

Rapid Speciation Through Black Queen Gene Loss in Bacteria and Digital Organisms. J. Jeffrey Morris^{1,2}, Spiridon E. Papoulis^{2,3}, Luis Zaman^{3,4}, and Richard E. Lenski^{2,3}, ¹ Department of Biology, University of Alabama at Birmingham, evolve@uab.edu, ² BEACON Center for the Study of Evolution in Action, ³ Department of Microbiology and Molecular Genetics, Michigan State University, ⁴ Department of Biology, University of Washington.

Introduction: Black Queen gene loss is an evolutionary phenomenon whereby organisms are able to gain fitness by not performing “leaky” functions. A biological function is considered leaky when some (but not all) of its products are available to the broader community and not just the organisms expending their own resources to perform the function. The Black Queen Hypothesis predicts that evolution will favor loss of leaky functions from individuals in a community until the number of function-performing “helpers” is low enough that the private advantage retained by helpers balances the fitness benefit of becoming a loss-of-function “beneficiary”. Evolution experiments using an *Escherichia coli* strain obligately dependent on a leaky, toxin-removing plasmid demonstrated that plasmid-containing helpers and plasmid-free beneficiaries coexisted for more than 1,000 generations despite both being in scramble competition over a single limiting resource. Genomic analysis of isolates taken from various time points within this experiment revealed evidence of speciation-like dynamics across 3 replicate populations: i) helpers and beneficiaries formed distinct phylogenetic clades, ii) different genes were consistently mutated in helper clones and in beneficiary clones, and iii) alleles that provided a fitness advantage for helpers were sometimes deleterious in beneficiaries (and vice versa). In order to test whether this relatively short-term ecological divergence would be stable over longer time scales, we recapitulated this system using the digital evolution platform Avida. We report here our efforts to examine the stability of Black Queen speciation over 100,000s of generations and in the presence of sexual recombination.