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Predicting Plasmid Promiscuity Could Help Fight Resistance



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Bacterial plasmids spread antibiotic resistance, virulence, and many other traits. Eva Top and colleagues of the University of Idaho, Moscow, show that the range of bacteria in which plasmids have resided over evolutionary time can be inferred based entirely on information from plasmid DNA. "Using a



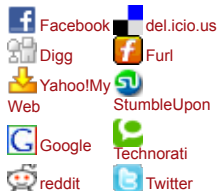
so-called genomic signature, we found that plasmids known to have narrow host ranges have signatures that are similar only to a set of closely related hosts," says Top. "In contrast, promiscuous plasmids, known to replicate in diverse

proteobacteria, have genomic signatures that are either similar to those of a wide range of bacterial chromosomes, or that are different from all bacterial chromosomes sequenced to date. This strongly suggests that the DNA sequence of a plasmid is like a book that tells stories about where-in which bacteria-the plasmid has previously resided." The research is important, she says, because it could help predict which additional bacteria might be serving as hosts for resistance- or virulence-carrying plasmids. "Our genomic signature tool can provide insight into the promiscuity and potential reservoirs of plasmids and other mobile genetic elements in the horizontal gene pool," she concludes.

(H. Suzuki, H. Yano. C. J. Brown, and E. M. Top. 2010. Predicting plasmid promiscuity based on genomic signature. J. Bacteriol. 192: 6045-6055.)

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