Pathogens adapting to new hosts or constantly shifting to escape the defenses of their natural hosts are subject to measurable evolutionary forces, and understanding these forces is critical to predicting emergence of infectious diseases. The avian pathogens *Mycoplasma synoviae* and *Mycoplasma gallisepticum* share two horizontally transferred traits, sialidase activity and VlhA adhesins, that are subject to distinct selective pressures and evolve at different rates in each species, making them an ideal system to study evolutionary dynamics. We genotypically and phenotypically assessed both traits in numerous strains of each species grown in axenic culture, and found distinct patterns favoring diversity in *M. synoviae* and conservation in *M. gallisepticum*. We used measured selection values from each species to calculate the evolvability, or capacity to permanently change in response to diversifying natural selection, of each trait. Both sialidase and VlhA were significantly evolvable in *M. synoviae* but not in *M. gallisepticum*, suggesting that the evolvability of a gene and its encoded trait can thus be driven by genomic context. To test the prediction that sialidase and VlhA will exert their calculated evolvability in their natural host habitat, we examined the input and out populations of a single strain of each pathogen before and after infection of leghorn chickens. Output populations of *M. synoviae* exhibited significant functional and genotypic diversity, whereas output populations of *M. gallisepticum* remained significantly unchanged from their input populations. These findings demonstrate the relevance of mathematically devised evolvability to *in vivo* disease states, and suggests that genomic context of potentially variable traits represent a new aspect to include in predictive modeling of evolution in pathogens and emerging infectious disease.