

Workshop: Bioinformatics Methods For Reconstruction Of Infectious Bronchitis Virus Quasispecies From Next Generation Sequencing Data

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Abstract—Viral infections cause a significant burden on animal health, reducing yields and increasing production costs due to expensive control programs. Vaccination is a vital part of control programs; however, its effectiveness is reduced by the quick evolution of escape viral quasispecies in animal hosts. Existing techniques for studying quasispecies evolution and response to vaccines have severely limited sensitivity and often require prior knowledge of sequence polymorphisms. By generating millions of short reads per run, with no need for culture or cloning, next-generation sequencing (NGS) technologies enable comprehensive identification of viral quasispecies infecting an animal. However, analysis of NGS data is challenging due to the huge amount of data on one hand, and to the short read lengths and high error rates on another. As a consequence, many tools developed for Sanger reads do not work at all or have impractical runtimes when applied to NGS data. Even newly developed algorithms for de novo genome assembly from NGS data are tuned for reconstruction of haploid genomes, and work poorly when the

sequenced sample contains a large number of closely related sequences, as is the case in viral quasispecies. To address these shortcomings we have developed computational methods for reconstructing quasispecies sequences and estimate their frequencies from both shotgun and amplicon NGS data. Preliminary analysis of 454 sequencing reads generated from synthetic pools of Infectious Bronchitis Virus (IBV) clones and field isolates collected at various intervals after vaccination with attenuated live IBV vaccine will be presented.

Keywords—next generation sequencing, viral quasispecies reconstruction, Infectious Bronchitis Virus

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