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Recent lateral gene transfer from *Pasteurella multocida* into *Haemophilus influenzae*

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Haemophilus influenzae is a gram-negative bacterium that exclusively colonizes humans. Nonencapsulated strains of the bacterium are found in the upper respiratory tract of healthy humans, but can also cause the respiratory diseases otitis media, bronchitis, and pneumonia. Many of the chromosomal genes of *H. influenzae* were acquired by lateral transfer from other bacterial genera. Recently, we investigated a cluster of unusually virulent nonencapsulated *H. influenzae* implicated in human invasive disease. An island between *aspA* and *groES* in which a urease gene cluster present in *H. influenzae* had been replaced by a homolog of *Neisseria meningitidis mtrF* was discovered (Erwin *et al.*, 2005). We compared the *aspA-groES* region with that of *Pasteurella multocida*, a member of the same family of bacteria. The two genomes have scattered synteny and share about 83% of their DNA. Both species have natural genetic transformation and use the same recognition site for DNA uptake. The *mtrF* gene is found between *aspA* and *groES* in *P. multocida*, within a somewhat larger island that includes a homolog of *fsxA*. The *H. influenzae mtrF* island is 95-100% identical to the region in *P. multocida*, as compared to 80% similarity in flanking genes. The direction of transfer is indicated by the presence of pseudogene fragments of *fsxA* persisting in *H. influenzae*. Because MtrF contributes to erythromycin resistance in *Neisseria*, we hypothesized that the gene transfer event occurred during the antibiotic era. To test this hypothesis, we collaborated with Dr. Vivek Kapur (University of Minnesota) to test isolates of *P. multocida* from domestic poultry and wild fowl for the presence of *mtrF*. Long and inverse PCR was used to identify genes between *aspA* and *groES* in six wild-type *Pasteurella* genomes. This is the first report of gene exchange between *H. influenzae* and a pathogen of our domestic species.