

## Letter to the Editor

Misidentification slanders *Pantoea agglomerans* as a serial killer

Madam,

*Pantoea agglomerans* is an ecologically versatile species that has important beneficial applications in agriculture as a biological alternative to antibiotic use for orchard protection against phytopathogenic bacteria.<sup>1</sup> Disease-suppressive, biocontrol isolates are among the most effective tools available to manage fire blight, an invasive threat to global apple and pear production. *P. agglomerans*-based products are registered for biocontrol in the USA, Canada and New Zealand, but clinical reports have been a regulatory obstacle in Europe. Thus, the recent report of a fatal bacteraemia outbreak attributed to *P. agglomerans* is alarming and would have significant socio-economic impact, if the conclusion of clinical pathogenicity was correct.<sup>2</sup>

There is mounting evidence that many, if not most, *P. agglomerans* clinical reports are based upon inaccurate isolate identification, resulting from investigators' reliance on inadequate identification methods and/or obsolete nomenclature.<sup>3</sup> The *P. agglomerans*–*Enterobacter agglomerans*–*Erwinia herbicola* complex has experienced several taxonomic revisions,<sup>3</sup> and both biochemical profiling as well as 16S rRNA gene sequencing lack the resolution needed to discriminate *P. agglomerans sensu stricto* isolates.<sup>4</sup> Despite conclusive demonstration using *gyrB* sequencing and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) that a number of clinical strains archived in reputable culture collections do not belong to the genus *Pantoea* and even less to the species *P. agglomerans*, most remain erroneously catalogued.<sup>3,5</sup> Inaccurate identification has been shown for 95.5% of '*P. agglomerans*' clinical strains in the American Type Culture Collection (ATCC), a reference used to identify the Brazilian outbreak pathogen.<sup>3</sup>

The authors correctly recognized the difficulties involved in routine biochemical identification of *P. agglomerans* and appropriately applied *gyrB* sequencing in their characterization of isolates from a nosocomial outbreak in Brazil.<sup>2</sup> They reported their isolates as *P. agglomerans* based on a 100% sequence identity of their *gyrB* sequences with that of strain ATCC 27990, which was deposited in GenBank by our laboratory (GenBank nucleotide database: FJ617358). However, this strain is not *P. agglomerans* but rather belongs to an unnamed

new species most closely related to *Enterobacter* spp. included within the Brenner's Biotype XII.<sup>3,5</sup> Nucleotide sequence identity between ATCC 27990 and type strain *P. agglomerans* LMG 1286<sup>T</sup> is 83% for *gyrB*, well below accepted species or genus thresholds (Figure 1). We have reconfirmed that a BLAST search of both the nucleotide and the protein databases using the *gyrB* sequence of ATCC 27990 returns not a single *Pantoea* within the 100 best hits, indicating a simple author error in database navigation and/or reporting. Regrettably, this error has resulted in an alarming misrepresentation of *P. agglomerans* as a 'serial killer'. The potential for serious, lasting consequences on regulatory evaluation of plant-beneficial *P. agglomerans* biocontrol products necessitates correction of the clinical report and the related GenBank entries (nucleotide database: JN051137 and JN084037).

## Conflict of interest statement

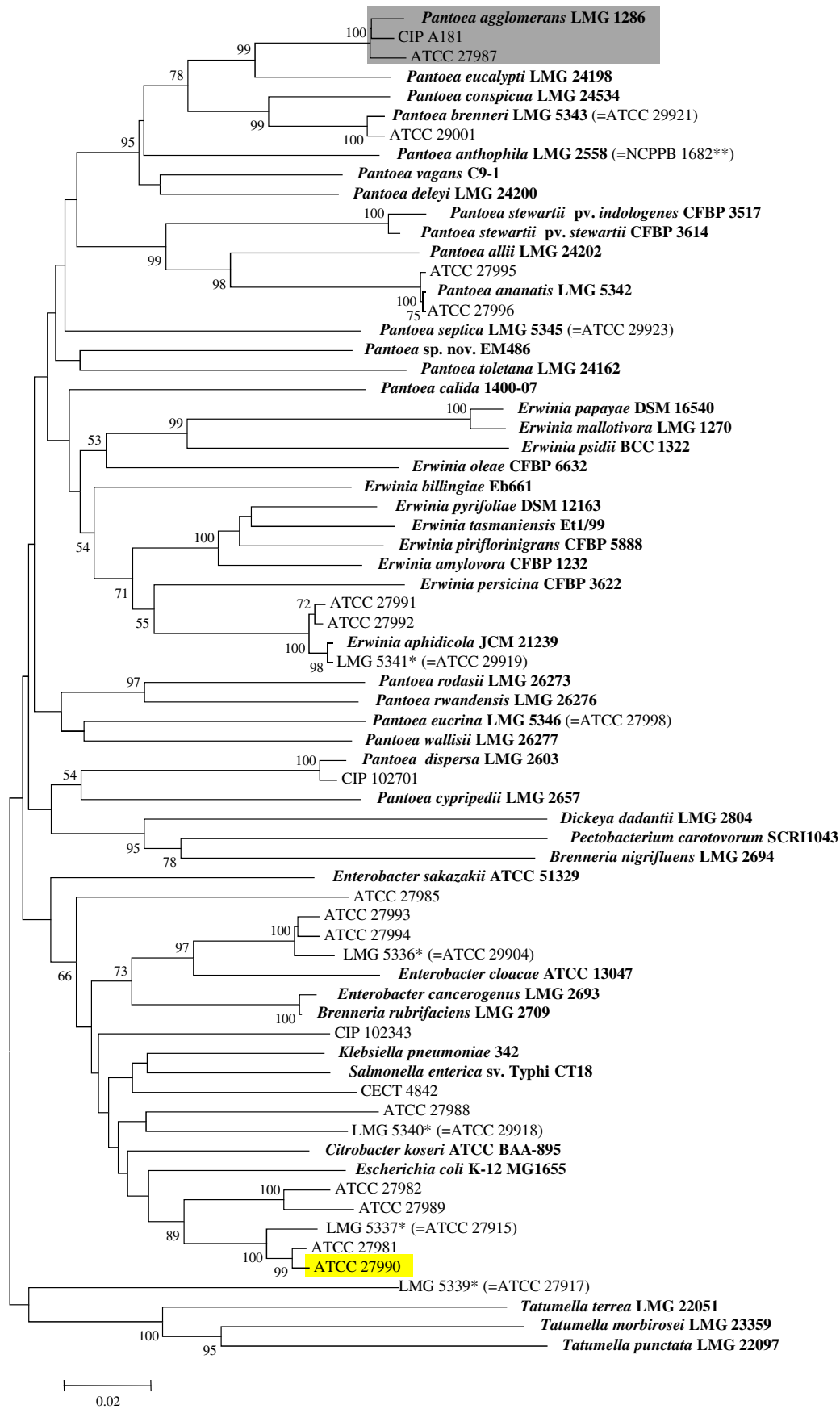
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## References

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**Figure 1.** Phylogenetic position of ATCC 27990 (yellow box) used as the reference to identify a Brazilian outbreak pathogen, compared with true *Pantoea agglomerans* (grey box) and clinical isolates received from culture collections as *P. agglomerans* or basonyms *Erwinia herbicola* and *Enterobacter agglomerans*.

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