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Genomic epidemiology of *Neisseria meningitidis* serogroup W isolates collected in Switzerland between 2010 and 2016

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Introduction. *Neisseria meningitidis*, also known as meningococcus (Men) can cause bacterial meningitis and septicaemia. Virulent isolates are classified in serogroups according to capsule components. In Switzerland the incidence of serogroup W (MenW) has steadily increased from 5% in 2005 to 35% in 2015. Sequence Type (ST)-11 was the prevalent genetic lineage and the only ST identified in 2016. MenW ST-11 strains are hypervirulent and often cause outbreaks world-wide mainly due to two circulating lineages: one originating from a South-American and the other from Saudi Arabian (Hajj clone) outbreaks.

Aim. We investigated potential clonal relationships among Swiss MenW by whole-genome sequencing (WGS).

Methods. Illumina MiSeq 2x300 sequencing was performed on 40 Swiss MenW isolates collected between 2010 and 2016. Multi-Locus Sequencing Typing (MLST) was inferred on *de novo* assembled genomes and phylogenetic analyses were performed with a core genome MLST (cgMLST) gene approach. ST-11 samples were further analysed by considering cgMLST Single Nucleotide Polymorphisms (SNPs). Potential outbreaks were evaluated by considering the relative amount of SNPs between samples, the canton and date of sample isolation. Swiss isolates were also connected to reference European strains of South-American and Hajj-clone-related lineages.

Results. Of the 40 MenW samples analysed, 34 belonged to ST-11. SNPs analyses revealed that ST-11 isolates were clustered in three main blocks. Block I contained 14 samples, 7 of which were isolated between February and July 2015 in the canton of Basel (5) and in its neighbouring regions: Bern (1) and Aargau (1). Given the narrow time window and the low number of SNPs (range = 1-4), our results argue in favor of a monoclonal outbreak. The block II contained 3 samples isolated between January and February 2014 in the canton of Ticino. No SNPs were found among these 3 samples, thereby they represented the same circulating strain. The block III contained 2 and 7 isolates from 2015 and 2016, respectively, with 1-37 SNPs identified in pairwise comparisons. These isolates likely resulted from the expansion of a strain circulating in 2015 in the German and French speaking Swiss cantons. Comparisons with other European strains showed that samples of Block-I derive from the Hajj clone lineage whereas Block-II and Block-III isolates are related to the South-American lineage.

Conclusions We identified potential monoclonal outbreaks by WGS and we also established connections between Swiss MenWs and other European strains.