of the same *N. meningitidis* strain within the outbreak, the most relevant changes in terms of sequence length and predicted function were selected for further investigation and validation through primer-specific cycle sequencing in the two sequenced *N. meningitidis* strains and in the other seven ST-11/ET-37 isolates collected in 2007-2008 in the same area. This analysis confirmed findings provided by next generation sequencing and bioinformatic comparison and demonstrated that the other five isolates from the same outbreak shared the same sequences of the outbreak index strain, whereas the isolate from sporadic meningitis shared sequence identity with isolates from other sporadic cases of meningitis occurring in Veneto Region both before and after the outbreak, during the same season. All genetic differences among strains occurred in the capsule locus and were compatible with horizontal acquisition of a cluster of genes involved in lipooligosaccharide biosynthesis from commensal meningococci. Conclusions: The results of this study showed that an outbreak strain of *N. meningitidis* serogroup C was characterized by horizontal acquisition of a capsule biosynthesis operon that could contribute to its highly virulent phenotype.