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LETTER TO THE EDITOR

The *Pseudomonas aeruginosa* Population among Cystic Fibrosis Patients in Quebec, Canada: a Disease Hot Spot without Known Epidemic Isolates

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The Canadian province of Quebec has prevalence rates of cystic fibrosis (CF) that are among the highest in the world, with an average of 1 in 2,500 newborns (1; http://www.cysticfibrosis.ca), and up to 1 in 902 in the region of Saguenay–Lac-Saint-Jean (2–4). Still, unlike in other provinces (5–7), molecular epidemiology data are not available for the most common respiratory pathogen associated with this disease, *Pseudomonas aeruginosa* (8). A recent national molecular typing study included isolates from two clinics in Montreal, the largest city in Quebec (9), but analyses were not directed toward investigating each province individually. Here, we sought to describe the population structure of *P. aeruginosa* in Quebec to improve the epidemiological basis for infection control and patient management. We were mainly interested in the prevalences of epidemic strains, which have been reported in the Prairie Provinces and Ontario and are generally associated with worse clinical prognoses (7, 9, 10).

We selected all sequenced Quebec isolates from the International *Pseudomonas* Consortium Database (http://ipcd.ibis.ulaval.ca) (11) and 11 reference strains (Data Set S1). The final data set of 298 genomes comprised isolates from five CF clinics scattered across southern Quebec, as well as from environmental sources. We performed a core genome phylogenetic analysis with SaturnV (https://github.com/ejfresch/saturnV) (12), and produced *in silico* molecular typing using Short Read Sequence Typing for Bacterial Pathogens (SRST2) v0.2.0 (13).

No geographic structure emerged from the five CF clinics represented (Fig. 1). However, multiple clones were shared among two or more clinics. Based on molecular sequence typing (14; https://pubmlst.org/), the most pervasive clones (sequence type 17 [ST17], ST155, and ST179), including well-characterized clone C (15), are all widely distributed around the world and likely reflect environmental abundance rather than patient-to-patient transmission (16). This is further supported by the presence of environmental isolates, which incidentally came from hospital sinks (Data Set S1), within ST155 and ST179. Encouragingly, not a single isolate in this study corresponded to epidemic strains identified in Ontario (Liverpool epidemic strain and epidemic strain B [7]) or the Prairies (Prairie epidemic strain [PES; ST192] [5]). It is not clear whether this is due to

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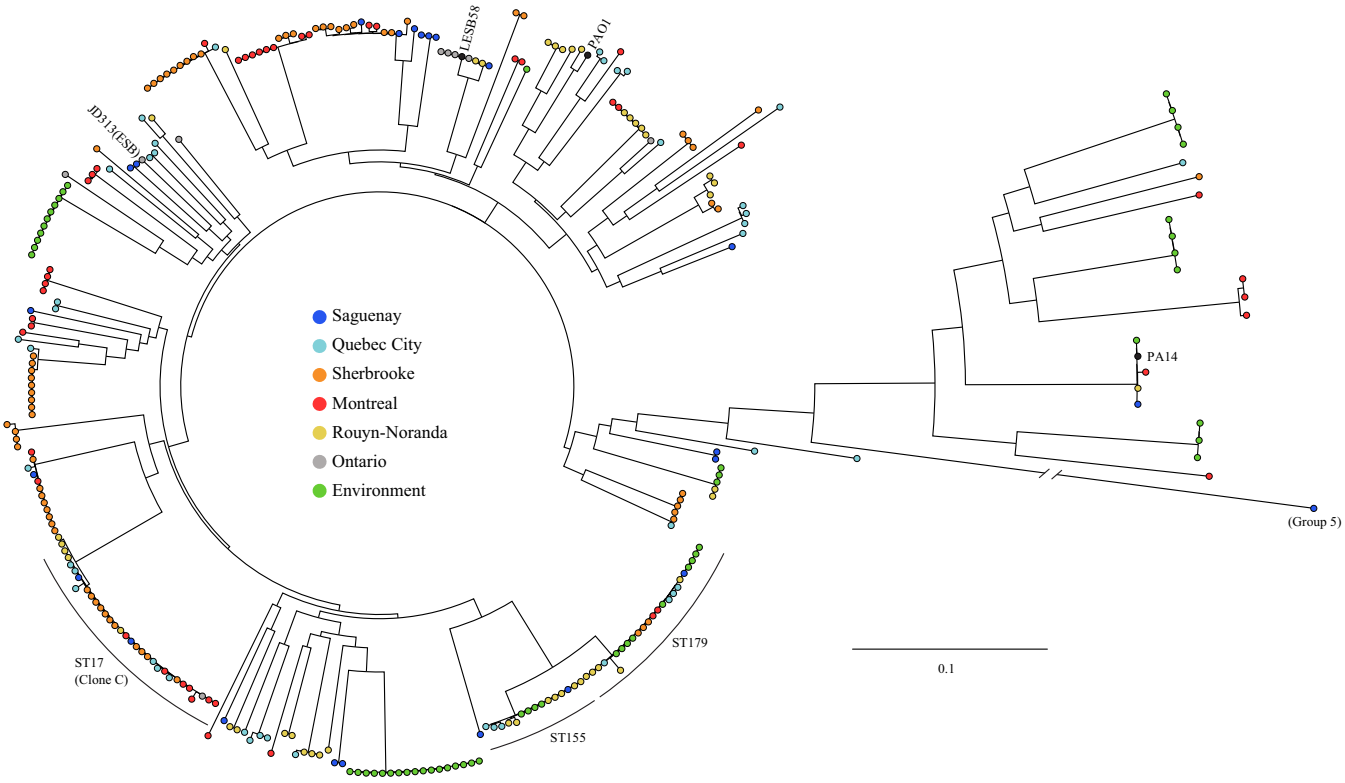

FIG 1 Phylogenetic tree of 298 *P. aeruginosa* isolates (66,805 SNPs, 1,000 bootstraps). Three refence isolates are labeled and represented in black (LESB58 is the reference for the Liverpool epidemic strain). Ontario's epidemic strain B (ESB) is also labeled. The most pervasive sequence types (STs) are identified. Group 5 isolates are relatively rare among CF patients (21). The same tree with genome IDs, detailed STs, and bootstrap values is provided in Fig. S1. Most environmental isolates are from hospitals and dental clinics of the greater Montreal area. Intrapatient redundancy, i.e., identical strains from the same patient, was not removed (numbers of patients: Quebec City, $n = 33$; Rouyn-Noranda, $n = 31$; Montreal, $n = 27$; Sherbrooke, $n = 20$; and Saguenay, $n = 17$). Isolates from the same clinic spanned up to a year for Montreal, Quebec City, and Saguenay, 3 years for Sherbrooke, and 6 years for Rouyn-Noranda; all clinical isolates were collected between 2007 and 2016 (see Data Set S1 for details).

differences in infection control, human population demographics, or environmental *P. aeruginosa* populations among Canadian provinces. Australian studies provide evidence that, except for known epidemic strains (17), CF strains are a sample of the environmental *P. aeruginosa* population (18, 19). More in-depth analyses are forthcoming for CF clinics where genomic data can be associated with patient identifier (ID), age, study time point, etc. Unfortunately, this type of information, although essential to direct further investigation of genomic data, proved extremely difficult to obtain.

Heterogeneity in *P. aeruginosa* population structure across Canada alone emphasizes the need for more customized patient care in the context of CF respiratory infections. This, of course, only adds to the great variability in antimicrobial resistance among *P. aeruginosa* isolates (11, 20). Canadian molecular epidemiology of *P. aeruginosa* may benefit from similar nationwide data from the United States. But, as mentioned in a recent review (16), there is a void to be filled in the literature in this regard.

Accession number(s). Assembled genomes used in this study are available as part of BioProject accession number PRJNA325248 (International *Pseudomonas aeruginosa* Consortium [IPC] genome sequencing project). The accession numbers for newly sequenced genomes are RWKX00000000 to RWVK00000000. The complete list of accession numbers is provided in Data Set S1 in the Supplemental Material.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/JCM.02019-18.

SUPPLEMENTAL FILE 1, PDF file, 0.3 MB.

SUPPLEMENTAL FILE 2, XLS file, 0.1 MB.

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