**#S9: Rapid Transmission of a Hyper-Virulent Meningococcal Clone Due to High Effective Contact Numbers and Super Spreaders**

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Rapid transmission, a critical contributory factor in outbreaks of invasive meningococcal disease, requires naïve populations of sufficient size and intermingling. We examined genomic variability and transmission dynamics in a student population subject to an 11-fold increase in carriage of a hypervirulent Neisseria meningitidis serogroup W ST-11 clone. Phylogenetic clusters, mutation and recombination rates were derived by bioinformatic analyses of whole-genome sequencing data. Transmission dynamics were determined by combining observed carriage rates, cluster sizes and distributions with simple SIS models. Between 9 and 15 genetically-distinct clusters were detected and associated with seven residential halls. Clusters had low mutation accumulation rates and infrequent recombination events. Modeling indicated that effective contacts decreased from 10 to 2 per day between the start and mid-point of the university term. Transmission rates fluctuated between 1 and 4% while the R(t) for carriage decreased from an initial rate of 47 to 1. Decreases in transmission values correlated with a rise in vaccine-induced immunity. Observed carriage dynamics could be mimicked by populations containing 20% of super spreaders with 2.3-fold higher effective contact rates. We conclude that spread of this hypervirulent ST-11 meningococcal clone depends on the levels of effective contacts and immunity rather than genomic variability. Additionally, we propose that super-spreaders enhance meningococcal transmission and that a 70% MenACWY immunization level is sufficient to retard, but not fully prevent, meningococcal spread in close-contact populations.

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