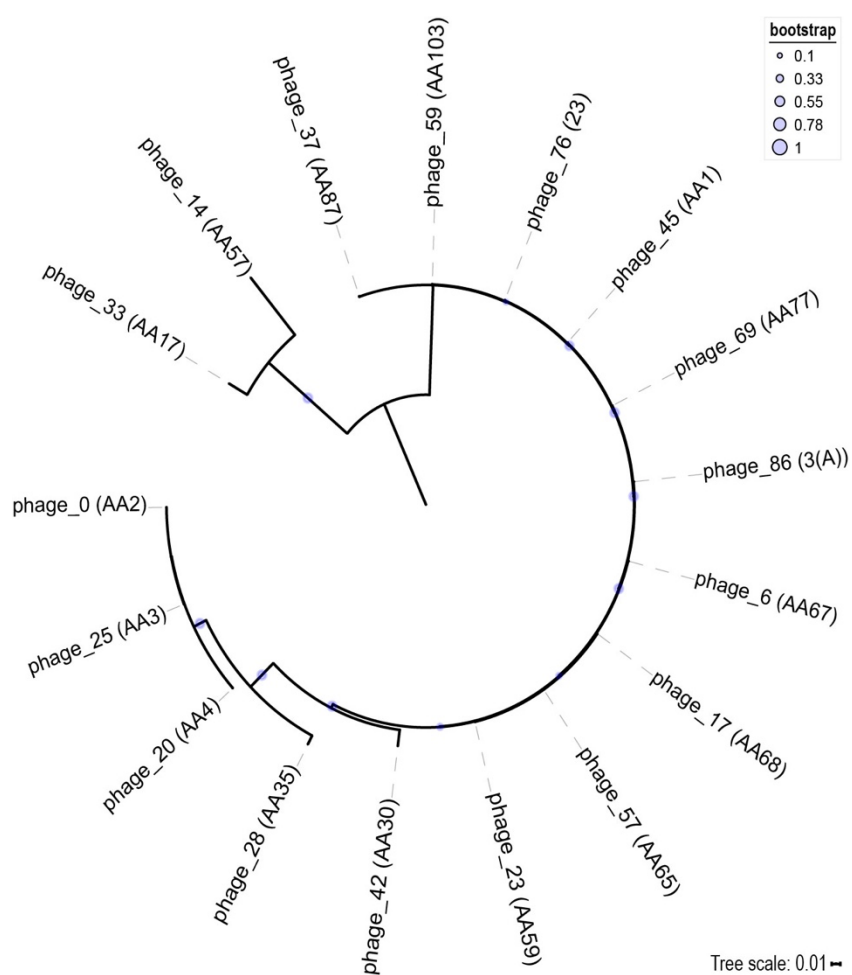


Examination of *Staphylococcus aureus* prophages circulating in Egypt

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Supplementary Materials

Supplemental Figures



Supplemental Figure 1. Phylogenetic tree for prophage cluster A prophage sequences. The *S. aureus* host strain is indicated in parentheses.

Supplemental Tables

Table S1. Prophage prediction statistics by strain.

Strain	WGS Accession	Isolation Source	# Prophages		
			Intact	Questionable	Incomplete
AA1	JAEOUR000000000	BAL	1	0	0
AA2	JAEOUZ000000000	Blood	3	0	0
AA3	JAEOVE000000000	BAL	3	0	1
AA4	JAEOVM000000000	Pus	3	0	0
AA5	JAEOVQ000000000	Blood	1	1	2
AA6	JAEOVX000000000	Aspirate	1	1	2
AA8	JAEOWM000000000	Blood	1	0	3
AA13	JAEOUV000000000	BAL	0	1	3
AA14	JAEOUW000000000	Pus	0	1	2
AA17	JAEOUX000000000	Blood	2	0	0
AA18	JAEOUY000000000	Pus	1	0	2
AA22	JAEOVA000000000	Pus	1	2	1
AA23	JAEOVB000000000	Pus	0	1	2
AA27	JAEOVC000000000	Pus	0	1	1
AA29	JAEOVD000000000	Urine	0	1	2
AA30	JAEOVF000000000	Blood	2	0	3
AA31	JAEOVG000000000	Pus	1	1	2
AA32	JAEOVH000000000	Pus	1	0	2
AA33	JAEOVI000000000	Pus	1	2	1
AA35	JAEOVJ000000000	Pus	2	0	2
AA36	JAEOVK000000000	Blood	2	0	2
AA39	JAEOVL000000000	Aspirate	1	0	3
AA41	JAEOVN000000000	Blood	1	0	2
AA45	JAEOVO000000000	Blood	2	0	0
AA46	JAEOVP000000000	Pus	0	2	1
AA51	JAEOVR000000000	Pus	2	0	1
AA52	JAEOVS000000000	Pus	0	1	3
AA53	JAEOVT000000000	Urine	1	1	3
AA55	JAEOVU000000000	Pus	1	1	2
AA57	JAEOVV000000000	Sputum	2	1	2
AA59	JAEOVW000000000	Pus	2	1	1
AA60	JAEOVY000000000	MiniBAL	0	1	2

Strain	WGS Accession	Isolation Source	# Prophages		
			Intact	Questionable	Incomplete
AA61	JAEOVZ000000000	Pus	0	1	3
AA62	JAOWA000000000	Pus	1	2	1
AA63	JAOWB000000000	MiniBAL	1	1	3
AA64	JAOWC000000000	Pus	1	1	3
AA65	JAOWD000000000	Urine	3	0	1
AA67	JAOWE000000000	Blood	3	0	1
AA68	JAOWF000000000	Blood	3	0	0
AA69	JAOWG000000000	Blood	2	0	1
AA70	JAOWH000000000	Pus	3	0	1
AA76	JAOWI000000000	Pus	1	1	6
AA77	JAOWJ000000000	Pus	3	0	0
AA78	JAOWK000000000	Pus	1	0	0
AA79	JAOWL000000000	Sputum	0	2	2
AA80	JAOWN000000000	Urine	1	1	7
AA87	JAOWO00000000	Pus	2	0	1
AA91	JAOWP000000000	Pus	1	1	2
AA92	JAOWQ000000000	Pus	0	1	1
AA93	JAOWR000000000	Pus	1	1	2
AA94	JAOWS000000000	Blood	1	0	1
AA95	JAOWT000000000	Pus	1	0	1
AA99	JAOWU000000000	Sputum	1	0	1
AA101	JAOUS000000000	BAL	1	1	2
AA103	JAOUT000000000	Pus	1	0	1
AA104	JAOUU000000000	unknown	1	0	3
42 (B)	SUKU000000000	unknown	0	1	2
48	SUKQ000000000	unknown	1	0	3
41	SUKN000000000	unknown	0	1	4
6 (A)	SUKY000000000	unknown	3	0	1
42	SULE000000000	unknown	0	1	1
23	SUKK000000000	unknown	2	0	0
50	SUKR000000000	unknown	1	2	2
3 (B)	SUKH000000000	unknown	3	0	1
19	SUKG000000000	unknown	0	1	2
46	SUKP000000000	unknown	0	2	2
40	SUKM000000000	unknown	0	2	2
43	SUKO000000000	unknown	2	0	0

Strain	WGS Accession	Isolation Source	# Prophages		
			Intact	Questionable	Incomplete
15	SULC00000000	unknown	0	0	1
14	SULB00000000	unknown	1	1	5
16	SULD00000000	unknown	0	0	1
3 (A)	SUKX00000000	unknown	3	0	1
17	SWMQ00000000	unknown	0	0	1

Table S2. BLAST hits for the Egyptian *S. aureus* prophages.

Prophage ID	Host Strain	Length	Description	Accession #	Query Coverage	% ID
phage_0	AA2	26511	Staphylococcus phage SA780ruMSSAST101	NC_048711.1	100	99.95
phage_1	AA2	29363	Staphylococcus phage SA97	KJ716334.1	89	96.14
phage_2	AA2	43262	Staphylococcus phage phi7401PVL DNA	AP012341.1	100	99.94
phage_3	AA94	49880	Staphylococcus phage 55-3	KR709303.1	66	96.3
phage_4	AA67	62863	Staphylococcus phage Sa2wa_st8	MK940809.1	73	99.94
phage_5	AA67	35427	Staphylococcus phage SA97	KJ716334.1	75	97.24
phage_6	AA67	28410	Staphylococcus phage SAP090B	GQ915271.1	81	97.73
phage_7	AA5	29682	Staphylococcus phage B166	KP893289.1	84	97.61
phage_8	AA93	16210	Staphylococcus phage SA13	JX094501.1	92	97.84
phage_9	AA51	64168	Staphylococcus phage SAP090B	GQ915271.1	36	97.7
phage_10	AA51	31799	Staphylococcus phage Sa2wa_st8	MK940809.1	99	99.97
phage_11	AA69	62863	Staphylococcus phage Sa2wa_st8	MK940809.1	73	99.94
phage_12	AA69	27700	Staphylococcus phage tp310-1	EF462197.1	79	97.34
phage_13	AA33	27203	Bacteriophage 92	AY954967.1	78	97.3
phage_14	AA57	34045	Staphylococcus phage IME1361_01	NC_048657.1	75	98.16
phage_15	AA57	13833	Bacteriophage 92	AY954967.1	70	98.16
phage_16	AA68	62862	Staphylococcus phage Sa2wa_st8	MK940809.1	73	99.94
phage_17	AA68	28102	Staphylococcus phage SAP090B	GQ915271.1	82	97.73
phage_18	AA68	31053	Staphylococcus phage TEM123	JQ779024.1	100	99.99
phage_19	AA4	70082	Staphylococcus phage SA97	KJ716334.1	39	96.14
phage_20	AA4	26350	Staphylococcus phage SA780ruMSSAST101	NC_048711.1	100	99.94
phage_21	AA4	43262	Staphylococcus phage phi7401PVL	AP012341.1	100	99.94
phage_22	AA59	53697	Staphylococcus phage Sa2wa_st8	MK940809.1	78	99.94
phage_23	AA59	28102	Staphylococcus phage SAP090B	GQ915271.1	82	97.73

Prophage ID	Host Strain	Length	Description	Accession #	Query Coverage	% ID
phage_24	AA3	34077	Staphylococcus phage phi7401PVL DNA	AP012341.1	96	99.84
phage_25	AA3	26511	Staphylococcus phage SA780ruMSSAST101	NC_048711.1	100	99.95
phage_26	AA3	29363	Staphylococcus phage SA97	KJ716334.1	89	96.14
phage_27	AA95	19196	Staphylococcus phage 55-3	KR709303.1	65	94.91
phage_28	AA35	48171	Staphylococcus phage SA7	KY695153.1	72	99.98
phage_29	AA35	40061	Staphylococcus phage SA97	KJ716334.1	62	97.55
phage_30	AA32	42886	Staphylococcus phage phiMR25	AB370205.1	61	94.7
phage_31	AA101	36605	Staphylococcus phage phiETA, strain: TY32	AP008954.1	74	96.98
phage_32	AA17	62671	Staphylococcus phage phiSa2wa_st121mssa	MG029518.1	68	98.57
phage_33	AA17	48021	Staphylococcus aureus phage SA345ruMSSAST8	NC_048713.1	82	99.84
phage_34	AA18	36270	Staphylococcus phage B166	KP893289.1	71	97.47
phage_35	AA80	45707	Staphylococcus aureus phage phi 12	AF424782.1	60	99.79
phage_36	AA87	60588	Staphylococcus phage phiSa2wa_st121mssa	MG029518.1	65	99.19
phage_37	AA87	59321	Staphylococcus phage SAP090B	GQ915271.1	39	97.74
phage_38	AA45	63945	Bacteriophage 85	AY954953.1	55	96.34
phage_39	AA45	34865	Staphylococcus phage SA780ruMSSAST101	NC_048711.1	100	99.33
phage_40	AA39	54537	Staphylococcus phage SA7	KY695153.1	63	99.97
phage_41	AA30	34597	Staphylococcus phage phi 11	AF424781.1	76	96.55
phage_42	AA30	28121	Staphylococcus phage tp310-1	EF462197.1	78	96.43
phage_43	AA64	22302	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	91	96.98
phage_44	AA6	54537	Staphylococcus phage SA7	KY695153.1	63	99.98
phage_45	AA1	45741	Staphylococcus phage SAP090B	GQ915271.1	50	97.73
phage_46	AA63	19610	Staphylococcus virus B122	MK290764.1	94	96.27
phage_47	AA55	30666	Bacteriophage 92	AY954967.1	70	97.3
phage_48	AA8	54537	Staphylococcus phage SA7	KY695153.1	63	99.98

Prophage ID	Host Strain	Length	Description	Accession #	Query Coverage	% ID
phage_49	AA99	49880	Staphylococcus phage 55-3	KR709303.1	66	96.3
phage_50	AA31	24806	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	92	96.89
phage_51	AA36	42543	Staphylococcus phage SA137ruMSSAST121PVL	MH384261.1	86	97.82
phage_52	AA36	55314	Staphylococcus phage SA7	KY695153.1	62	99.98
phage_53	AA53	44305	Staphylococcus aureus phage SA345ruMSSAST8	NC_048713.1	61	99.51
phage_54	AA62	36176	Staphylococcus phage UPMK_2	MG564297.1	70	97.1
phage_55	AA91	28172	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	86	96.98
phage_56	AA65	52914	Staphylococcus phage Sa2wa_st8	MK940809.1	77	99.94
phage_57	AA65	28102	Staphylococcus phage SAP090B	GQ915271.1	82	97.73
phage_58	AA65	25618	Staphylococcus phage TEM123	JQ779024.1	100	99.99
phage_59	AA103	59360	Staphylococcus phage SAP090B	GQ915271.1	39	97.73
phage_60	AA104	54549	Staphylococcus phage SA7	KY695153.1	63	99.93
phage_61	AA78	63535	Staphylococcus phage SAP090B	GQ915271.1	36	97.74
phage_62	AA76	47328	Staphylococcus phage phiMR11 DNA	AB370268.1	52	95.16
phage_63	AA22	27079	Bacteriophage 92	AY954967.1	78	97.3
phage_64	AA70	81781	Staphylococcus aureus phage phi 12	AF424782.1	50	99.82
phage_65	AA70	50286	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	69	98.3
phage_66	AA70	45450	Staphylococcus phage SA1014ruMSSAST7	NC_048710.1	68	99.17
phage_67	AA77	62863	Staphylococcus phage Sa2wa_st8	MK940809.1	73	99.94
phage_68	AA77	32539	Staphylococcus phage SA97	KJ716334.1	80	97.24
phage_69	AA77	31268	Staphylococcus phage SAP090B	GQ915271.1	73	97.73
phage_70	AA41	47772	Staphylococcus phage phiPVL108 DNA	AB243556.1	56	98.89
phage_71	50	14162	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	99	96.92
phage_72	48	48768	Staphylococcus phage phiETA3, strain: TY32	AP008954.1	50	98.08

Prophage ID	Host Strain	Length	Description	Accession #	Query Coverage	% ID
phage_73	43	60926	Staphylococcus phage Sa2wa_st8	MK940809.1	75	99.95
phage_74	43	55555	Staphylococcus phage SAP090B	GQ915271.1	41	97.73
phage_75	23	62863	Staphylococcus phage Sa2wa_st8	MK940809.1	73	99.95
phage_76	23	59360	Staphylococcus phage SAP090B	GQ915271.1	39	97.73
phage_77	14	45661	Staphylococcus aureus phage phi 12	AF424782.1	60	99.79
phage_78	6(A)	58967	Staphylococcus phage Sa2wa_st8	MK940809.1	70	99.94
phage_79	6(A)	21378	Staphylococcus phage TEM123	JQ779024.1	100	99.99
phage_80	6(A)	28368	Staphylococcus phage SAP090B	GQ915271.1	81	97.73
phage_81	3(B)	28368	Staphylococcus phage SAP090B	GQ915271.1	81	97.73
phage_82	3(B)	21378	Staphylococcus phage TEM123	JQ779024.1	100	99.99
phage_83	3(B)	58967	Staphylococcus phage Sa2wa_st8	MK940809.1	70	99.94
phage_84	3(A)	58967	Staphylococcus phage Sa2wa_st8	MK940809.1	70	99.94
phage_85	3(A)	24379	Staphylococcus phage TEM123	JQ779024.1	100	99.99
phage_86	3(A)	28496	Staphylococcus phage SAP090B	GQ915271.1	81	97.73

Table S3. Coding region statistics of Egyptian *S. aureus* prophages.

Prophage ID	Host Strain	Length	# CDS	Antibiotic resistance & virulence factors	Prophage Cluster
phage_0	AA2	26511	26	<i>sak; scn</i>	A
phage_1	AA2	29363	37		G
phage_2	AA2	43262	58	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_3	AA94	49880	70		B
phage_4	AA67	62863	73	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_5	AA67	35427	41		G
phage_6	AA67	28410	29	<i>sak; scn; sea</i>	A
phage_7	AA5	29682	38		B
phage_8	AA93	16210	19		-
phage_9	AA51	64168	72	<i>sak; scn; hld; sea; selk; selq</i>	D
phage_10	AA51	31799	31	<i>lukS</i> -PV; <i>lukF</i> -PV	F
phage_11	AA69	62863	73	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_12	AA69	27700	27	<i>sak; scn; sea</i>	D
phage_13	AA33	27203	31		B
phage_14	AA57	34045	45		A
phage_15	AA57	13833	17		B
phage_16	AA68	62862	73	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_17	AA68	28102	27	<i>sak; scn; sea</i>	A
phage_18	AA68	31053	40		H
phage_19	AA4	70082	83		G
phage_20	AA4	26350	25	<i>sak; scn</i>	A
phage_21	AA4	43262	58	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_22	AA59	53697	67		E
phage_23	AA59	28102	27	<i>sak; scn; sea</i>	A
phage_24	AA3	34077	40	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_25	AA3	26511	26	<i>sak; scn</i>	A
phage_26	AA3	29363	37		G
phage_27	AA95	19196	40		-
phage_28	AA35	48171	64	<i>sak; scn</i>	A
phage_29	AA35	40061	68		-
phage_30	AA32	42886	60		H
phage_31	AA101	36605	47		B
phage_32	AA17	62671	76	<i>lukS</i> -PV; <i>lukF</i> -PV	E
phage_33	AA17	48021	61	<i>sak; scn</i>	A

Prophage ID	Host Strain	Length	# CDS	Antibiotic resistance & virulence factors	Prophage Cluster
phage_34	AA18	36270	54		C
phage_35	AA80	45707	47	<i>tet(M)</i>	E
phage_36	AA87	60588	68		F
phage_37	AA87	59321	67	<i>sak; scn; sea; selk; selq</i>	A
phage_38	AA45	63945	85		H
phage_39	AA45	34865	43	<i>sak; scn</i>	D
phage_40	AA39	54537	70	<i>sak; scn</i>	D
phage_41	AA30	34597	38	<i>hlgA; lukE; lukD</i>	H
phage_42	AA30	28121	28	<i>sak; scn; sea</i>	A
phage_43	AA64	22302	28		B
phage_44	AA6	54537	70	<i>sak; scn</i>	D
phage_45	AA1	45741	53	<i>sak; scn; sea; selk; selq</i>	A
phage_46	AA63	19610	20		C
phage_47	AA55	30666	36		B
phage_48	AA8	54537	70	<i>sak; scn</i>	D
phage_49	AA99	49880	70		C
phage_50	AA31	24806	28		C
phage_51	AA36	42543	58		F
phage_52	AA36	55314	74	<i>sak; scn</i>	D
phage_53	AA53	44305	68	<i>sak; chp; scn</i>	-
phage_54	AA62	36176	51		G
phage_55	AA91	28172	37		C
phage_56	AA65	52914	65		E
phage_57	AA65	28102	27	<i>sak; scn; sea</i>	A
phage_58	AA65	25618	29		G
phage_59	AA103	59360	67	<i>sak; scn; sea; selk; selq</i>	A
phage_60	AA104	54549	70	<i>sak; scn</i>	D
phage_61	AA78	63535	72	<i>sak; scn; hld; sea; selk; selq</i>	D
phage_62	AA76	47328	52	<i>splA; splB; splC; seg; sei; yent1; yent2; selm; seln; selo; hlgA; lukE; lukD</i>	G
phage_63	AA22	27079	30		C
phage_64	AA70	81781	94	<i>tet(M)</i>	F
phage_65	AA70	50286	72		C
phage_66	AA70	45450	66	<i>sak; scn; selp</i>	D
phage_67	AA77	62863	73	<i>lukS-PV; lukF-PV</i>	E

Prophage ID	Host Strain	Length	# CDS	Antibiotic resistance & virulence factors	Prophage Cluster
phage_68	AA77	32539	40		H
phage_69	AA77	31268	35	<i>sak; scn; sea</i>	A
phage_70	AA41	47772	67		F
phage_71	50	14162	17		B
phage_72	48	48768	55	<i>splA; splB; splC; splD; splE; splF; hlgA; lukE; lukD</i>	C
phage_73	43	60926	73	<i>lukS-PV; lukF-PV</i>	F
phage_74	43	55555	65	<i>sak; scn; sea; selk; selq</i>	D
phage_75	23	62863	73	<i>lukS-PV; lukF-PV</i>	E
phage_76	23	59360	67	<i>sak; scn; sea; selk; selq</i>	A
phage_77	14	45661	48	<i>tet(M)</i>	E
phage_78	6(A)	58967	73		F
phage_79	6(A)	21378	26		G
phage_80	6(A)	28368	29	<i>sak; scn; sea</i>	D
phage_81	3(B)	28368	29	<i>sak; scn; sea</i>	D
phage_82	3(B)	21378	26		G
phage_83	3(B)	58967	73		F
phage_84	3(A)	58967	73		F
phage_85	3(A)	24379	35		G
phage_86	3(A)	28496	29	<i>sak; scn; sea</i>	A