



Article

Staphylococcus aureus Host Spectrum Correlates with Methicillin Resistance in a Multi-Species Ecosystem

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Supplementary data

Table S1. List of abbreviations.

- Biological terms:
- NHP: Non-human primate
- MRSA: methicillin-resistant *Staphylococcus aureus*
- CC: Clonal Complex
- SAID: *S. aureus* identification
- microm: micromammals
- mec A: gene found in bacterial cells which allows them to be resistant methicillin.
- Nuc: amplified gene for *S. aureus* identification
- SSR: Short Sequence Repeats
- DNA: Deoxyribose Nucleic Acid
- PCR: Polymerase Chain Reaction
- PVL: Panton-Valentine (toxin)
- ST: Sequence Typing
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- Research structures and Non-governmental organisations:
- CDP: Centre de Primatologie (Primate Centre)
- CIRMF: Centre International de Recherches Médicales de Franceville (Gabon)
- IRD: Institut de Recherche pour le Développement
- CNE: Centre National d’Ethique (Gabonese National Ethics Committee)
- IUCN: International Union for Conservation of Nature
- GRASP: Great Apes Survival Partnership
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- Host spectrum:
- S: strains classified as specialist
- G: strains observed in humans and classified as generalist

- GH: strains observed in NHP classified as generalist and that were also observed in humans
- GnH: strains observed in NHP classified as generalist but were not observed in humans
- GE: strains observed in a non exposed species (micromammals or bat), classified as generalist and that were also observed in at least one exposed species (humans or NHP)
- GnE: strains observed in a non exposed species (micromammals or bat), classified as generalist but were not observed in any exposed species (humans or NHP)
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- Statistical terms:
- AIC: Akaike Information Criterium
- LRT: Likelihood Ratio Test
- OR: Odd Ratio
- factor1 * factor2: interaction between factor1 and factor2
- H0: null hypothesis (model without any explanatory cofactor)
- CI: confidence interval
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- Cofactors:
- s: sex
- a: age
- spe: species
- d: distance from NHP installations
- h: housing
- g: degree of generalism
- sw: seniority at work

Table S2. Species sampled, *S. aureus* and MSRA strains. *N*= Number of individuals sampled; *Ni*= Number of *S. aureus* isolates among *N*; *Ns* = Number of MRSA isolates among *Ni*. NHPs (Non-Human Primates), “Microm.” stands for Micromammals.

Host		Swabs collected		
Group	Species	<i>N</i>	<i>Ni</i> (%: <i>Ni/N</i>)	<i>Ns</i>
Humans	<i>H.sapiens sapiens</i>	39	18 (46.15)	12
	<i>Pan t. troglodytes</i>	83	36	7
	<i>Gorilla g. gorilla</i>	6	5	-
	<i>Mandrillus sphinx</i>	380	180	66
	<i>Cercopithecus torquatus</i>	2	0	-
	<i>Chlorocebus Aethiops</i>	9	1	-
NHPs	<i>Macaca sp.</i>	86	43	6
	<i>Cercopithecus solatus</i>	12	4	1
	<i>Cercopithecus cephus</i>	2	1	-
Total NHPs		580	270 (46.55)	80
Bats	<i>Epomops franqueti</i>	121	49	11
	<i>Hypsignathus monstrosus</i>	20	9	2
Total Bats		141	58 (41.13)	13
Microm.	<i>Lemniscomys striatus</i>	93	18	-
	<i>Lophuromys nudicaudus</i>	52	17	2
	<i>Mastomys natalensis</i>	38	14	2
	<i>Praomys sp</i>	89	24	5
	<i>Rattus norvegicus</i>	98	36	8
	<i>Rattus Rattus</i>	40	16	2

	shrews	10	3	1
Total Micromam.		420	128 (30.48)	20
Total		1180	474 (40.17)	125

Table S3. Generalized linear model (GLM) tested to explain observed variation in MRSA carriage in infected hosts, as well as GE strains carriage (in micromammals for prediction P4). The conditions of the models are described in the Methods section. The model with the smallest AIC was retained to test our predictions (in yellow for P2 and P4, in green for P3). Correcting cofactors *a* (age), *s* (sex), *sw* (work seniority), *d* (distance), *g* (generalist or specialist strains of *S. aureus*), *spe* (species). 'NA' means that the inference algorithm failed.

Infected Hosts	Response Variable	GLM	AIC
Humans	MRSA carriage	H0	21.095 (P3)
		<i>s</i>	22.436
		<i>sw</i>	23.095
		<i>s+sw</i>	24.34
		<i>s*sw</i>	24.34
		<i>d+g</i>	101.50
		<i>s+d+g</i>	103.45
		<i>g</i>	104.09
		<i>d+spe+g</i>	105.31
		<i>s+g</i>	106.08
		<i>esp+g</i>	106.39
		<i>s+d+spe+g</i>	107.13
		<i>a+s+d+g</i>	107.22
		<i>a+g</i>	108.02
		<i>d</i>	108.67 (P3)
Micromammals: all	MRSA carriage	<i>a*s+d+g</i>	109.01
		<i>a+s+d+esp+g</i>	109.54
		<i>a+s+g</i>	110.00
		<i>s+d</i>	110.5
		<i>d+esp</i>	111.64
		<i>a*s+g</i>	111.93
		<i>a*s+d+esp+g</i>	111.98
		<i>a+d</i>	112.65
		H0	112.95 (P4a)
		<i>s+d+spe</i>	113.49
		<i>a+s+d</i>	114.49
		<i>esp</i>	114.79
		<i>s</i>	114.94
		<i>a*s+d</i>	116.29
		<i>s+esp</i>	116.78
		<i>a</i>	116.94
		<i>a+s+d+esp</i>	117.08
		<i>a+esp</i>	118.55
		<i>a+s</i>	118.93
		<i>a*s+d+esp</i>	119.3
		<i>a*s</i>	120.12
		<i>a+s+esp</i>	120.54
		<i>a*s+esp</i>	122
		<i>s</i>	165.43 (P4b)
		H0	166.24
		<i>a+s</i>	167.11
		<i>a</i>	167.37
		<i>s+esp</i>	172.44
		<i>esp</i>	172.71
Micromammals: all	GE carriage		

		<i>a*s</i>	167.87
		<i>a+esp</i>	174.05
		<i>a+s+esp</i>	174.44
		<i>a*s+esp</i>	175.78
Micromammals: infected by GE	MRSA carriage	H0	78.478 (P4c)
		s	79.985
		esp	81.53
		a	82.207
		s+esp	82.522
		a*s	83.348
		a+s	83.573
		a+esp	85.156
		a+s+esp	86.255
		a*s+esp	NA
		H0	63.723 (P3)
		s	64.66
Bats	MRSA carriage	a	67.21
		a*s	68.22
		a+s	68.25
		spe	68.68
		s+spe	69.22
		a*s+spe	71.83
		a+spe	72.20
		a+s+spe	72.82
		a+s+spe+g	264.08
		a*s+g	265.39 (P2)
NHPs	MRSA carriage	s+spe+g	265.49
		a+spe+g	265.87
		a+g	267.17
		spe+g	267.57
		s+g	269.52
		g	271.53
		a+s+spe	276.76 (P3)
		a+spe	278.70
		a+s	278.79
		a*s	278.85
		a	279.58
		s+spe	280.14
		spe	281.77
		s	283.07
		H0	284.06

Table S4. General Linear Models (GLM) for prediction P3 in different host groups comparing generalist and specialist MRSA strains. GE: generalist strains also infecting humans and/or NHPs, i.e., at least one of the two species that are directly exposed to antibiotics; GnE: generalist strains only infecting untreated species to antibiotics (micromammals and bats); GH: generalist strains infecting humans (whether infecting or not they were also found in bats and/or micromammals); GnH: generalist strains infecting other species but not humans. The abbreviation ‘microm.’ stands for micromammals.

Hosts	Base Model	Variables	Estimate	Std. Error	z Value	p-Value
Humans	H0	<i>g</i>	0.44	1.14	0.38	0.69
		<i>d</i>	−0.0045	0.0024	−1.821	0.068
Microm.	<i>d</i>	<i>g</i> : GE	2.31	0.68	3.41	0.0006 *
		<i>g</i> : GnE	−∞	NA	NA	0.99
Bats	H0	<i>g</i> : GE	1.93	0.73	2.61	0.009 *
		<i>g</i> : GnE	NA	NA	NA	NA
		<i>age</i> : adolescent	0.30	0.42	0.70	0.49
		<i>age</i> : juvenile	−1.48	0.80	−1.83	0.07
		<i>sex</i> : male	0.63	0.33	1.92	0.05
		<i>species</i> : <i>C. cephus</i>	−15.41	2399.54	−0.006	−0.99
		<i>species</i> : <i>Pan t. troglodytes</i>	−1.20	0.52	−2.32	0.02 *
NHPs	<i>a+s+spe</i>	<i>species</i> : <i>Gorilla g. gorilla</i>	−15.90	1085.60	−0.015	0.99
		<i>species</i> : <i>Macaca sp.</i>	−1.13	0.51	−2.23	0.03 *
		<i>species</i> : <i>C. solatus</i>	−0.06	1.26	−0.05	0.95
		<i>species</i> : <i>Ch. Aethiops</i>	−15.41	2399.60	−0.006	0.99
		<i>g</i> : GH	0.92	0.46	2.01	0.04 *
		<i>g</i> : GnH	0.85	0.39	2.19	0.03 *