In bacteria, plasmids can move horizontally between cells of the same and different species through the process of conjugation. When a plasmid imposes a fitness cost on its bacterial host, a sufficiently high level of conjugation is required to maintain the extrachromosomal element in the population (effectively as a molecular parasite). For costly plasmids with low conjugation rates, their long-term persistence presents a paradox. Prime examples of this paradoxical persistence concern plasmids that house antibiotic resistance genes, which can be costly in the absence of antibiotics. Focusing on such plasmids, in this talk, I will describe how plasmid-host coevolution produces more persistent plasmids (and thereby greater stability of drug resistance), offering a potential resolution of the plasmid paradox. Furthermore, in multi-plasmid multi-species communities, evolved persistence can also lead to heightened emergence of multi-drug resistant bacteria. Underlying the evolution of persistence is not only the diminution of plasmid-associated costs, but also an increase in the rate of conjugation itself. In order to properly measure conjugation rate in our system, it turns out that a new estimation approach is required. Thus, I will present a novel estimate derived from a branching process framework and implemented via an adjustment of the classic fluctuation analysis of Luria and Delbrück. Not only does conjugation itself evolve in our system, but conjugation between species has the potential to dramatically impact the evolution of antibiotic resistance. I will end with some preliminary data and models to understand how the adaptive trajectories for plasmid-borne genes are impacted by the presence of horizontal transfer, revisiting Wright’s fitness landscape metaphor in the process. In sum, the process of conjugation is critical to a deeper understanding of plasmid biology, affecting the persistence of these elements as well as the evolution of the genes they contain.