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Letter to the Editor

Pantoea clinical isolates cannot be accurately assigned to species based on metabolic profiling

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To the Editor

We wish to comment on a recent clinical report of *Pantoea agglomerans* (1), motivated by the enduring influence that such reports have on regulatory assessment of *P. agglomerans* biocontrol strains for beneficial agricultural application as natural plant disease control alternatives.

Pantoea and *P. agglomerans* are ecologically diverse taxa that have undergone substantial taxonomic revisions, which can confuse identification efforts (2, 3). Identification in clinical reports (1, 4) is often based on metabolic phenotyping, an inadequate approach for *Pantoea* species resolution (5, 6). Databases for standard metabolic tests such as an API system (bioMerieux SA, Marcy l'Etoile, France) lack reference depth essential to discriminate *P. agglomerans* from the other 13 *Pantoea* species, and best-available matching can deliver false identity as *P. agglomerans*. Use of API Coryne (a gram-positive Actinobacteria kit) in this report (1) probably further complicates identification.

Recently, multilocus sequencing and proteomic analyses of clinical isolates initially reported as *P. agglomerans* found that many were misidentified and deserved reassignment to other *Pantoea* species or even other enterobacterial genera (2, 5, 6).

We appreciate the impracticality of integrating additional steps in routine clinical diagnostics, but in published case reports application of the most sensitive technology must be warranted to ensure unambiguous identification. Moreover, although conservation of published isolates by authors or culture collections is imperative for independent identity confirmation as technology and taxonomy advance, obtaining even recently published clinical isolates unfortunately is rarely successful. This is a major obstacle to investigating "pathogenic potential of *P. agglomerans*" (1, 4), a recurrent inference despite historical misidentification of this species and absence of evidential support for animal pathogenicity/toxicity (2).

We hope this comment will foster dialog and collaboration between clinical and environmental bacteriology communities essential to resolve the enigma of *P. agglomerans*.

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