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Talk Title:

“Detecting selection: what can amino acid changes tell us about evolution?”

Abstract:

Proteins evolve in two ways: in leaps by adding or losing whole domains and in incremental steps by changing one amino acid at a time. Single amino acid substitutions are the protein-level manifestation of single nucleotide substitutions - the most common point mutations and are largely responsible for evolution of new functions. Vast majority of amino acid substitutions reach fixation neutrally, by genetic drift. How can we detect among them those few that were driven to fixation by positive selection and therefore are likely to be functionally significant? There are several ways to do this: by comparing the frequency of amino acid substitutions to that of synonymous changes (that are almost certainly evolve by drift), by comparing frequencies of amino acid changes in different parts of the same protein and by analyzing amino acid changes occurring in different evolutionary lineages in parallel. I will discuss several recent examples of using these approaches to detect adaptive evolution in proteins in fruit flies, endemic species flocks and the coronavirus.

Bio:

Dr. Yampolsky earned a BS in Biology in 1986 from Moscow State University and a PhD in Genetics in 1992 from the Russian Academy of Sciences. He then came to the U.S. for a series of postdoc appointments: 1993 – 1994, Northern Illinois University; 1994 – 1996, Cornell University; 1997 – 1999, University of Georgia; 1999 – 2001, University of Maryland/NIST. He has been a faculty member at ETSU since 2001. His major research interest is in the area of the evolution of gene expression in response to changes in the environment (temperature, nutrients, xenobiotics) or genetic background (chromosomal aberrations, gene duplications). Differential gene expression is the molecular basis of phenotypic plasticity. Dr. Yampolsky investigates the role of adaptation and environmental constraints in the shaping of differential gene expression. Does plastic gene expression impede adaptive evolution or provide a new

target for selection? If plasticity of gene expression is lost in a constant environment, does it occur by neutral processes or by selection operating through across-environmental trade-offs? He attempts to answer these and other questions using microarray and RNAseq technology as well as bioinformatics. His study organisms include *Drosophila* *Daphnia* and Lake Baikal (Siberia) endemic crustaceans.