

**Prevalence of ST1193 clone and IncI1/ST16 plasmid in E-coli
isolates carrying blaCTX-M-55 gene from urinary tract
infections patients in China**

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**Table S1. Susceptibility of 111 CTX-M-55-producing *Escherichia coli* isolates
from UTIs patients against common antimicrobial agents**

| Agent | Resistant(%) | Susceptible(%) | MIC50(ug/ml) | MIC90(ug/ml) |
|--------------------------|--------------|----------------|--------------|--------------|
| Imipenem | 2 | 98 | 0.125 | 0.25 |
| Meropenem | 0 | 100 | <=0.06 | <=0.06 |
| Ertapenem | 2 | 98 | <=0.06 | 0.25 |
| Tigecycline | 6 | 94 | 0.25 | 0.5 |
| Colistin | 0 | 100 | 1 | 2 |
| Cefoperazone/sulbactam | 9.6 | 76.2 | 8 | 16 |
| Piperacillin/ tazobactam | 5 | 93 | 2 | 4 |
| Cefepime | 98 | 2 | >32 | >32 |
| Cefotaxime | 94 | 6 | >64 | >64 |
| Ceftazidime | 97 | 3 | 32 | >64 |
| Ceftriaxone | 97.4 | 2.6 | >64 | >64 |
| Aztreonam | 97 | 3 | >8 | >8 |

| | | | | |
|---------------|----|----|-----|------|
| Amikacin | 18 | 82 | 4 | >128 |
| Levofloxacin | 76 | 16 | 16 | >16 |
| Ciprofloxacin | 85 | 15 | >16 | >16 |
| Minocycline | 26 | 58 | 4 | >16 |

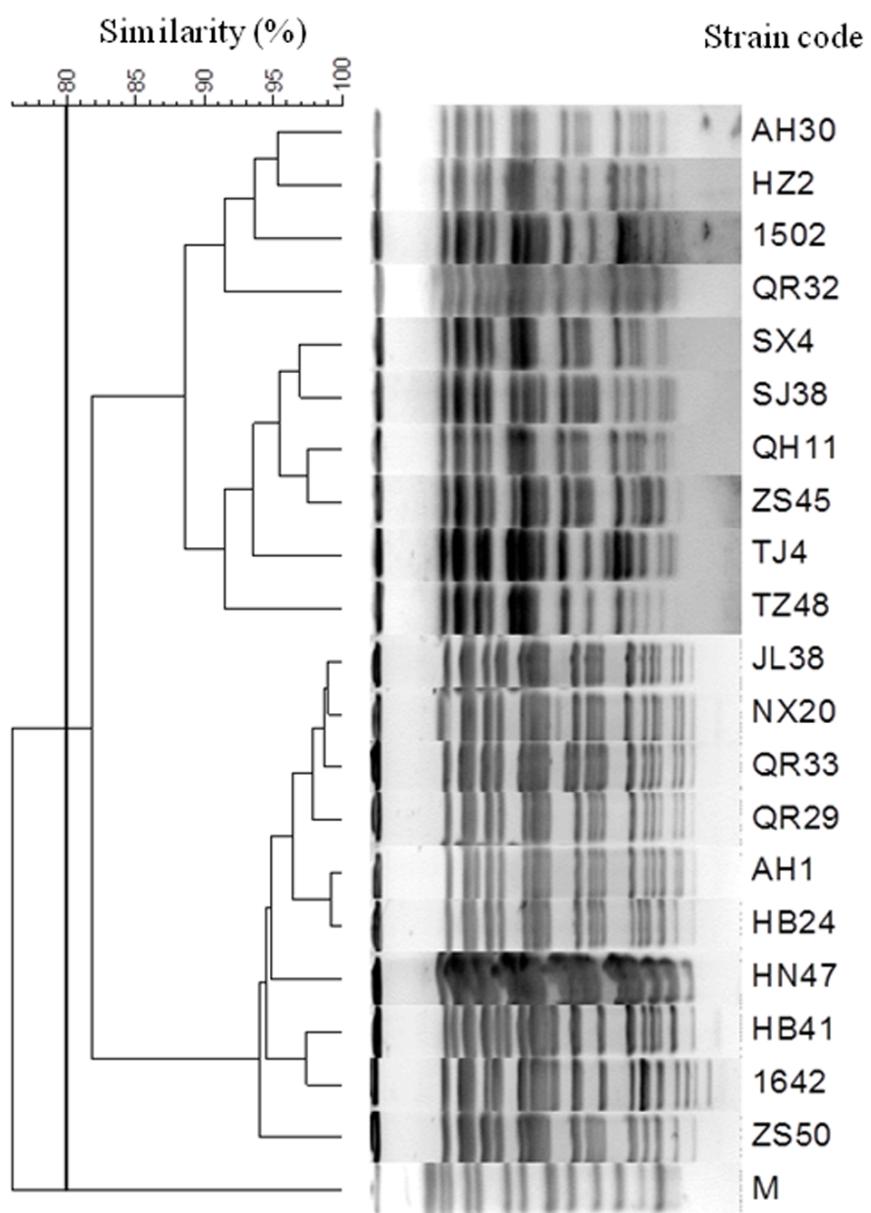


Figure S1 Dendrogram showing the relationship of Cluster I . PFGE profiles were generated by XbaI digestion of genomic DNA. The thick black line indicates 80% banding pattern similarity, used to define strains.

Table S2. Distribution of sequence types(ST) among 111 *E.coli* UTIs isolates carrying *bla*_{CTX-M-55} gene

| ST | Number(%) of isolates |
|-----------------------------|-----------------------|
| ST1193 | 20(18.0) |
| ST405 | 9(8.1) |
| ST156 | 5(4.5) |
| ST2003 | 5(4.5) |
| ST12 | 4(3.6) |
| ST95 | 4(3.6) |
| ST167 | 4(3.6) |
| ST354 | 4(3.6) |
| ST10 | 3(2.7) |
| ST38 | 3(2.7) |
| ST101 | 3(2.7) |
| ST131 | 3(2.7) |
| ST4207 ^a | 1(0.9) |
| ST4208 ^a | 1(0.9) |
| ST4210 ^a | 1(0.9) |
| Various others ^b | |
| Untypable | 5(4.5) |

^a ST4207,4208 and ST4210 were novel to this study

^b Various others: A total of 36 STs occurring in one or 2 isolates each

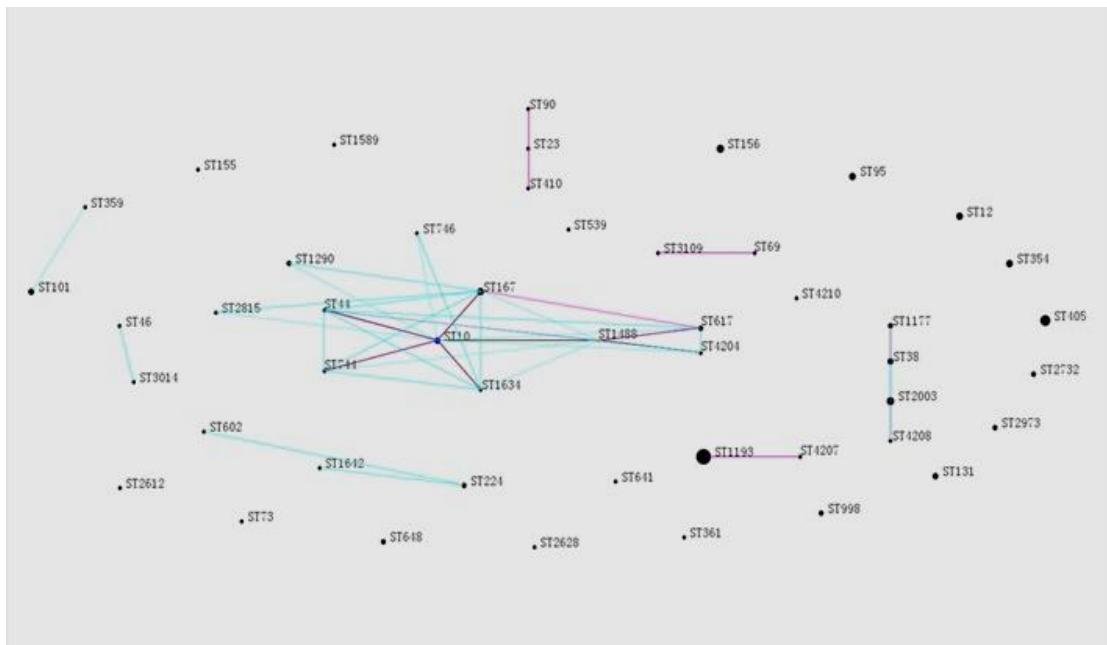


Figure S2 eBURST diagram of ST from isolates in the present study. Each ST is represented by a dot, the size of the dots represents the relative frequency of the ST. Predicted founders are positioned centrally in each cluster and shown in blue, SLVs and DLVs are shown in purple and green, respectively.

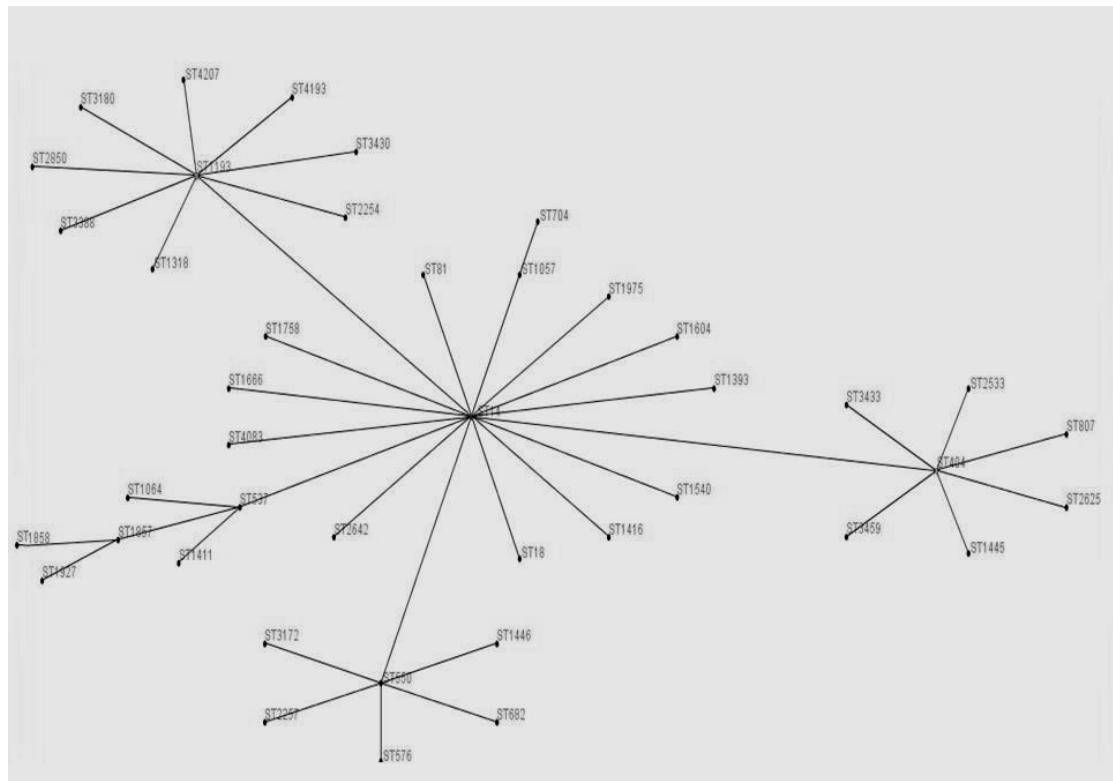


Figure S3 A snapshot of CC14 is shown in an eBURST comparison between the current dataset and all of the information held in the international online database.