

AUTHOR'S CORRECTION

Genetic Evidence that *Legionella pneumophila* RpoS Modulates Expression of the Transmission Phenotype in Both the Exponential Phase and the Stationary Phase

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Volume 72, no. 5, p. 2468–2476, 2004. Pages 2468–2474: “*mip*” should read “*magA*.” The *mip* nucleotide sequence file (GenBank accession number S71704), used to design probes for Northern analysis (Fig. 1), was mislabeled in GenBank and instead describes the gene *magA* (P. Hoffman, personal communication). As recently reported (M. F. Hiltz, G. R. Sisson, A. K. C. Brassinga, E. Garduno, R. A. Garduno, and P. S. Hoffman, J. Bacteriol. **186**:3038–3045, 2004), this error, which has now been corrected, led to incorrect assignment of Mip homology to MagA homologues in other bacterial species. MagA is a 20-kDa protein containing a conserved motif of AhpD-type reductases, encoded within the 65-kb pathogenicity island of *Legionella pneumophila* Philadelphia-1 strains and highly expressed in the mature intracellular form of *L. pneumophila* (R. A. Garduno, E. Garduno, M. Hiltz, and P. S. Hoffman, Infect. Immun. **70**:6273–6283, 2002; A. K. C. Brassinga, M. F. Hiltz, G. R. Sisson, M. G. Morash, N. Hill, E. Garduno, P. H. Edelstein, R. A. Garduno, and P. S. Hoffman, J. Bacteriol. **185**:4630–4637, 2003; and M. F. Hiltz, G. R. Sisson, A. K. C. Brassinga, E. Garduno, R. A. Garduno, and P. S. Hoffman, J. Bacteriol. **186**:3038–3045, 2004). Consistent with the presence of RhoS-specific promoter sequences upstream of *magA* and Western analysis (M. F. Hiltz, G. R. Sisson, A. K. C. Brassinga, E. Garduno, R. A. Garduno, and P. S. Hoffman, J. Bacteriol. **186**:3038–3045, 2004), RpoS and, to a lesser extent, LetA/LetS and LetE induce expression of *magA* in the stationary phase. We did not analyze expression of *mip*, encoding the macrophage infectivity potentiator. The results of the paper are not affected by this correction.