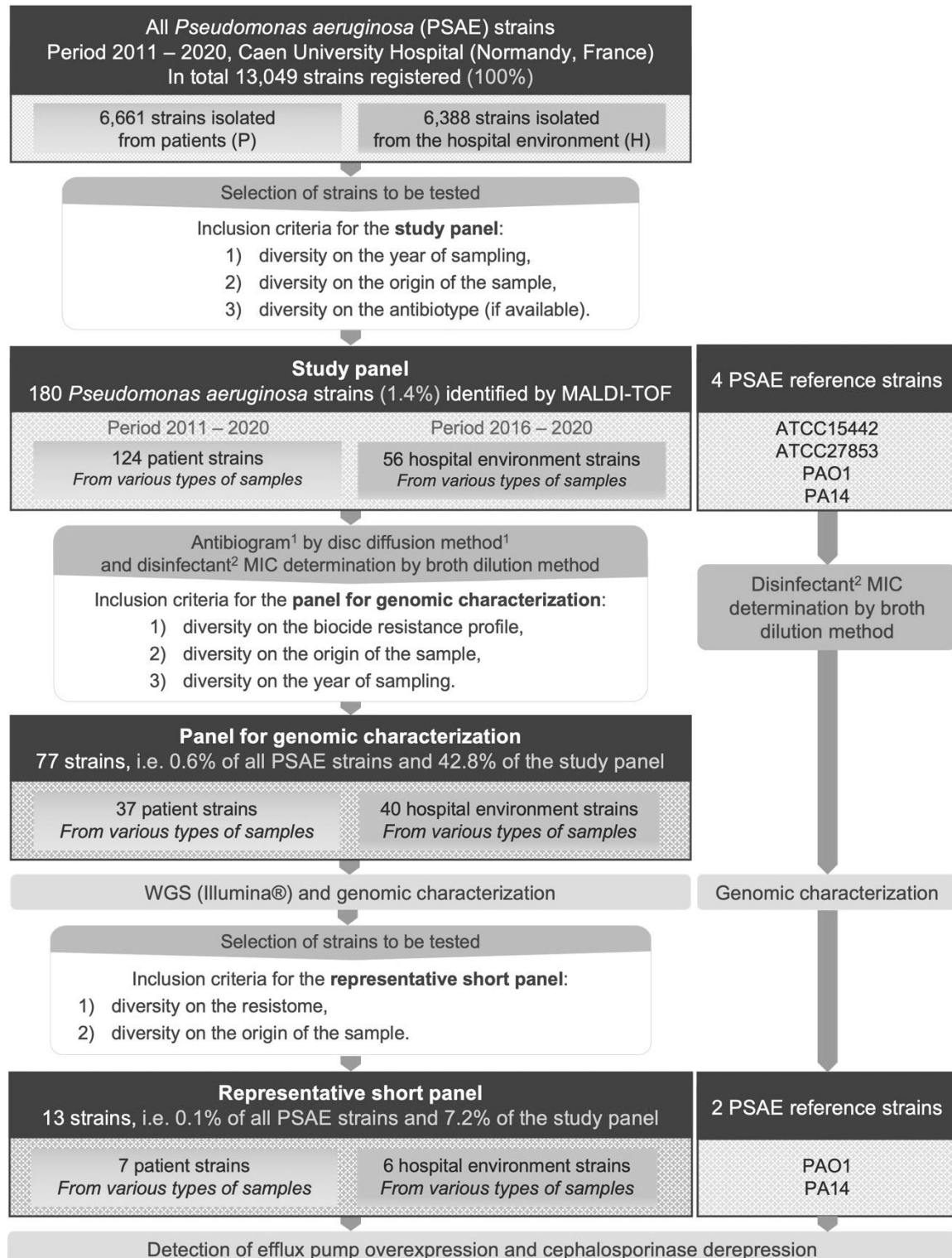


Supplementary Material

Supplementary Data 1. Characteristic of the strains used in the study panel (Part 1), in the panel for genomic characterization (Part 2) and in the representative short panel (Part 3).

Please see the joined Excel file named Supplementary_data1.xls

Supplementary Data 2. Selection diagram for the study and reference strains. ¹: 6 classes tested, i.e., 16 antibiotics for hospital use; ²: didecyldimethylammonium chloride; ATCC: American Type Culture Collection; H: strains isolated from the hospital environment; MALDI-TOF: Matrix Assisted Laser Desorption Ionisation/Time Of Flight; P: strains isolated from patients; PSAE: *Pseudomonas aeruginosa*; UHC: University Hospital Center; WGS: Whole Genome Sequencing.



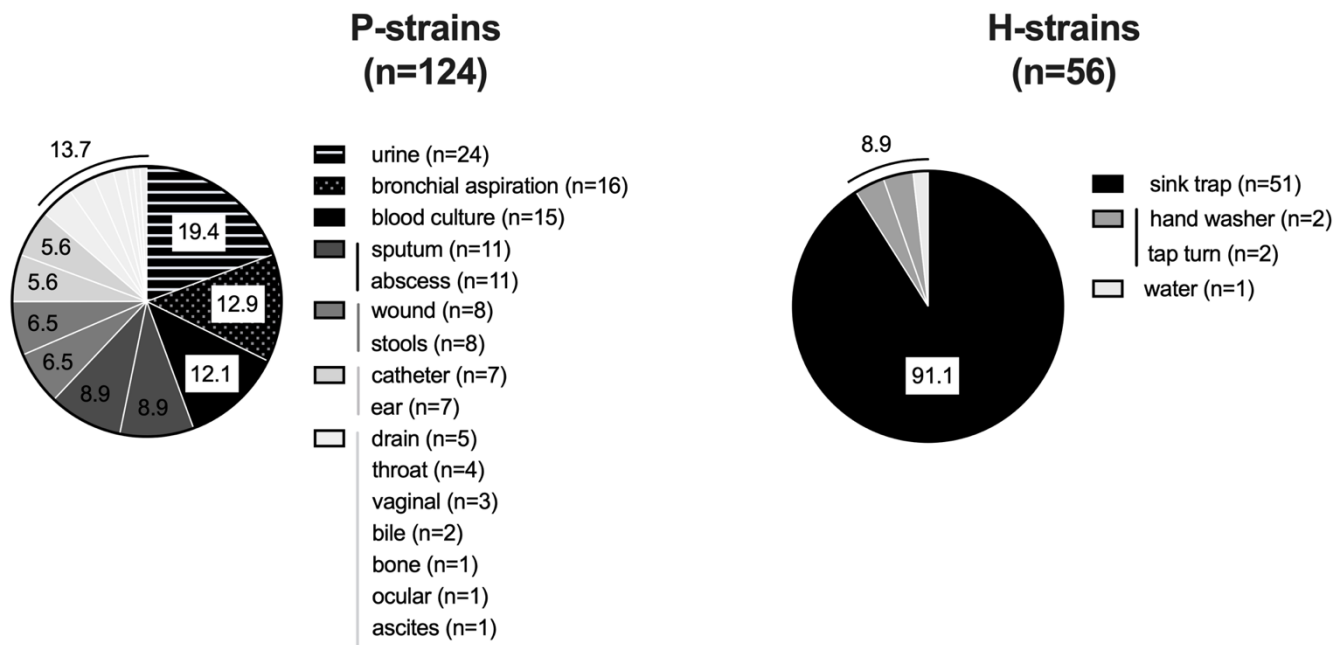
Supplementary Data 3. The sequence of oligonucleotide primers.

Target gene	Type	Sequence 5'-3'
<i>mexA</i>	Forward	CTGGAAGGTCGCCTCGAATT
	Reverse	AGGATGGCCTTCTGCTTGAC
<i>mexB</i>	Forward	CGATCGTGATGACCTCCCTG
	Reverse	TACCCAGAAGATCGCCAGGA
<i>oprM</i>	Forward	CCTGGACTACGCGAAGATCC
	Reverse	GAGCTGGTAGTACTCGTCGC
<i>mexE</i>	Forward	GGTCTACGCCTACTTCGACG
	Reverse	CCTGGTTGTGCGAGGAAGTCC
<i>mexF</i>	Forward	TGATCCTGATCGTGCCGATG
	Reverse	GCGAACTCGACGATCAGGAT
<i>oprN</i>	Forward	GGGTCTGTTCACTCTGCTG
	Reverse	GGTCGGATCGTCGAACTGTT
<i>gyrB</i>	Forward	CACGTACGACTCTTCCAGCA
	Reverse	GAACACCATGTGGTGCAGAC

Supplementary Data 4. Temporal distribution: of all *Pseudomonas aeruginosa* strains isolated at Caen UHC over 2011-2020, the study panel, and of genomic characterization panel.

		All <i>P. aeruginosa</i> strains isolated (N=13,049)		Study panel (n=180)	Panel for genomic characterization (n=77)
Sampling year		Strains/year	Average strains/year [IC95%]	Strains/year	Strains/year
P-strains	2011	630	666.1 [615.1-717.1]	11	4
	2012	526		14	3
	2013	576		12	2
	2014	655		14	5
	2015	659		12	3
	2016	737		12	6
	2017	715		11	4
	2018	725		16	7
	2019	722		10	-
	2020	716		12	3
	Total	6,661	-	124	37
H-strains	2011	283	638.8 [389.2-888.4]	-	-
	2012	284		-	-
	2013	291		-	-
	2014	310		-	-
	2015	589		-	-
	2016	1,026		20	11
	2017	542		19	14
	2018	989		12	12
	2019	957		4	2
	2020	1,117		1	1
	Total	6,388	-	56	40
General total		13,049	1,304.9 [1,012.1-1,597.7]	180	77

Supplementary Data 5. Distribution by sample type of the study panel (n=180). H: strains isolated from the hospital environment; P: strains isolated from patients.



Supplementary Data 6. Antimicrobial resistance for the study panel (n=180). (a) Occurrence of antibiotics resistance for patient strains (n=124) and hospital environment strains (n=56) of the study panel. For antibiotics, resistance breakpoints were set according to the CASFM/EUCAST 2021, or 2019 edition if a breakpoint was not available, and for DDAC, the DS breakpoint was the concentration in the disinfectant solution following the manufacturer's instructions. Fisher's test for populations independence for human and environmental hospital strains resistance frequency. (b) Number of strains (in percent) of the study panel (n=180) showing resistance for 0 to 7 antibiotic classes. The hatched areas represent profiles that also accumulate DS to the disinfectant DDAC. The different antibiotic categories are penicillins (ticarcillin, ticarcillin-clavulanic acid, piperacillin, piperacillin-tazobactam), carbapenems (imipenem, meropenem), monobactam (aztreonam), cephalosporins (ceftazidime, ceftolozane-tazobactam, cefepime), phosphonic acid (fosfomycin), aminoglycosides (amikacin, tobramycin, gentamicin) and fluoroquinolones (ciprofloxacin and levofloxacin) were considered. Fisher's test for populations independence for DS to DDAC and loss of susceptibility to more than three categories of antibiotics. ns: p-value > 0.05, *: p-value ≤ 0.05, **: p-value ≤ 0.01, and ****: p-value ≤ 0.0001 after analysis by Fisher's independence test. DDAC: didecylmethylammonium chloride; DS: decreased susceptibility; H: hospital environment; MDR: multidrug-resistant; P: strains isolated from patients; XDR: extensively drug-resistant.

