**Abstract: Modeling the Viral Fitness of Novel Swine H1N1 in Concentrated Animal Feeding Operations**

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RNA viruses are characterized by their high mutation rates, which lead to variant genomes within the population, termed quasispecies [1,2]. This creates deviate strains that are either resistant or susceptible to defensive mechanisms by the host/acquired immunity. While a great deal is known about the pathogenesis of the novel H1N1 strain, relatively little research has gone to viral fitness within concentrated animal feeding operations (CAFOs). In previous studies, swine flu-like infections peaked in counties with licensed swine operations [3]. We hypothesize that the generation of new variants will exceed the biosecurity/immune measures, thus expanding that variant’s host range. To test this assumption, we will create a phylogenic tree based upon the variant genomes deviated from the novel H1N1 strain to measure the point mutation rate per generation. We will also create a model that reflect societal (environmental) parameters as they relate to the mutation rate. We further hypothesize that biosecurity policies have low fidelity for preventing or reducing endemic factors. We will analyze the data using python and Linux programs that will create a predictive model for viral fitness within CAFOs. Our research will provide insight on what factors lead to the emergence of zoonotic strains within CAFOs.

**References**

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