

ORIGINAL ARTICLE

Study of *Staphylococcus aureus* N315 Pathogenic Genes by Text Mining and Enrichment Analysis of Pathways and Operons

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SUMMARY

Background: *Staphylococcus aureus* (*S. aureus*) is a versatile pathogen found in many environments and can cause nosocomial infections in the community and hospitals. *S. aureus* infection is an increasingly serious threat to global public health that requires action across many government bodies, medical and health sectors, and scientific research institutions.

Methods: In the present study, *S. aureus* N315 genes that have been shown in the literature to be pathogenic were extracted using a bibliometric method for functional enrichment analysis of pathways and operons to statistically discover novel pathogenic genes associated with *S. aureus* N315.

Results: A total of 383 pathogenic genes were mined from the literature using bibliometrics, and subsequently a few new pathogenic genes of *S. aureus* N315 were identified by functional enrichment analysis of pathways and operons.

Conclusions: The discovery of these novel *S. aureus* N315 pathogenic genes is of great significance to treat *S. aureus* induced diseases and identify potential diagnostic markers, thus providing theoretical fundamentals for epidemiological prevention.

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Supplementary Table

Table S1. The list of pathogenic genes participated in at least five pathways.

Locus tag	No.	Pathway
SA1736	16	sau00010 sau00053 sau00071 sau00280 sau00310 sau00330 sau00340 sau00380 sau00410 sau00561 sau00620 sau00625 sau01100 sau01110 sau01120 sau01130
SA0143	12	sau00010 sau00071 sau00350 sau00620 sau00625 sau00626 sau00650 sau01100 sau01110 sau01120 sau01130 sau01220
SA1226	10	sau00260 sau00261 sau00270 sau00300 sau01100 sau01110 sau01120 sau01130 sau01210 sau01230
SA1225	10	sau00260 sau00261 sau00270 sau00300 sau01100 sau01110 sau01120 sau01130 sau01210 sau01230
SA2008	9	sau00290 sau00650 sau00660 sau00770 sau01100 sau01110 sau01130 sau01210 sau01230
SA1184	9	sau00020 sau00630 sau01100 sau01110 sau01120 sau01130 sau01200 sau01210 sau01230
SA2204	9	sau00010 sau00260 sau00680 sau01100 sau01110 sau01120 sau01130 sau01200 sau01230
SA0679	9	sau00340 sau00350 sau00360 sau00400 sau00401 sau01100 sau01110 sau01130 sau01230
SA0512	9	sau00270 sau00280 sau00290 sau00770 sau01100 sau01110 sau01130 sau01210 sau01230
SA0471	8	sau00270 sau00920 sau01100 sau01110 sau01120 sau01130 sau01200 sau01230
SA1164	8	sau00260 sau00270 sau00300 sau01100 sau01110 sau01120 sau01130 sau01230
SA1150	8	sau00220 sau00250 sau00630 sau00910 sau01100 sau01120 sau01230 sau02020
SA2395	8	sau00010 sau00270 sau00620 sau00640 sau01100 sau01110 sau01120 sau01130
SA1245	8	sau00020 sau00310 sau00380 sau01100 sau01110 sau01120 sau01130 sau01200
SA1609	8	sau00010 sau00020 sau00620 sau01100 sau01110 sau01120 sau01130 sau01200
SA1227	7	sau00261 sau00300 sau01100 sau01110 sau01120 sau01130 sau01230
SA1228	7	sau00261 sau00300 sau01100 sau01110 sau01120 sau01130 sau01230
SA0431	7	sau00250 sau00910 sau01100 sau01110 sau01120 sau01130 sau01230
SA0430	7	sau00250 sau00910 sau01100 sau01110 sau01120 sau01130 sau01230
SA1858	7	sau00290 sau00770 sau01100 sau01110 sau01130 sau01210 sau01230
SA2155	7	sau00020 sau00620 sau01100 sau01110 sau01120 sau01130 sau01200
SA2334	7	sau00072 sau00280 sau00650 sau00900 sau01100 sau01110 sau01130
SA1244	7	sau00020 sau00310 sau01100 sau01110 sau01120 sau01130 sau01200
SA2127	7	sau00030 sau01100 sau01110 sau01120 sau01130 sau01200 sau01230
SA2318	7	sau00260 sau00270 sau01100 sau01110 sau01130 sau01200 sau01230
SA2319	7	sau00260 sau00270 sau01100 sau01110 sau01130 sau01200 sau01230
SA1545	7	sau00260 sau00680 sau01100 sau01120 sau01130 sau01200 sau01230
SA2425	6	sau00220 sau00230 sau00910 sau01100 sau01120 sau01200
SA0822	6	sau00220 sau00250 sau01100 sau01110 sau01130 sau01230
SA0821	6	sau00220 sau00250 sau01100 sau01110 sau01130 sau01230
SA0177	6	sau00220 sau01100 sau01110 sau01130 sau01210 sau01230
SA2294	6	sau00030 sau01100 sau01110 sau01120 sau01130 sau01200
SA2288	6	sau00040 sau00052 sau00500 sau00520 sau01100 sau01130
SA0697	6	sau00260 sau00561 sau00630 sau01100 sau01120 sau01130
SA1165	6	sau00260 sau00750 sau01100 sau01110 sau01120 sau01230
SA1199	6	sau00400 sau01100 sau01110 sau01130 sau01230 sau02024
SA1200	6	sau00400 sau01100 sau01110 sau01130 sau01230 sau02024
SA2427	5	sau00220 sau01100 sau01110 sau01130 sau01230
SA1299	5	sau00400 sau01100 sau01110 sau01130 sau01230
SA1347	5	sau00280 sau00640 sau01100 sau01110 sau01130
SA1940	5	sau00230 sau00240 sau00760 sau01100 sau01110

Table S1. The list of pathogenic genes participated in at least five pathways (continue).

Locus tag	No.	Pathway
SA1811	5	sau00562 sau00564 sau01100 sau01110 sau02024
SA1170	5	sau00380 sau00630 sau01110 sau01130 sau01200
SA1724	5	sau00230 sau00250 sau01100 sau01110 sau01130
SA1166	5	sau00260 sau01100 sau01110 sau01120 sau01230
SA1202	5	sau00400 sau01100 sau01110 sau01130 sau01230
SA1201	5	sau00400 sau01100 sau01110 sau01130 sau01230
SA1203	5	sau00400 sau01100 sau01110 sau01130 sau01230

Table S2. The novel pathogenic genes identified in the present study.

	Pathway analysis	Operon analysis	GO analysis
Most likely pathogenic genes	SA0819 SA0922 SA2397	SA1049 SA0849	
Probably pathogenic genes	SA0977 SA2285 SA0221 SA1004 SA1003 SA1001SA1751 SA0616 SA0617SA0793 SA0795 SA1193 SA1812 SA1813	SA0151 SA0152 SA0154	
May be pathogenic genes			SA2220 SA1924 SA0162 SA0605 SA0606 SA1072 SA1187 SA1548 SA1714 SA0875 SA0674