



Figure S1: Distribution of participating hospitals. The number of hospitals from each Spanish region is indicated.

Figure S2. Minimum-spanning trees (MST) of the cgMLST of the XDR *P. aeruginosa* isolates from 2017 and 2022 studies. PAO1 (ST549), PA14 (ST253) and PA7 (1195) reference strains assemblies were included in the schema seed. After the exclusion of paralogous loci and poor-quality assemblies, the cgMLST for loci presence threshold of 95% in the isolates was composed of 4487 genes, following chewBBACCA v3.1.2. instructions. For trees visualization Grape Tree program was used. Each circle represents a single ST and the size of that circle corresponds to the number of isolates ascribed to that particular ST. **A.** Each colour represents a different region and year. PAO1, PA14 and P7 are represented with white circles **B.** Each colour represents a different acquired β -lactamase.

