

Additional file 1 for “Evidence of antimicrobial resistance-conferring genetic elements among pneumococci isolated prior to 1974”

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Supplementary Table 1.

Genes identified in the phage-Tn916 composite element found in pneumococcal isolate 18C/3.

| Gene ^a | O ^b | Bp ^c | Predicted Product |
|-------------------------------|----------------|------------------|--|
| ICESp18C_3_00001 | R | 957 | phage lytic amidase |
| ICESp18C_3_00002 | R | 336 | phage holin, LL-H family |
| ICESp18C_3_00003 | R | 300 | hypothetical protein |
| ICESp18C_3_00004 | R | 351 | hypothetical protein |
| ICESp18C_3_00005 | R | 204 | conserved domain protein |
| ICESp18C_3_00006 | R | 117 | hypothetical protein |
| ICESp18C_3_00007 | R | unk ^d | -- |
| ICESp18C_3_00008 | R | 351 | prophage protein |
| ICESp18C_3_00009 | R | 3606 | TMP repeat family |
| ICESp18C_3_00010 | R | 351 | hypothetical protein |
| ICESp18C_3_00011 | R | 381 | prophage protein |
| ICESp18C_3_00012 | R | 414 | putative major tail protein |
| ICESp18C_3_00013 | R | 369 | putative conserved structural protein |
| ICESp18C_3_00014 | R | 327 | hypothetical protein |
| ICESp18C_3_00015 | R | 339 | hypothetical protein |
| ICESp18C_3_00016 | R | 312 | hypothetical protein |
| ICESp18C_3_00017 | R | 189 | hypothetical protein |
| ICESp18C_3_00018 | R | 183 | hypothetical protein |
| ICESp18C_3_00019 | R | 846 | major phage head protein |
| ICESp18C_3_00020 | R | 585 | phage scaffold protein |
| ICESp18C_3_00021 | R | 1349 | putative phage head morphogenesis protein |
| ICESp18C_3_00022 | R | 1302 | phage portal |
| ICESp18C_3_00023 | R | 1299 | phage terminase large subunit |
| ICESp18C_3_00024 | R | 501 | phage terminase small subunit |
| ICESp18C_3_00025 | R | 405 | phage protein |
| ICESp18C_3_00026 | R | 438 | hypothetical protein |
| ICESp18C_3_00027 | R | 459 | hypothetical protein |
| ICESp18C_3_00028 | R | 162 | hypothetical protein |
| ICESp18C_3_00029 | R | 696 | hypothetical protein |
| ICESp18C_3_00030 | R | 1344 | hypothetical protein |
| ICESp18C_3_00031 | R | 822 | hypothetical protein |
| ICESp18C_3_00032 | R | 507 | hypothetical protein |
| ICESp18C_3_00033 | R | 828 | hypothetical protein |
| ICESp18C_3_00034 | R | 318 | hypothetical protein |
| ICESp18C_3_00035 ^e | F | 120 | hypothetical protein |
| ICESp18C_3_00036 ^e | F | 315 | conjugative transposon protein |
| ICESp18C_3_00037 ^e | F | 384 | conjugative transposon protein |
| ICESp18C_3_00038 ^e | F | 1386 | conjugative transposon FtsK/SpoIIIE-family protein |

| | | | |
|-------------------------------|---|------|---|
| ICESp18C_3_00039 ^e | F | 186 | conjugative transposon FtsK/SpoIIIE-family |
| ICESp18C_3_00040 ^e | F | 1206 | putative conjugative transposon replication initiation factor |
| ICESp18C_3_00041 ^e | F | 222 | conjugative transposon protein |
| ICESp18C_3_00042 ^e | F | 498 | conjugative transposon protein |
| ICESp18C_3_00043 ^e | F | 231 | putative conjugative transposon membrane protein |
| ICESp18C_3_00044 ^e | F | 2448 | conjugative transposon ATP/GTP-binding protein |
| ICESp18C_3_00045 ^e | F | 2178 | conjugative transposon membrane protein |
| ICESp18C_3_00046 ^e | F | 1002 | putative cell wall hydrolase |
| ICESp18C_3_00047 ^e | F | 915 | putative conjugative transposon exported protein |
| <i>tet(M)</i> ^e | F | 1920 | conjugative transposon tetracycline resistance protein, <i>tet(M)</i> |
| ICESp18C_3_00049 ^e | R | 354 | putative conjugative transposon regulatory protein |
| ICESp18C_3_00050 ^e | F | 147 | hypothetical protein |
| ICESp18C_3_00051 ^e | F | 423 | putative conjugative transposon regulatory protein |
| ICESp18C_3_00052 ^e | F | 231 | hypothetical protein |
| ICESp18C_3_00053 ^e | R | 129 | hypothetical protein |
| ICESp18C_3_00054 ^e | R | 252 | hypothetical protein |
| <i>xis</i> ^e | F | 204 | excisionase |
| <i>int</i> ^e | F | 1218 | integrase |
| ICESp18C_3_00057 | R | 1203 | hypothetical protein |
| ICESp18C_3_00058 | R | 486 | hypothetical protein |
| ICESp18C_3_00059 | R | 360 | hypothetical protein |
| ICESp18C_3_00060 | R | 483 | hypothetical protein |
| ICESp18C_3_00061 | R | 765 | hypothetical protein |
| ICESp18C_3_00062 | R | 231 | hypothetical protein |
| ICESp18C_3_00063 | R | 342 | hypothetical protein |
| ICESp18C_3_00064 | F | 240 | hypothetical protein |
| ICESp18C_3_00065 | R | 171 | hypothetical protein |
| ICESp18C_3_00066 | R | 204 | hypothetical protein |
| ICESp18C_3_00067 | F | 690 | hypothetical protein |
| ICESp18C_3_00068 | F | 792 | hypothetical protein |
| ICESp18C_3_00069 | F | 951 | hypothetical protein |
| <i>int</i> | F | 1128 | phage integrase |

a. Genes listed in order from left to right as depicted in Figure 1.

b. Orientation of the gene: F, forward; R, reverse.

c. Bp: gene length in base pairs.

d. Precise length of the sequence gap is unknown.

e Tn916-associated region.

Supplementary Table 2.**Genes identified in the novel ICE element, ICESpPN1, which was found in the pneumococcal isolate PN1.**

| Gene ^a | O ^b | Bp ^c | Predicted Product |
|-------------------|----------------|-----------------|--|
| PN1_ICE_00001 | F | 174 | hypothetical protein |
| <i>repA</i> | F | 780 | replication initiation protein A, RepA |
| PN1_ICE_00003 | F | 102 | hypothetical protein |
| PN1_ICE_00004 | F | 1359 | putative DNA methylase |
| PN1_ICE_00005 | F | 450 | hypothetical protein |
| PN1_ICE_00006 | F | 381 | arsenate reductase-like glutaredoxin family protein |
| PN1_ICE_00007 | F | 234 | hypothetical protein |
| PN1_ICE_00008 | F | 663 | putative caax amino protease family protein |
| PN1_ICE_00009 | F | 591 | hypothetical protein |
| PN1_ICE_00010 | F | 810 | hypothetical protein |
| PN1_ICE_00011 | F | 729 | truncated traD/traG family protein |
| PN1_ICE_00012 | F | 243 | hypothetical protein |
| PN1_ICE_00013 | F | 855 | putative membrane protein |
| PN1_ICE_00014 | F | 360 | hypothetical protein |
| PN1_ICE_00015 | F | 2358 | hypothetical protein |
| PN1_ICE_00016 | F | 2814 | M23 peptidase domain protein |
| PN1_ICE_00017 | R | 609 | hypothetical protein pseudogene |
| PN1_ICE_00018 | R | 165 | hypothetical protein |
| PN1_ICE_00019 | F | 411 | Ig domain protein, 2 domain protein |
| PN1_ICE_00020 | F | 6225 | putative conjugative transposon DNA recombination protein pseudogene |
| PN1_ICE_00021 | F | 285 | hypothetical protein |
| PN1_ICE_00022 | F | 300 | hypothetical protein |
| PN1_ICE_00023 | F | 183 | hypothetical protein |
| PN1_ICE_00024 | F | 183 | hypothetical protein |
| PN1_ICE_00025 | F | 177 | hypothetical protein |
| PN1_ICE_00026 | F | 108 | hypothetical protein |
| PN1_ICE_00027 | F | 738 | ABC-type antimicrobial peptide transport protein |
| PN1_ICE_00028 | F | 2016 | ABC transporter permease |
| PN1_ICE_00029 | F | 1575 | histidine kinase |
| PN1_ICE_00030 | F | 597 | response regulator |
| PN1_ICE_00031 | F | 2955 | putative lantibiotic biosynthesis protein |
| PN1_ICE_00032 | F | 2124 | putative lantibiotic transporter protein |
| PN1_ICE_00033 | F | 642 | putative parvulin-like peptidyl-prolyl isomerase |
| PN1_ICE_00034 | F | 498 | hypothetical protein |
| <i>plcR</i> | F | 867 | putative transcriptional regulator, PlcR |
| PN1_ICE_00036 | F | 135 | hypothetical protein |
| PN1_ICE_00037 | F | 252 | hypothetical protein |
| PN1_ICE_00038 | F | 303 | hypothetical protein |
| PN1_ICE_00039 | F | 1347 | putative protein kinase |
| PN1_ICE_00040 | F | 918 | ABC transporter, ATP-binding protein |
| PN1_ICE_00041 | F | 801 | putative ABC-2 transporter permease protein |
| PN1_ICE_00042 | F | 474 | transposase, IS200 family |
| PN1_ICE_00043 | F | 222 | hypothetical protein |
| PN1_ICE_00044 | F | 270 | putative excisionase |

PN1_ICE_00045 F 1509 putative integrase

- a. Genes listed in order from left to right as depicted in Figure 1.
- b. Orientation of the gene: F, forward; R, reverse.
- c. Bp: gene length in base pairs.