Transmission of Staphylococcus aureus in social networks

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Background: The heterogeneity of bacterial populations is associated with variability in pathogenicity, infectivity and sensitivity to antimicrobial agents. Thus, predictions of how various strains are distributed in a host population are important in a public health perspective. Network epidemiology, in addition to individual biological properties of microbe hosts predicts that strains, including resistant strains, will not spread randomly but will cluster based on the contact structure. Among the known structuring factors are demographic characteristics such as age and sex, in addition to determinants of social relations such as school grade and school affiliation. In our study we address how social structure influences Staphylococcus aureus strain clustering via statistical modeling of social network data.

Material/methods: The analysis is based on social network data from 1038 first-year upper-secondary school students’ age 15-19 years, who participated in a survey on lifestyle and health, the Tromsø Study Fit Futures, North Norway, in 2010/11 (508 girls and 530 boys from all eight upper-secondary schools in the Tromsø region; 93% attendance rate). Each participant was asked to list five other students they have had contact with recently to map the social network. Swab samples were collected from both tonsils to assess Staphylococcus aureus throat colonization. Social structure was assessed using statistical models including age, sex and school class affiliation as predictors of social links. Further, clustering and modularity of the social network were estimated. Staphylococcus aureus throat isolates, one from each carrier (N=631), were genotyped by spa-typing and assigned to clonal complexes (Spa-CCs). The genotype information was added to the social network data to explore whether the distribution is contingent on, and predictable from, contact structure.

Results: The social network was fully connected with 2772 links and maximum number of links per node of 16, on average 7.27. Social interactions were structured by demographic and social network determinants. The structuring factors influenced social clustering and were associated with S. aureus transmission. The two dominant strains were widespread (24,1% and 23,4%) whereas other strains formed more distinct clusters associated with the social network structure.
Conclusions: *Staphylococcus aureus* transmission in a healthy population is not random but rather follows the social network structure. Our findings have implications for the design of interventions in a public health context.