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[O4] PSEUDOMONAS STUTZERI CHANGES THE FITNESS LANDSCAPE OF EVOLVING BACILLUS VELEZENSIS

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Bacterial interaction can alter community structure, yet the mechanisms underpinning this effect remain unknown. Here, we investigate how bacterial interaction influences the evolution of phenotypic and genetic diversity. *Bacillus velezensis* SQR9 was allowed to evolve alone and in the presence of a partner species *Pseudomonas stutzeri* XL272 under biofilm condition. *B. velezensis* rapidly diversified into three ecotypes under both conditions but the frequency varied. These ecotypes displayed phenotypic trade-off among biofilm formation, swarming motility, free-living growing capacity, and exopolysaccharide production. Whole genome re-sequencing correlated these phenotypic changes with certain mutations, including *ywC*, *comP*, *degS*, *swrA* and *spoOF*. In contrast, *P. stutzeri* displayed no observable morphotype change when co-evolving with *B. velezensis*, but the parallel evolution in an unknown gene encoding capsular biosynthesis protein increased its exopolysaccharide production in coculture. The evolved *P. stutzeri* variants altered the fitness landscape of *B. velezensis* ecotypes, allowing a cheater ecotype to outcompete the matrix-producing ecotypes. These findings are in accordance with the “Black Queen Hypothesis”: adaptive function loss that occurs through the reliance on a partner species.