Supplement A.   Supplementary Tables For Applications

TABLE S1

Posterior mean (upper triangle) and 95% Bayesian credible interval (BCI - lower triangle) estimates for latent liability model correlations between antibiotic resistance traits in *Salmonela*.

	Nalidixic acid	Ciprofloxacin	Furazolidone	Kanamycin	Trimethoprim	Gentamicin	Netilmicin
Nalidixic acid	1.00	0.34	0.10	0.16	0.24	0.20	0.16
Ciprofloxacin	[-0.07, 0.68]	1.00	-0.20	-0.15	0.06	-0.20	-0.23
Furazolidone	[-0.31, 0.48]	[-0.73, 0.42]	1.00	0.18	0.21	0.53	0.57
Kanamycin	[-0.22, 0.51]	[-0.67, 0.45]	[-0.26, 0.56]	1.00	0.52	0.41	0.42
Trimethoprim	[-0.10, 0.54]	[-0.39, 0.50]	[-0.17, 0.55]	[0.23, 0.76]	1.00	0.52	0.21
Gentamicin	[-0.17, 0.54]	[-0.75, 0.47]	[0.02, 0.84]	[0.06, 0.71]	[-0.16, 0.53]	1.00	0.92
Netilmicin	[-0.21, 0.51]	[-0.77, 0.42]	[0.06, 0.87]	[0.06, 0.72]	[-0.15, 0.53]	[0.80, 0.98]	1.00
Spectinomycin	[-0.13, 0.51]	[-0.62, 0.42]	[0.04, 0.93]	[-0.21, 0.54]	[-0.26, 0.43]	[0.28, 0.97]	[0.30, 0.97]
Chloramphenicol	[-0.28, 0.41]	[-0.73, 0.23]	[0.20, 0.97]	[-0.07, 0.58]	[-0.13, 0.49]	[0.20, 0.98]	[0.24, 0.98]
Ampicillin	[-0.33, 0.38]	[-0.72, 0.28]	[0.10, 0.97]	[-0.16, 0.57]	[-0.18, 0.49]	[-0.02, 0.95]	[0.01, 0.95]
Tetracycline	[-0.26, 0.44]	[-0.69, 0.32]	[0.09, 0.97]	[-0.16, 0.53]	[-0.19, 0.47]	[0.10, 0.97]	[0.12, 0.97]
Sulphamethoxazole	[-0.25, 0.55]	[-0.63, 0.57]	[-0.15, 0.91]	[-0.16, 0.53]	[-0.13, 0.67]	[-0.19, 0.90]	[-0.17, 0.90]
Streptomycin	[-0.17, 0.52]	[-0.65, 0.42]	[0.00, 0.95]	[-0.30, 0.64]	[-0.24, 0.46]	[0.15, 0.96]	[0.17, 0.97]

	Spectinomycin	Chloramphenicol	Ampicillin	Tetracycline	Sulphamethoxazole	Streptomycin
Nalidixic acid	0.21	0.07	0.04	0.10	0.18	0.19
Ciprofloxacin	-0.13	-0.29	-0.26	-0.22	-0.02	-0.14
Furazolidone	0.66	0.79	0.76	0.77	0.62	0.70
Kanamycin	019	0.28	0.23	0.20	0.19	0.17
Trimethoprim	0.10	0.20	0.18	0.16	0.30	0.13
Gentamicin	0.78	0.70	0.58	0.66	0.46	0.72
Netilmicin	0.79	0.75	0.63	0.70	0.49	0.74
Spectinomycin	1.00	0.82	0.70	0.82	0.64	0.93
Chloramphenicol	[0.67, 0.92]	1.00	0.82	0.96	0.76	0.86
Ampicillin	[0.50, 0.85]	[0.86, 0.98]	1.00	0.93	0.78	0.77
Tetracycline	[0.68, 0.92]	[0.91, 0.98]	[0.86, 0.98]	1.00	0.82	0.89
Sulphamethoxazole	[0.36, 0.85]	[0.54, 0.91]	[0.55, 0.92]	[0.63, 0.93]	1.00	0.74
Streptomycin	[0.84, 0.98]	[0.73, 0.94]	[0.59, 0.89]	[0.78, 0.96]	[0.50, 0.91]	1.00

TABLE S2

Posterior mean and 95% Bayesian credible interval (BCI) estimates for pairwise correlation between the host trait (Animal/Human) and the different antibiotic resistance traits.

	Correlation	95% BCI
Ampicillin	0.0349	[-0.2357, 0.3036]
Chloramphenicol	-0.0610	[-0.3055, 0.1903]
Ciprofloxacin	0.1505	[-0.3313, 0.6099]
Gentamicin	-0.3651	[-0.6893, -0.0086]
Kanamycin	-0.1578	[-0.4641, 0.1715]
Furazolidone	0.0001	[-0.3131, 0.3098]
Nalidixic acid	-0.0967	[-0.4199, 0.2439]
Netilmicin	-0.3315	[-0.6551, 0.0145]
Spectinomycin	-0.2696	[-0.5130, 0.0009]
Streptomycin	-0.1392	[-0.4020, 0.1375]
Sulphamethoxazole	0.1399	[-0.2104, 0.4768]
Tetracycline	-0.0142	[-0.2716, 0.2471]
Trimethoprim	0.0049	[-0.2888, 0.2976]

TABLE S3

Posterior mean (upper triangle) and 95% Bayesian credible interval (BCI - lowwer triangle) estimates for latent liability model correlations between floral traits in *Aquilegia*.

	Orientation	Blade brightness	Spur brightness	Sepal length	Blade length	Pollinator
Orientation	1.00	0.54	0.42	0.50	0.55	0.74
Blade brightness	[0.32; 0.73]	1.00	0.52	0.49	0.60	0.50
Spur brightness	[0.17; 0.64]	[0.29; 0.71]	1.00	0.47	0.43	0.60
Sepal length	[0.26; 0.70]	[0.26; 0.69]	[0.22; 0.67]	1.00	0.74	0.64
Blade length	[0.33; 0.73]	[0.39; 0.76]	[0.17; 0.64]	[0.60; 0.85]	1.00	0.55
Pollinator	[0.56; 0.87]	[0.24; 0.70]	[0.38; 0.77]	[0.38; 0.83]	[0.27; 0.78]	1.00
Spur hue	[0.14; 0.63]	[0.09; 0.59]	[0.38; 0.76]	[0.19; 0.65]	[0.14; 0.63]	[0.74; 0.94]
Spur length	[0.34; 0.73]	[0.08; 0.59]	[0.17; 0.65]	[0.47; 0.80]	[0.47; 0.80]	[0.60; 0.88]
Blade hue	[-0.14; 0.42]	[-0.06; 0.49]	[0.05; 0.57]	[0.22; 0.67]	[0.10; 0.60]	[0.28; 0.75]
Blade chroma	[-0.71; -0.29]	[-0.75; -0.37]	[-0.57; -0.06]	[-0.55; -0.03]	[-0.55; -0.02]	[-0.56; -0.01]
Spur chroma	[-0.76; -0.38]	[-0.84; -0.55]	[-0.77; -0.41]	[-0.64; -0.17]	[-0.67; -0.21]	[-0.70; -0.24]
Anthocyanins	[-0.67; -0.19]	[-0.75; -0.34]	[-0.68; -0.22]	[-0.77; -0.30]	[-0.98; -0.83]	[-0.79; -0.27]

	Spur hue	Spur length	Blade hue	Blade chroma	Spur chroma	Anthocyanins
Orientation	0.40	0.56	0.15	-0.52	-0.59	-0.45
Blade brightness	0.36	0.35	0.22	-0.58	-0.71	-0.57
Spur brightness	0.59	0.43	0.33	-0.33	-0.61	-0.47
Sepal length	0.44	0.65	0.47	-0.31	-0.42	-0.56
Blade length	0.40	0.65	0.36	-0.30	-0.46	-0.92
Pollinator	0.86	0.76	0.54	-0.30	-0.49	-0.56
Spur hue	1.00	0.68	0.55	-0.03	-0.33	-0.55
Spur length	[0.50; 0.81]	1.00	0.50	-0.10	-0.19	-0.61
Blade hue	[0.33; 0.73]	[0.26; 0.70]	1.00	-0.28	-0.21	-0.34
Blade chroma	[-0.31; 0.26]	[-0.38; 0.18]	[-0.53; 0.00]	1.00	0.63	0.17
Spur chroma	[-0.57; -0.06]	[-0.45; 0.10]	[-0.47; 0.07]	[0.44; 0.79]	1.00	0.43
Anthocyanins	[-0.74; -0.32]	[-0.78; -0.39]	[-0.59; -0.05]	[-0.13; 0.45]	[0.16; 0.65]	1.00

TABLE S4

Posterior mean (upper triangle) and 95% Bayesian credible interval (BCI - lower triangle) estimates for latent liability correlations between floral traits in *Aquilegia* not controlling for phylogenetic relatedness.

	Orientation	Blade brightness	Spur brightness	Sepal length	Blade length	Pollinator
Orientation	1.00	0.56	0.51	0.59	0.71	0.70
Blade brightness	[0.35, 0.71]	1.00	0.53	0.52	0.60	0.44
Spur brightness	[0.28, 0.67]	[0.30, 0.68]	1.00	0.58	0.60	0.60
Sepal length	[0.38, 0.73]	[0.28, 0.67]	[0.37, 0.72]	1.00	0.78	0.74
Blade length	[0.55, 0.82]	[0.40, 0.74]	[0.40, 0.74]	[0.65, 0.86]	1.00	0.66
Pollinator	[0.51, 0.82]	[0.17, 0.62]	[0.39, 0.74]	[0.55, 0.86]	[0.44, 0.80]	1.00
Spur hue	[0.13, 0.58]	[-0.02, 0.47]	[0.28, 0.67]	[0.34, 0.70]	[0.22, 0.64]	[0.81, 0.94]
Spur length	[0.34, 0.71]	[0.027, 0.50]	[0.25, 0.65]	[0.52, 0.80]	[0.53, 0.80]	[0.74, 0.91]
Blade hue	[-0.06, 0.43]	[-0.04, 0.45]	[0.12, 0.57]	[0.40, 0.74]	[0.18, 0.61]	[0.48, 0.81]
Blade chroma	[-0.67, -0.27]	[-0.79, -0.50]	[-0.57, -0.12]	[-0.54, -0.08]	[-0.56, -0.11]	[-0.41, 0.11]
Spur chroma	[-0.77, -0.46]	[-0.84, -0.60]	[-0.78, -0.48]	[-0.64, -0.24]	[-0.71, -0.35]	[-0.63, -0.20]
Anthocyanins	[-0.78, -0.46]	[-0.73, -0.37]	[-0.78, -0.46]	[-0.82, -0.48]	[-0.98, -0.88]	[-0.86, -0.54]

	Spur hue	Spur length	Blade hue	Blade chroma	Spur chroma	Anthocyanins
Orientation	0.39	0.562	0.22	-0.457	-0.61	-0.62
Blade brightness	0.26	0.304	0.24	-0.637	-0.72	-0.54
Spur brightness	0.51	0.490	0.38	-0.326	-0.63	-0.61
Sepal length	0.56	0.693	0.60	-0.288	-0.43	-0.65
Blade length	0.47	0.697	0.43	-0.321	-0.52	-0.93
Pollinator	0.89	0.846	0.68	-0.121	-0.40	-0.70
Spur hue	1.00	0.798	0.70	0.150	-0.20	-0.63
Spur length	[0.68, 0.87]	1.000	0.63	0.061	-0.15	-0.72
Blade hue	[0.53, 0.80]	[0.43, 0.75]	1.00	-0.136	-0.17	-0.45
Blade chroma	[-0.14, 0.37]	[-0.23, 0.28]	[-0.41, 0.09]	1.000	0.68	0.16
Spur chroma	[-0.46, 0.02]	[-0.42, 0.08]	[-0.44, 0.05]	[0.50, 0.79]	1.00	0.47
Anthocyanins	[-0.79, -0.47]	[-0.85, -0.60]	[-0.67, -0.25]	[-0.14, 0.39]	[0.21, 0.64]	1.00

Table S5: Posterior mean and 95% Bayesian credible interval (BCI) estimates for significant correlations between sites in Influenza epitopes A and B.

	Sites	Correlation	95% BCI
1	[156(K)Q EpB, 158(E)K EpB]	0.7432	[0.3999, 0.9284]
2	[158(E)N EpB, 189(S)K EpB]	0.7365	[0.2806, 0.9499]
3	[144(V)N EpA, 158(E)K EpB]	0.7204	[0.3469, 0.9249]
4	[133(D)N EpA, 144(V)N EpA]	0.7180	[0.2908, 0.9391]
5	[159(Y)F EpB, 189(S)N EpB]	0.6913	[0.2655, 0.9174]
6	[144(V)I EpA, 156(K)Q EpB]	0.6883	[0.2880, 0.9161]
7	[133(D)N EpA, 158(E)K EpB]	0.6849	[0.2355, 0.9360]
8	[144(V)N EpA, 145(N)S EpA]	0.6826	[0.1411, 0.9304]
9	[131(A)T EpA, 159(Y)F EpB]	0.6792	[0.1932, 0.9353]
10	[145(N)S EpA, 188(D)Y EpB]	0.6726	[0.2276, 0.9137]
11	[144(V)N EpA, 188(D)Y EpB]	0.6640	[0.0368, 0.9332]
12	[144(V)N EpA, 156(K)Q EpB]	0.6602	[0.2393, 0.9076]
13	[159(Y)F EpB, 189(S)K EpB]	0.6586	[0.1364, 0.9346]
14	[156(K)H EpB, 159(Y)F EpB]	0.6585	[0.1583, 0.9204]
15	[158(E)K EpB, 188(D)Y EpB]	0.6534	[1.503e-05, 0.9262]
16	[144(V)N EpA, 144(V)D EpA]	0.6523	[0.0478, 0.9326]
17	[144(V)D EpA, 158(E)K EpB]	0.6516	[0.1447, 0.9094]
18	[131(A)T EpA, 156(K)H EpB]	0.6500	[0.1195, 0.9357]
19	[156(K)H EpB, 189(S)N EpB]	0.6381	[0.1477, 0.9119]
20	[144(V)N EpA, 156(K)H EpB]	0.6376	[0.0889, 0.9335]
21	[133(D)N EpA, 156(K)Q EpB]	0.6343	[0.1697, 0.9142]
22	[133(D)N EpA, 156(K)H EpB]	0.6328	[0.0869, 0.9432]
23	[145(N)S EpA, 156(K)H EpB]	0.6324	[0.0278, 0.9333]
24	[133(D)N EpA, 144(V)D EpA]	0.6320	[0.0886, 0.9170]
25	[144(V)I EpA, 158(E)K EpB]	0.6291	[0.1824, 0.8998]
26	[145(N)S EpA, 198(A)S EpB]	0.6195	[0.1026, 0.9115]
27	[156(K)H EpB, 198(A)S EpB]	0.6192	[0.0813, 0.9172]
28	[158(E)N EpB, 159(Y)F EpB]	0.6192	[0.0549, 0.9204]
29	[133(D)N EpA, 145(N)S EpA]	0.6190	[0.0058, 0.9267]
30	[189(S)K EpB, 193(S)Y EpB]	0.6138	[0.0330, 0.9231]
31	[131(A)T EpA, 189(S)N EpB]	0.6047	[0.0788, 0.9113]
32	[131(A)T EpA, 189(S)K EpB]	0.6030	[0.0881, 0.9200]
33	[144(V)D EpA, 156(K)Q EpB]	0.5898	[0.0680, 0.8939]
34	[159(Y)F EpB, 198(A)S EpB]	0.5780	[0.0158, 0.9013]

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Table S5: Posterior mean and 95% Bayesian credible interval (BCI) estimates for significant correlations between sites in Influenza epitopes A and B.

	Sites	Correlation	95% BCI
35	[145(N)S EpA, 158(E)K EpB]	0.5774	[0.0008, 0.8927]
36	[144(V)K EpA, 189(S)K EpB]	0.5738	[0.0089, 0.9101]
37	[131(A)T EpA, 158(E)N EpB]	0.5652	[0.0013, 0.9056]
38	[133(D)N EpA, 197(R)Q EpB]	0.5644	[0.0600, 0.8911]
39	[189(S)K EpB, 193(S)F EpB]	0.5149	[0.0128, 0.8652]
40	[131(A)T EpA, 193(S)F EpB]	0.4865	[0.0112, 0.8355]
41	[159(Y)F EpB, 193(S)F EpB]	0.4849	[0.0015, 0.8354]

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*The code for sites is as follows: of the number of the amino acid site in the aligned sequence; the one letter code for the reference amino acid for the site in parenthesis; the code for the amino acid corresponding to the latent trait; and the epitope to which the site belongs.