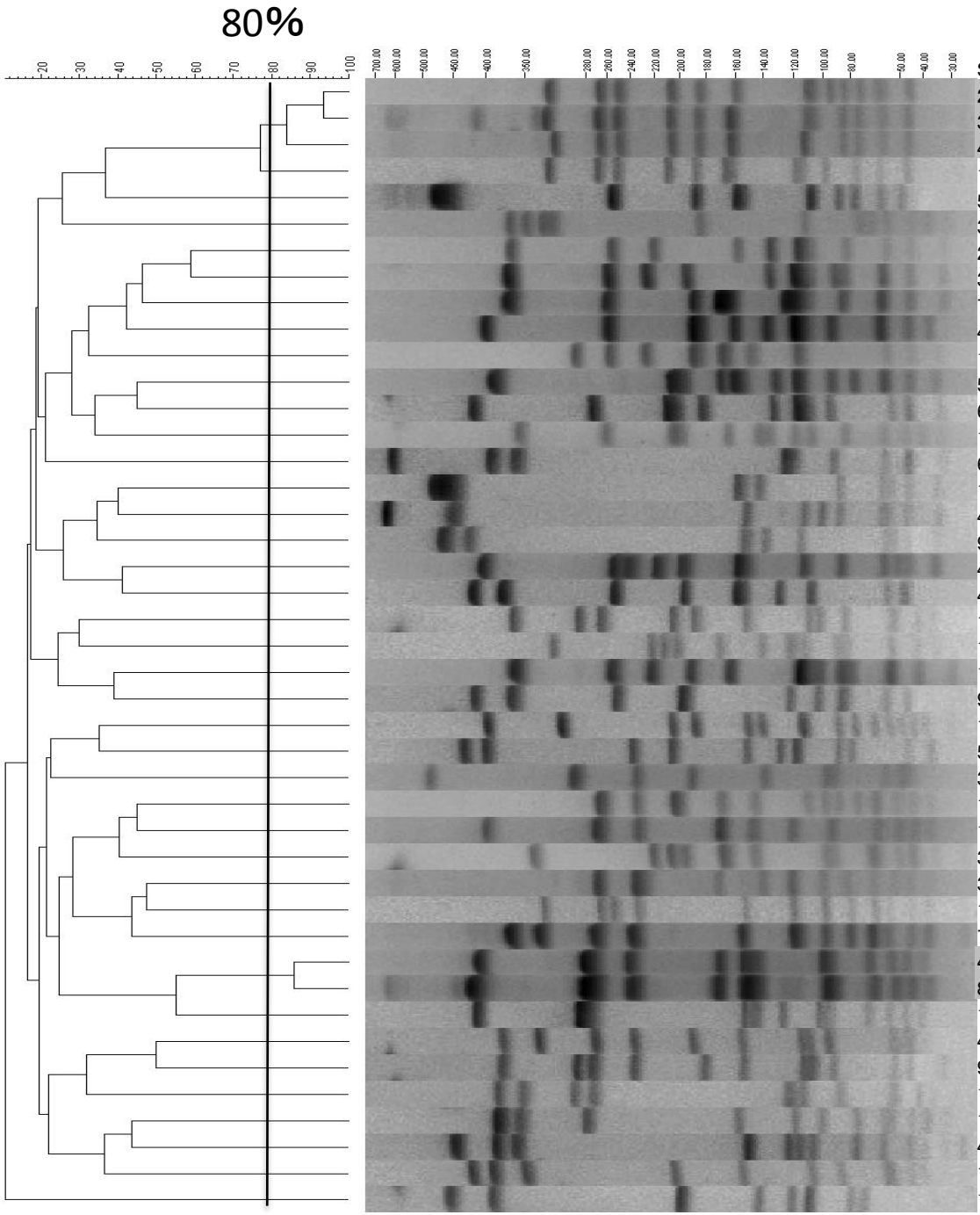

Strain	ST	β-l	PBP3 Group
21	161		Ⅲ
32	161		Ⅲ
40	161		Ⅲ
147	161		Ⅲ
58	3	TEM-1	Ⅲ
35	430		Ⅲ
27	1415		Ⅲ
31	535		Ⅲ
78	714		Ⅲ
41	1418		Ⅲ
19	1413		Ⅲ
54	107		Ⅲ
6	57	TEM-1	Ⅲ
109	1420		Ⅲ
68	1419	TEM-1	NC
146	3		Ⅲ
42	836	TEM-1	Ⅲ
93	3	TEM-1	Ⅲ
48	695		Ⅲ
4	3	TEM-1	others
120	259		Ⅲ
137	760		Ⅲ
106	535		Ⅱb
96	14	TEM-1	Ⅲ
140	1429		Ⅲ
5	165	TEM-1	Ⅲ
34	1029		Ⅲ
10	549		Ⅲ
100	549		Ⅲ
3	1428		Ⅲ
38	549		Ⅲ
138	249		Ⅲ+Ⅱc
79	249		Ⅲ
44	549		Ⅲ
84	549		Ⅲ
162	549		Ⅲ
45	57	ROB-1	Ⅲ
90	57	TEM-1	NC
111	242	TEM-1	Ⅲ
144	1422		Ⅲ
46	597	TEM-1	Ⅲ
141	160		Ⅲ
157	165	TEM-1	Ⅲ

Cluster 1

Cluster 2

SDC 3.
Pulsed-field gel electrophoresis (PFGE) of 43 *Haemophilus influenzae* strains with minimum inhibitory concentrations (MICs) of ampicillin ≥ 8 mg/L: genetically β-lactamase-nonproducing ampicillin resistant (gBLNAR) (n=30), genetically β-lactamase-producing ampicillin-resistant (gBLPAR) (n=2), and genetically β-lactamase-producing amoxicillin/clavulanic acid-resistant (gBLPACR) (n=11). Isolates with ≥ 80% relatedness were considered to belong to the same cluster (Clusters 1 and 2). On the right, the strain, the sequence type (ST), β-lactamase production, the group based on amino acid substitutions in penicillin-binding protein 3 (PBP3), and the genotype are reported. There are two clusters of BLNAR isolates with identical STs (ST161 and 549).