

Table S1. Capsular types and clones recovered from invasive disease and carriage between 2001 and 2003 in Portugal

Serotype	No. of isolates		Total no. of isolates	OR (CI _{95%}) ^a	No. of PFGE clusters	Most common clones ^b (n)	Fisher exact test p-value (heterogeneity of invasive potential) ^c
	Invasive disease	Carriage					
14	61	52	113	2.03 (1.35-3.06)	9	14-1 [ST156+ST790] (72), 14-2 [ST15+ST409] (31)	0.003*
19F	7	93	100	0.11 (0.04-0.24)	8	19F-1 [ST177+ST179] (84)	<0.001*
23F	20	70	90	0.44 (0.25-0.74)	12	23F-1 [ST338+ST732] (52), 23F-3 [ST33] (16)	0.003*
6B	14	69	83	0.31 (0.16-0.56)	15	6B-1 [ST887] (40), 6B-2 [ST176] (19)	<0.001*
6A	14	64	78	0.33 (0.17-0.61)	19	6A-1 [ST460+ST1880] (19), 6A-2 [ST1879] (12), 6A-3 [ST1878] (14)	<0.001*
3	43	28	71	2.63 (1.57-4.47)	6	3-1 [ST180+ST232] (51), 3-2 [ST162+ST1220+ST1646] (14)	0.004*
19A	25	45	70	0.89 (0.52-1.51)	11	19A-1 [ST81+ST634+ST994] (27), 19A-4 [ST193+ST202+ST416] (9), 19A-5 [ST416+ST1151] (9)	<0.001*
11A	10	42	52	0.37 (0.16-0.76)	4	11A-1 [ST62+ST408] (47)	0.004*
1	44	1	45	78.09 (13.22-3115.57)	2	1-1 [ST228+ST306] (31), 1-2 (14) [ST304+ST350]	1.000
35F	3	35	38	0.13 (0.03-0.43)	3	35F-1 [ST1368] (22), 35F-2 (15) [ST446]	0.040
16F	1	36	37	0.04 (0.00-0.26)	3	16F-1 [ST30] (34)	0.027
4	32	4	36	13.78 (4.84-54.02)	6	4-1 [ST1221] (18), 4-2 (10) [ST247]	0.530
15B/C	2	33	35	0.09 (0.01-0.37)	1	15B/C-1 [ST411] (34)	1.000
18C	18	13	31	2.29 (1.05-5.13)	9	18C-1 [ST1233+ST1381] (11)	0.083
NT ^d	7	24	31	0.46 (0.17-1.12)	13	NT-1 [ST344] (10)	<0.001*
9V	16	14	30	1.88 (0.85-4.20)	2	9V-1 [ST156+ST162+ST557+ST838] (29)	1.000
8	27	1	28	46.17 (7.55-1878.37)	3	8-1 [ST53+ST327] (22)	1.000
10A	9	19	28	0.76 (0.30-1.78)	3	10A-1 [ST97+ST1226] (26)	0.095
7F	21	3	24	11.78 (3.49-62.06)	1	7F-1 [ST191] (24)	1.000

34	3	18	21	0.27 (0.05-0.92)	5	34-1 [ST2001] (12)	0.003*
6C	4	14	18	0.46 (0.11-1.47)	3	6C-1 [ST1150] (7), 6C-2 [ST395] (6)	0.114
22F	8	8	16	1.63 (0.53-5.01)	3	22F-1 [ST443] (6), 22F-2 [ST433] (8)	0.001*
18A	4	12	16	0.54 (0.13-1.78)	4	18A-1 [ST241] (8)	0.021
23B	3	11	14	0.44 (0.08-1.67)	2	23B-1 [ST439] (13)	1.000
5	12	0	12	Inf (4.58-Inf)	1	5-1 [ST1223] (12)	1.000
23A	1	11	12	0.15 (0.00-1.01)	3	23A-1 [ST2404] (8)	1.000
20	10	0	10	Inf (3.68-Inf)	5	20-1 [ST235] (4)	1.000
12B	10	0	10	Inf (3.68-Inf)	3	12B-1 [ST218] (5)	1.000
31	3	7	10	0.69 (0.11-3.05)	3	31-1 [ST1766+ST2002] (8)	1.000
24F	6	3	9	3.26 (0.69-20.24)	4	24F-1 [ST72](3), 24F-3 (3) [ST230+ST1708]	0.786
33F	5	4	9	2.03 (0.43-10.29)	1	33F-1 [ST1655] (9)	1.000
37	0	9	9	0.00 (0.00-0.81)	1	37-1 [ST447] (9)	1.000
9N	6	1	7	9.80 (1.18-451.08)	2	9N-1 [ST66] (6)	0.143
9L	6	0	6	Inf (1.92-Inf)	2	9L-1 [ST1654] (6)	1.000
15A	2	4	6	0.81 (0.07-5.67)	1	15A-1 [ST63+ST2108] (6)	1.000
21	0	6	6	0.00 (0.00-1.37)	2	21-1 [ST1877] (4)	1.000
Other ^e	18	15	33				
Total	475	769	1244				

^a OR and CI_{95%} are shown for serotypes that had at least five isolates. Highlighted in bold are OR estimates whose confidence interval does not include one. Inf, infinite.

^b Clones defined as described in Materials and Methods. Numbers in parenthesis indicate the number of isolates found in each clone.

^c Evidence for heterogeneity of invasive disease potential of clones sharing the same serotype is indicated by significant p-values after FDR correction marked by asterisks.

^d NT – non-typable

^e Other serotypes: 15F, 29, 39, and 42 found only in carriage; 7C, 10F, 13, 19C, 24B, 25F, and 35B found only in invasive disease; 9A, 17F, and 38 found in both.