## SARS-CoV-2 outbreak dynamics at a United States Marine recruit training facility: An observational, phylogenetic cohort study

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## Abstract:

**Summary**: Recruit training environments can efficiently spread respiratory infections threatening the heath of trainees and long-term military staffing goals. We studied the epidemiology and transmission dynamics of Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) in the recruit setting using a prospective, longitudinal study at Marine Corps Recruit Depot Parris Island (MCRDPI), South Carolina, USA.

**Methods:** We analyzed data on 2469 unvaccinated, mostly male, United States Marine Corps recruits between May and November 2020. We enrolled participants at the beginning of a supervised two-week quarantine. After testing negative for SARS-CoV-2 by polymerase chain reaction (PCR), recruits were transferred to basic training, tested biweekly for 6 weeks by PCR, and administered a clinical questionnaire at each study encounter. We assessed the effects of COVID-19 prevention measures on other respiratory infections, performed phylogenetic analysis on genomes from representative SARS-CoV-2 strains, and calculated the basic reproduction number (R<sub>0</sub>) of person-person transmission.

**Results:** COVID-19 preventive measures reduced other viral etiologies of respiratory illnesses and pneumonia. However, 1107 (44.8%) participants tested SARS-CoV-2 PCR positive during the first six weeks of basic training. Phylogenetic analysis of viral genomes from 580 participants revealed five monophyletic outbreaks and transmission of mutations emerging during transmission, one of which was associated with fewer symptoms. The R<sub>0</sub> among the 20 training companies that were observed was 5.5 [95% Cl 5.0-6.1]) (Figure 1).

**Conclusion**: Despite measures that reduced other respiratory infections, five SARS-CoV-2 introductory events entered the training depot and proliferated. The  $R_0$  of the ancestral SARS-CoV-2 strain in the training environment approximated that now

reported for contemporary variants of concern demonstrating the influence a congregant setting has on viral transmission.