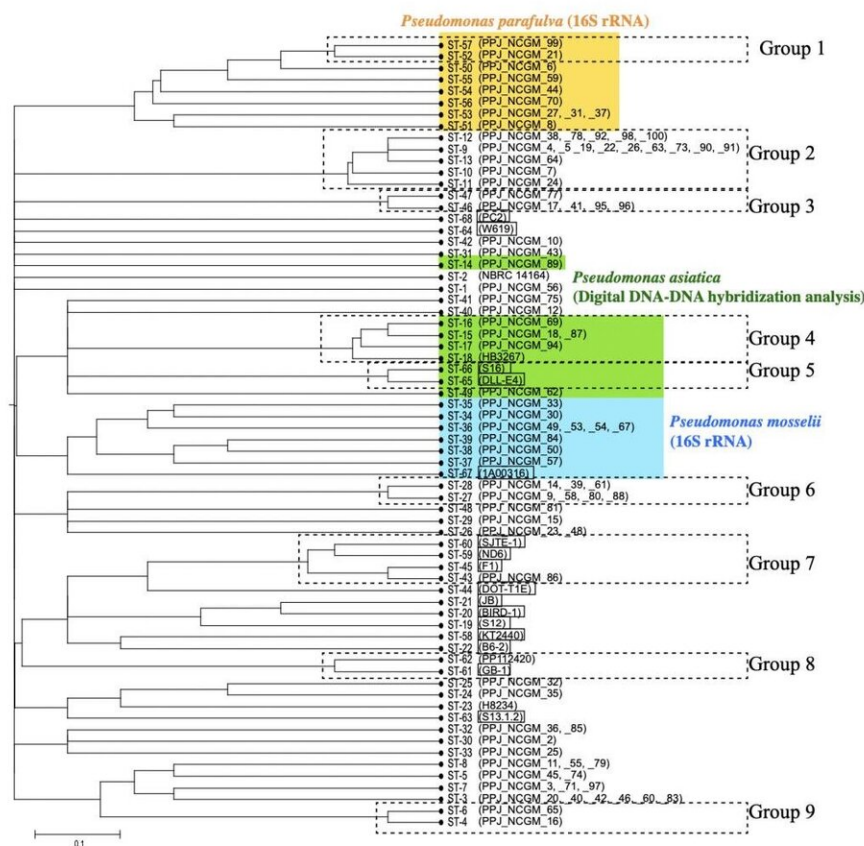


Genetic typing of a bacterium with biotechnological potential

December 6 2019



Tree of *P. putida* sequence types (STs). Squares indicate environmental isolates. Dash lines indicate clonal complex (relatively close ST types). Credit: Kanazawa University

Pseudomonas putida is a bacterium occurring in soil, aquatic environments and plants. Although the virulence of *Pseudomonas p.*—the ability of the bacterium to infect its host and inflict a disease—is considered to be low, infection in severely ill patients can be lethal. *P. putida* strains (also called isolates) have been found in hospitals, e.g. in urine, blood or wound discharge from patients, and such clinical isolates have been found to display resistance to drugs. Now, Kohei Ogura from Kanazawa University and colleagues have performed gene sequencing for various *P. putida* isolates originating from both environmental and clinical sites.

Genetic typing of different *P. putida* strains enables researchers to determine which are the more virulent ones. This is important because *P. putida* has high biotechnological value. Indeed, *P. putida* is a perfect microbiological platform for '[metabolic engineering](#),' in which selected biochemical processes within the cells of an organism are stimulated so that the cells produce more of a particular substance. (Examples of metabolic engineering include the industrial production of beer, wine and cheese.)

The researchers applied a technique known as multilocus sequence typing (MLST), a method used in [molecular biology](#) for the genetic typing of more than one locus—a locus refers to the position on a chromosome where a specific gene is located.

The MLST technique is based on obtaining DNA sequences of several so-called 'housekeeping [genes](#)': genes that are needed for the maintenance of the basic functioning of a cell. In order to arrive at a valid MLST scheme, typically 100 isolates are required. Ogura and colleagues used 106 isolates, with 16 having an environmental origin and 90 coming from clinical sites. For the MLST scheme, the scientists used 8 housekeeping genes.

The scientists not only obtained the first MLST scheme for *P. putida*, they also were able to deduce that the studied bacterium isolates are clonal, meaning that they share common ancestry. At the same time, the researchers found that "our MLST scheme reflects the genetic diversity of *P. putida* group isolated from both clinical and environmental sites."

More information: Kohei Ogura et al, A multilocus sequence typing scheme of *Pseudomonas putida* for clinical and environmental isolates, *Scientific Reports* (2019). [DOI: 10.1038/s41598-019-50299-6](https://doi.org/10.1038/s41598-019-50299-6)

Provided by Kanazawa University

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