Choice of High-Efficacy Strains for the Annual Influenza Vaccine

MICHAEL DEEM, Rice University — We introduce a model of protein evolution to explain limitations in the immune system response to vaccination and disease [1]. The phenomenon of original antigenic sin, wherein vaccination creates memory sequences that can increase susceptibility to future exposures to the same disease, is explained as stemming from localization of the immune system response in antibody sequence space. This localization is a result of the roughness in sequence space of the evolved antibody affinity constant for antigen and is observed for diseases with high year-to-year mutation rates, such as influenza. We show that the order parameter within this theory correlates well with efficacies of the H3N2 influenza A component of the annual vaccine between 1971 and 2004 [2,3]. This new measure of antigenic distance predicts vaccine efficacy significantly more accurately than do current state-of-the-art phylogenetic sequence analyses or ferret antisera inhibition assays. We discuss how this new measure of antigenic distance may be used in the context of annual influenza vaccine design and monitoring of vaccine efficacy. 1) M. W. Deem and H. Y. Lee, Phys. Rev. Lett. 91 (2003) 068101. 2) E. T. Munoz and M. W. Deem, q-bio.BM/0408016. 3) V. Gupta, D. J. Earl, and M. W. Deem, “Choice of High-Efficacy Strains for the Annual Influenza Vaccine,” submitted.

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