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Pneumococcal genomics, vaccines and AMR

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Streptococcus pneumoniae (the pneumococcus) is an important cause of pediatric meningitis, which has been well controlled with pneumococcal conjugate vaccines (PCVs). Nevertheless, PCVs target only a fraction of the strains in the population and their use has been followed by increases in non-vaccine serotypes, some of which can cause disease. Predicting how pathogen populations will change over time is challenging. Here, we use the frequencies of pneumococcal accessory genes to predict changes in the pneumococcal population after vaccination, hypothesizing that these frequencies reflect the results of negative frequency-dependent selection (NFDS) on the gene products. We find that the standardized predicted fitness of a strain estimated by an NFDS-based model at the time the vaccine is introduced accurately predicts whether the strain increases or decreases in prevalence following vaccination. Further, we are able to predict the equilibrium post-vaccine population composition and assess the invasion capacity of emerging lineages using predicted fitness and quadratic programming. In general, we provide a method for predicting the impact of an intervention on pneumococcal populations with potential application to other bacterial pathogens in which NFDS is a driving force.