**Table S5.** Genetic determinants of antimicrobial resistance in 818 Bangladeshi *S.* Typhi isolates

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| **Resistance patterns** | **H58 isolates (n=479)** | **Non H58 isolates (n=339)** | **Total isolates (n=818)** |
| **Acquired AMR genes** | **422 (88.1%)** | **1 (0.29%)** | **422 (51.6%)** |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB* / *gyrA-*S83F | 211 (44.1%) | 0 (0.00%) | 211 (25.79%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB* / *gyrA-*S83Y | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strA*B / *gyrA-*D87N | 9 (1.9%) | 0 (0.00%) | 9 (1.10%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB /* *gyrA-*D87G | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB /* *gyrA-*S83F, *parC-*E84K | 4 (0.84%) | 0 (0.00%) | 4 (0.49%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB /* *gyrA-*S83F, *parC-*S80R | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strA, strB /* *gyrA* D87G, *parC* E84K | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB /* *gyrA-*S83F, *gyrA-*D87G, *parC-*E84K | 7 (1.5%) | 0 (0.00%) | 7 (0.86%) |
| *blaTEM-1, catA1, dfrA7, sul1, sul2, strAB* | 2 (0.42%) | 0 (0.00%) | 2 (0.25%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB, tetB* / *gyrA-*S83Y | 48 (10.1%) | 0 (0.00%) | 48 (5.88%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB, tetB* / *gyrA-*S83F | 2 (0.42%) | 0 (0.00%) | 2 (0.25%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB, tetB* / *gyrA-*D87N | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB, tetB* / *gyrA-*S83Y, *parC-*S80R | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1 , catA1, dfrA7, sul1, sul2, strAB, qnrS, tetA /* gyrA-S83F | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1, catA1, dfrA7, sul1, strAB, tetB / gyrA-S83Y* | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1, sul2, strAB, tetB* | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1 , catA1, sul2, strAB / gyrA-S83Y* | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1* *, catA1, dfrA7, sul1/ gyrA-*S83F | 2 (0.42%) | 0 (0.00%) | 2 (0.25%) |
| *blaTEM-1* *, catA1, dfrA7, sul1 / gyrA-*S83Y | 6 (1.26%) | 0 (0.00%) | 6 (0.74%) |
| *catA1, dfrA7, sul, tetB /* gyrA-S83Y | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *catA1,sul2, strA, strB /* gyrA-S83F | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *catA1, dfrA7, sul1/ gyrA-*S83F | 47 (9.81%) | 0 (0.00%) | 47 (5.76%) |
| *catA1, dfrA7, sul1/ gyrA-*D87N | 2 (0.42%) | 0 (0.00%) | 2 (0.25%) |
| *catA1, dfrA7, sul1/ gyrA-*S83F, *gyrA-D87G, parC-*E84K | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *catA1, dfrA7, sul1* | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1, sul2, qnrS, tetA /* *gyrA-*S83Y | 62 (12.94%) | 0 (0.00%) | 62 (7.59%) |
| *sul1, strAB, tetB / gyrA-*S83Y | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| *blaTEM-1, sul2, qnrS / gyrA-*S83Y | 5 (1.05%) | 0 (0.00%) | 5 (0.61%) |
| *blaTEM-1, blaCTX-*M | 0 (0.00%) | 1 (0.29%) | 1 (0.12%) |
| **Only QRDR mutation** | **51 (10.6%)** | **248 (73.16%)** | **299 (36.55%)** |
| *gyrA-*S83F | 19 (3.98%) | 190 (56.05%) | 209 (25.6%) |
| *gyrA-*S83Y | 27 (5.66%) | 13 (3.83%) | 40 (4.9%) |
| *gyrA-D87G* | 2 (0.42%) | 1 (0.29%) | 3 (0.37%) |
| *gyrA-D87N* | 0 (0.00%) | 37 (10.91%) | 37 (4.52%) |
| *gyrA-D87Y* | 2 (0.42%) | 6 (1.77%) | 8 (0.98%) |
| *gyrA-*S83F, *parC-*E84K | 0 (0.00%) | 1 (0.29%) | 1 (0.12%) |
| *gyrA-*S83F, *gyrA-*D87N, *parC-*S80I | 1 (0.21%) | 0 (0.00%) | 1 (0.12%) |
| **Susceptible to all antibiotics** | **6 (1.25%)** | **90 (26.55%)** | **96 (11.74%)** |