**Supplementary information**

**Riverine antibacterial resistance gradient determined by environmental factors**

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|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Site  | Sampling location | Distance from source (km) | Elevation (m) | Co-ordinates |
| 1 | Conservation area | 36 | 666 | 22°47'35.5"N, 120°27'46.9"E |
| 2 | Fuxingdiao bridge | 44 | 569 | 22°47'11.9"N, 120°27'19.3"E |
| 3 | Mount Zion foot | 57 | 354 | 22°54'23.4"N, 120°29'28.3"E |
| 4 | Side bridge | 65.5 | 267 | 22°57'39.3"N, 120°31'20.3"E |
| 5 | Shanlin bridge | 72 | 117 | 22°59'26.7"N, 120°33'05.4"E |
| 6 | Yuemei bridge | 83.5 | 91 | 23°05'47.6"N, 120°35'39.7"E |
| 7 | Qishan town | 88.5 | 44 | 23°09'24.9"N, 120°38'07.3"E |
| 8 | Qimei WWTP | 113 | 31 | 23°14'47.8"N, 120°41'38.2"E |
| 9 | Kaoping river | 120 | 20 | 23°17'17.2"N, 120°43'12.0"E |

**Table S1** Information and website link of the 9 sampling sites along the Qishan river, Kaohsiung city.

<https://www.google.com/maps/d/viewer?mid=1ECk9vgIGULDdrgJHY7AcUEkp86OYWzDf&usp=sharing>

|  |  |  |  |
| --- | --- | --- | --- |
| Antibacterial agent  | Solvent | Diluent | Storage condition |
| Ampicillin  | Water a | Water a | 4°C; light exposure |
| Chloramphenicol  | 95% ethanol  | Water a | 4°C; light protection b |
| Cefotaxime  | Water a | Water a | 4°C; light exposure |
| Ciprofloxacin | Water a | Water a | 4°C; light protection b |
| Erythromycin | 95% ethanol  | Water a | 4°C; light protection b |
| Gentamicin  | Water a | Water a | 4°C; light exposure |
| Tetracycline | 95% ethanol  | Water a | 4°C; light protection b |
| Trimethoprim | DMSO c | Water a | 4°C; light protection b |
| Trimethoprim-sulfamethoxazole (1:19) | DMSO c | Water a | 4°C; light protection b |
| Vancomycin | Water a | Water a | 4°C; light exposure |

**Table S2** Preparation of each stock solution of antibacterial agent for resistance tests

a Double-distilled water

b Shielding with Aluminum foil

c Dimethyl sulfoxide

**Table S3** DNA sequencing of each tested bacterial species

|  |  |  |
| --- | --- | --- |
| **Strain** | **Genbank** | **16s ribosomal RNA sequence** |
| *Escherichia coli* strainNUBRI-E | MN453448.1 | ATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACAGGAAGCAGCTTGCTGCTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAGTAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAATGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGACCTGCGGTTGGATCACCTCCTT |
| *Klebsiella pneumonia* strain 1910ICUP5 | MT225697.1 | GCAAGTCGAGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGTGGGGGACCTTCGGGCCTCATGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTCAGCGGGGAGGAAGGCGTTAAGGTTAATAACCTTGGCGATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGATTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGC |
| *Enterobacter* sp.strain R1W | MG280962.1 | GCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACAGGAAGCAGCTTGCTGCTTCGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGTGTTGAGGTTAATAACCTCAGCAATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTTACCAGAGATGCTTTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTAGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAGTC |
| *Serratia marcescens* strain M9 | KR856196.1 | TGCAGTCGAGCGGTAGCACAAGGAGAGCTTGCTCTCTGGGTGACGAGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTCAGCGAGGAGGAAGGTGGTGAACTTAATACGTTCATCAATTGACGTTACTCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTTGAAACTGGCAAGCTAGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTC |
| *Acinetobacter* sp. WCHAc060042 | MH428811.1 | AGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGGGAAGGTAGCTTGCTACCTAACCTAGCGGCGGACGGGTGAGTAATGCTTAGGAATCTGCCTATTAGTGGGGGACAACATTTCGAAAGGGATGCTAATACCGCATACGCCCTAAGGGGGAAAGCAGGGGATCTTCGGACCTTGCGCTAATAGATGAGCCTAAGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCGACGATCTGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACCGAGATTAATACTCTTGGATAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGATTTACTGGGCGTAAAGCGTGCGTAGGCGGCTTTTTAAGTCGGATGTGAAATCCCCGAGCTTAACTTGGGAATTGCATTCGATACTGGGAAGCTAGAGTATGGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAATACTGACGCTGAGGTACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGCCGTAAACGATGTCTACTAGCCGTTGGGGCCTTTGAGGCTTTAGTGGCGCAGCTAACGCGATAAGTAGACCGCCTGGGGAGTACGGTCGCAAGACTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATAGTAAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTTACATACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTTTCCTTATTTGCCAGCACTTCGGGTGGGAACTTTAAGGATACTGCCAGTGACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGTCGGTACAAAGGGTTGCTACCTAGCGATAGGATGCTAATCTCAAAAAGCCGATCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCACCAGAAGTAGGTAGTCTAACCGCAAGGAGGACGCTTACCACGGTGTGGCCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCT |
| *Staphylococcus aureus* strain ATCC 12600 | NR\_118997.2 | TTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACGGACGAGAAGCTTGCTTCTCTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGTCTTGCTGTCACTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAACTGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCCTTCCCCTTCGGGGGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTACATGAAGCTGGAATCGCTAGTAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTATTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCTTTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTT |
| *Staphylococcus epidermidis*strain: ATCC 14990 | D83363.1 | AGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGTTAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGTTTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTCTGACCCCTCTAGAGATAGAGTTTTCCCCTTCGGGGGACAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAGTAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTG |
| *Bacillus megaterium* strain IMAU80222 | GU125638.1 | GGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACTGATTAGAAGCTTGCTTCTATGACGTTAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCCTGTAAGACTGGGATAACTTCGGGAAACCGAAGCTAATACCGGATAGGATCTTCTCCTTCATGGGAGATGATTGAAAGATGGTTTCGGCTATCACTTACAGATGGGCCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAACAAGTACGAGAGTAACTGCTCGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGAAAAGCGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTTTTTGGTCTGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTTGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTTGACAACTCTAGAGATAGAGCGTTCCCCTTCGGGGGACAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCATTTAGTTGGGCACTTTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGATGGTACAAAGGGCTGCAAGACCGCGAGGTCAAGCCAATCCCATAAAACCATTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGAGTAACCGTAAGGAGCTAGCCGCCTAAGGTGGGACAGATGATTGGGGGAAGTCGTA |
| *Bacillus cereus* strain SP31 | JX317637.1 | CGGGTGCTATACATGCAAGTCGAGCGAATGGATTAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATAACATTTTGAACTGCATGGTTCGAAATTGAAAGGCGGCTTCGGCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGAAAACCCTAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTGGAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTAACCTTTTTGGAGCCAGCCGCCTAAGGTGACAGAGC |
| *Bacillus subtilis* strain XN-80-5 | EU668175.1 | CACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGTAAGAACAAGTGCCGTTCAAATAGGGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGACAATCCTAAGAGATAGGACGTCCCCTTCGGGGCAAGGTGACAGGTGGTGGCATTAGGAAGACAAGTCGTTCAATAAGCGGCACTTGACGGTACTACCAGAAAGGCCACGCTAACTACGTGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTGTCGGAATATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTTCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGACAATCCTAGAGATAGGACGTCCCCTTCGGGGGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCATTCAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGGCAGAACAAAGGGCAGCGAAACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGCTGGAATCGTTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCG |

**Table S4** Principal component analysis (PCA) for physiochemical and bacteriological parameters in Qishan River water.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Variable | PC 1 | PC 2 | PC 3 | PC 4 | PC 5 | PC 6 | PC 7 | PC 8 |
| Temp. | 0.9734 | -0.0128 | 0.0089 | -0.1236 | 0.1129 | 0.1555 | 0.0003 | 0.0070 |
| pH | -0.9817 | -0.0587 | -0.0710 | 0.0749 | -0.0276 | -0.0745 | 0.0887 | -0.0899 |
| Conduct. | 0.9993 | -0.0307 | -0.0214 | 0.0097 | 0.0024 | -0.0005 | -0.0002 | 0.0001 |
| TDS | 0.9991 | -0.0134 | 0.0366 | 0.0036 | 0.0133 | -0.0060 | -0.0010 | 0.0005 |
| Sal. | 0.9979 | -0.0616 | 0.0150 | -0.0096 | -0.0112 | 0.0038 | 0.0013 | -0.0003 |
| DO | -0.9854 | -0.0221 | -0.0573 | -0.0186 | -0.0099 | -0.0821 | 0.1110 | -0.0758 |
| BOD | 0.9854 | -0.0014 | 0.1119 | -0.0091 | -0.0077 | 0.0826 | -0.0915 | 0.0341 |
| TVC | 0.9862 | 0.1646 | -0.0040 | -0.0152 | -0.0034 | -0.0017 | -0.0001 | 0.0001 |
| TE | 0.9881 | 0.1509 | -0.0178 | -0.0173 | 0.0105 | -0.0042 | 0.0033 | -0.0105 |
| TEP | 0.8647 | -0.2960 | -0.1650 | -0.2484 | 0.2479 | 0.1140 | -0.0191 | -0.0309 |
| TC | 0.8553 | 0.4320 | 0.0931 | 0.2655 | -0.0347 | 0.0351 | -0.0055 | -0.0127 |
| TCP | 0.7851 | 0.2874 | 0.1295 | 0.3736 | 0.2845 | 0.1408 | -0.1943 | -0.0787 |
| EC | 0.8566 | 0.4231 | 0.1182 | 0.2525 | -0.0806 | 0.0515 | -0.0135 | 0.0132 |
| ECP | 0.8061 | 0.1889 | 0.2550 | 0.3248 | -0.2580 | 0.1139 | -0.2451 | 0.0667 |
| TS | 0.8360 | 0.5026 | 0.0637 | 0.2054 | -0.0160 | 0.0162 | 0.0404 | 0.0130 |
| TSP | 0.5075 | 0.5656 | 0.0717 | 0.0080 | 0.5906 | -0.0512 | 0.2426 | 0.0839 |
| AB | 0.9810 | 0.1575 | -0.0026 | -0.0344 | 0.0179 | 0.0735 | -0.0553 | 0.0528 |
| ABP | -0.9574 | 0.1591 | -0.0434 | 0.2041 | -0.0868 | -0.0539 | -0.0155 | 0.0618 |
| TB | 0.9901 | 0.1029 | 0.0091 | -0.0431 | 0.0530 | 0.0654 | 0.0062 | 0.0017 |
| TBP | -0.9885 | 0.0595 | -0.0062 | 0.0664 | 0.0545 | 0.0026 | 0.1088 | 0.0055 |
|  |  |  |  |  |  |  |  |  |
| Eigen value | 82441.0000 | 571.8070 | 40.9401 | 31.7871 | 9.0787 | 3.8401 | 1.5724 | 0.3909 |
| Variance | 99.21% | 0.69% | 0.05% | 3.83% | 1.09% | 0.46% | 0.19% | 0.05% |

**Table S5A** Results of growth zone diameters (GIDs) for*E. coli*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 19.67 a | 18.67 a | 15.33 b | 10.33 c | 159.3333 | <0.0001 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.58 |  |  |
| Chl | Mean | 19.00 a | 16.00 b | 11.67 c | 11.67 c | 231.1700 | <0.0001 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Cip | Mean | 24.00 a | 23.00 a | 16.33 b | 13.33 c | 192.2700 | <0.0001 |
|  | SD | 0.00 | 1.00 | 0.58 | 0.58 |  |  |
| Ctx | Mean | 30.33 a | 30.00 a | 29.67 a | 30.33 a | 0.6111 | 0.6265 |
|  | SD | 0.58 | 1.00 | 0.58 | 0.58 |  |  |
| Ery | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Gen | Mean | 17.00 a | 16.00 b | 16.33ab | 16.00 b | 8.0000 | 0.0086 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.00 |  |  |
| Sxt | Mean | 16.00 a | 16.33 ab | 17.00 b | 16.00 a | 8.0000 | 0.0086 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.00 |  |  |
| Tet | Mean | 16.00 a | 15.00 a | 10.33 b | 9.67 b | 185.8300 | <0.0001 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Tmp | Mean | 18.00 a | 16.67 b | 17.00 ab | 16.33 b | 9.3333 | 0.0054 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.58 |  |  |
| Van | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|   | SD | 0.00 | 0.00 | 0.00 | 0.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5B** Results of growth zone diameters (GIDs) for *K. pneumonia*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 23.00 a | 22.00 a | 22.33 a | 14.00 b | 162.0000 | <0.0001 |
|  | SD | 0.00 | 1.00 | 0.58 | 0.00 |  |  |
| Chl | Mean | 18.00 a | 15.00 b | 11.00 c | 10.33 c | 465.0000 | <0.0001 |
|  | SD | 0.00 | 0.00 | 0.00 | 0.58 |  |  |
| Cip | Mean | 21.67 a | 21.33 a | 18.00 b | 18.00 b | 29.5330 | 0.0001 |
|  | SD | 1.15 | 0.58 | 0.00 | 0.00 |  |  |
| Ctx | Mean | 29.67 a | 29.00 a | 29.33 a | 29.00 a | 0.3333 | 0.8018 |
|  | SD | 1.15 | 0.00 | 1.53 | 0.00 |  |  |
| Ery | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Gen | Mean | 20.00 a | 20.00 a | 19.00 b | 18.67 b | 17.0000 | 0.0008 |
|  | SD | 0.00 | 0.00 | 0.00 | 0.58 |  |  |
| Sxt | Mean | 19.00 a | 18.67 a | 19.00 a | 18.33 a | 1.8333 | 0.2192 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.58 |  |  |
| Tet | Mean | 16.00 a | 15.67 a | 10.00 b | 12.67 c | 143.1700 | <0.0001 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.58 |  |  |
| Tmp | Mean | 20.00 a | 19.67 a | 19.00 a | 19.33 a | 3.3333 | 0.0770 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.58 |  |  |
| Van | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|   | SD | 0.00 | 0.00 | 0.00 | 0.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5C** Results of growth zone diameters (GIDs) for *Enterobacter* sp.; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 5 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 18.67 a | 18.00 a | 17.67 a | 14.67 b | 37.6667 | <0.0001 |
|  | SD | 0.58 | 0.00 | 0.58 | 0.58 |  |  |
| Chl | Mean | 19.00 a | 13.00 b | 8.67 c | 9.67 c | 391.1700 | <0.0001 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Cip | Mean | 25.00 a | 25.33 a | 25.00 a | 19.67 b | 133.8300 | <0.0001 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.58 |  |  |
| Ctx | Mean | 27.00 a | 27.00 a | 27.00 a | 27.00 a | ─ | ─ |
|  | SD | 0.00 | 1.00 | 1.00 | 0.00 |  |  |
| Ery | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Gen | Mean | 20.00 a | 19.67 ab | 19.33 ab | 18.67 b | 3.8889 | 0.0553 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Sxt | Mean | 19.67 ab | 20.00 a | 19.00 ab | 18.67 b | 6.6667 | 0.0144 |
|  | SD | 0.58 | 0.00 | 0.00 | 0.58 |  |  |
| Tet | Mean | 16.00 a | 12.33 b | 11.00 b | 12.00 c | 172.0000 | <0.0001 |
|  | SD | 0.00 | 0.58 | 0.00 | 0.00 |  |  |
| Tmp | Mean | 17.33 a | 17.33 a | 16.33 a | 16.33 a | 3.0000 | 0.0951 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.58 |  |  |
| Van | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|   | SD | 0.00 | 0.00 | 0.00 | 0.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5D** Results of growth zone diameters (GIDs) for *S. marcescens*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 18.33 a | 17.33 ab | 17.00 b | 12.00 c | 144.6667 | <0.0001 |
|  | SD | 0.58 | 0.58 | 0.00 | 0.00 |  |  |
| Chl | Mean | 23.67 a | 22.33 a | 20.33 b | 20.67 b | 21.5830 | 0.0003 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.58 |  |  |
| Cip | Mean | 27.00 a | 27.00 a | 24.33 b | 17.00 c | 201.0000 | <0.0001 |
|  | SD | 1.00 | 0.00 | 0.58 | 0.00 |  |  |
| Ctx | Mean | 30.00 a | 29.67 a | 29.67 a | 29.67 a | 0.2963 | 0.8272 |
|  | SD | 1.00 | 0.58 | 0.58 | 1.15 |  |  |
| Ery | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Gen | Mean | 24.00 a | 23.33 a | 23.00 a | 22.67 a | 1.4583 | 0.2970 |
|  | SD | 1.00 | 0.58 | 1.00 | 0.58 |  |  |
| Sxt | Mean | 16.00 a | 16.00 a | 15.67 ab | 15.00 b | 8.0000 | 0.0086 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.00 |  |  |
| Tet | Mean | 16.00 a | 14.00 b | 13.33 b | 13.67 b | 25.8330 | 0.0002 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Tmp | Mean | 21.00 a | 20.67 a | 20.67 a | 19.33 b | 6.5556 | 0.0151 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Van | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|   | SD | 0.00 | 0.00 | 0.00 | 0.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5E** Results of growth zone diameters (GIDs) for *Acinetobacter* sp.; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Chl | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Cip | Mean | 24.00 a | 23.00 a | 22.33 a | 15.33 b | 112.2700 | <0.0001 |
|  | SD | 1.00 | 0.00 | 0.58 | 0.58 |  |  |
| Ctx | Mean | 26.33 a | 26.00 a | 25.33 a | 26.00 a | 1.2667 | 0.3493 |
|  | SD | 0.58 | 0.00 | 0.58 | 1.00 |  |  |
| Ery | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Gen | Mean | 20.00 a | 18.00 b | 18.00 b | 18.00 b | 12.0000 | 0.0025 |
|  | SD | 0.00 | 0.00 | 0.00 | 1.00 |  |  |
| Sxt | Mean | 20.00 a | 20.00 a | 20.00 a | 20.00 a | 0.0000 | 1.0000 |
|  | SD | 0.00 | 0.00 | 0.00 | 0.00 |  |  |
| Tet | Mean | 17.33 a | 14.00 b | 10.67 c | 9.67 c | 145.2200 | <0.0001 |
|  | SD | 0.58 | 0.00 | 0.58 | 0.58 |  |  |
| Tmp | Mean | 22.00 a | 22.33 a | 21.67 a | 21.67 a | 1.2220 | 0.3630 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Van | Mean | 0.00 | 0.00 | 0.00 | 0.00 | ─ | ─ |
|   | SD | 0.00 | 0.00 | 0.00 | 0.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5F** Results of growth zone diameters (GIDs) for *S. aureus*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 32.67 a | 32.00 ab | 31.00 ab  | 30.00 b | 4.9000 | 0.0321 |
|  | SD | 1.15 | 1.00 | 0.00 | 1.00 |  |  |
| Chl | Mean | 21.67 a | 14.33 b | 11.67 c  | 12.00 c | 259.8900 | <0.0001 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.00 |  |  |
| Cip | Mean | 24.33 a | 24.67 a | 24.33 a | 21.67 b | 10.0480 | 0.0043 |
|  | SD | 0.58 | 1.15 | 0.58 | 0.58 |  |  |
| Ctx | Mean | 28.33 a | 27.67 a | 27.67 a | 27.33 a | 0.6333 | 0.6140 |
|  | SD | 0.58 | 0.58 | 1.53 | 0.58 |  |  |
| Ery | Mean | 25.00 a | 24.00 a | 19.67 b | 18.33 c | 189.9300 | <0.0001 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Gen | Mean | 18.00 a | 17.67 a | 17.67 a | 17.33 a | 0.4440 | 0.7278 |
|  | SD | 0.00 | 0.58 | 1.15 | 0.58 |  |  |
| Sxt | Mean | 17.00 a | 17.33 a | 17.67 a | 17.00 a | 1.8333 | 0.2192 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.00 |  |  |
| Tet | Mean | 20.00 a | 19.67 a | 14.67 b | 12.67 c | 160.3333 | <0.0001 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Tmp | Mean | 22.00 a | 21.67 a | 21.33 a | 21.33 a | 1.2220 | 0.3630 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Van | Mean | 20.67 a | 20.67 a | 15.33 b | 15.67 b | 80.2500 | <0.0001 |
|   | SD | 0.58 | 0.58 | 0.58 | 0.58 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5G** Results of growth zone diameters (GIDs) for *S. epidermidis*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 4 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 32.00 a | 32.33 a | 31.33 ab | 29.00 b | 5.8095 | 0.0208 |
|  | SD | 0.00 | 1.53 | 1.53 | 0.00 |  |  |
| Chl | Mean | 19.67 a | 15.33 b | 11.67 c | 11.33 c | 136.3333 | <0.0001 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.58 |  |  |
| Cip | Mean | 23.33 a | 23.33 a | 23.00 a | 21.67 b | 7.5556 | 0.0101 |
|  | SD | 0.58 | 0.58 | 0.00 | 0.58 |  |  |
| Ctx | Mean | 27.67 a | 27.33 a | 27.00 a | 26.33 a | 0.9722 | 0.4521 |
|  | SD | 0.58 | 1.53 | 1.00 | 0.58 |  |  |
| Ery | Mean | 28.00 a | 25.67 b | 20.33 c | 19.67 c | 66.1850 | <0.0001 |
|  | SD | 1.00 | 1.15 | 0.58 | 0.58 |  |  |
| Gen | Mean | 17.33 a | 17.67 a | 17.00 a | 17.00 a | 0.7333 | 0.5607 |
|  | SD | 0.58 | 0.58 | 1.00 | 0.00 |  |  |
| Sxt | Mean | 16.67 a | 16.33 a | 16.00 a | 16.33 a | 0.4440 | 0.7278 |
|  | SD | 0.58 | 0.58 | 1.00 | 0.58 |  |  |
| Tet | Mean | 21.67 a | 20.67 a | 16.00 b | 15.33 b | 61.9440 | <0.0001 |
|  | SD | 0.58 | 0.58 | 1.00 | 0.58 |  |  |
| Tmp | Mean | 21.33 a | 20.33 ab | 20.33 ab | 20.00 b | 4.0000 | 0.0519 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.00 |  |  |
| Van | Mean | 20.33 a | 20.00 a | 15.67 b | 15.33 b | 87.5560 | <0.0001 |
|   | SD | 0.58 | 0.00 | 0.58 | 0.58 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5H** Results of growth zone diameters (GIDs) for *B. megatium*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 34.67 a | 34.00 ab | 33.33 b | 31.33 c | 24.8889 | 0.0002 |
|  | SD | 0.58 | 0.00 | 0.58 | 0.58 |  |  |
| Chl | Mean | 21.33 a | 19.67 ab | 18.67 b | 18.33 b | 9.3333 | 0.0054 |
|  | SD | 0.58 | 1.15 | 0.58 | 0.58 |  |  |
| Cip | Mean | 24.33 a | 25.00 a | 24.33 a | 18.33 b | 29.3333 | 0.0001 |
|  | SD | 1.53 | 1.00 | 0.58 | 0.58 |  |  |
| Ctx | Mean | 24.00 a | 23.33 a | 23.00 a | 22.67 a | 0.8333 | 0.5122 |
|  | SD | 1.00 | 1.15 | 1.00 | 1.15 |  |  |
| Ery | Mean | 23.33 a | 21.33 ab | 19.67 b | 20.00 b | 16.6110 | 0.0008 |
|  | SD | 0.58 | 0.58 | 0.58 | 1.00 |  |  |
| Gen | Mean | 20.67 a | 20.67 a | 19.67 a | 20.33 a | 1.1429 | 0.3889 |
|  | SD | 0.58 | 0.58 | 0.58 | 1.15 |  |  |
| Sxt | Mean | 20.00 a | 19.00 a | 19.67 a | 19.33 a | 3.3333 | 0.0770 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.58 |  |  |
| Tet | Mean | 20.67 a | 19.33 b | 19.00 b | 18.67 b | 9.2222 | 0.0056 |
|  | SD | 0.58 | 0.58 | 0.00 | 0.58 |  |  |
| Tmp | Mean | 19.00 a | 18.00 b  | 18.67 ab | 18.00 b | 9.0000 | 0.0061 |
|  | SD | 0.00 | 0.00 | 0.58 | 0.00 |  |  |
| Van | Mean | 18.67 a | 18.33 a | 14.67 b | 15.00 b | 27.1110 | 0.0002 |
|   | SD | 0.58 | 0.58 | 0.58 | 1.00 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5I** Results of growth zone diameters (GIDs) for *B. cereus*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 34.33 a | 33.33 ab | 33.00 b | 31.33 c | 18.6667 | 0.0006 |
|  | SD | 0.58 | 0.58 | 0.00 | 0.58 |  |  |
| Chl | Mean | 25.00 a | 23.33 a | 19.33 b | 20.67 b | 26.1850 | 0.0002 |
|  | SD | 1.00 | 1.15 | 0.58 | 0.58 |  |  |
| Cip | Mean | 26.33 a | 25.00 a | 25.67 a | 20.00 b | 27.2420 | 0.0001 |
|  | SD | 0.58 | 1.00 | 1.53 | 0.00 |  |  |
| Ctx | Mean | 21.67 a | 21.00 a | 22.33 a | 21.67 a | 0.8889 | 0.4872 |
|  | SD | 0.58 | 1.00 | 1.15 | 1.15 |  |  |
| Ery | Mean | 23.67 a | 22.67 ab  | 21.33 b | 21.33 b | 6.6190 | 0.0147 |
|  | SD | 0.58 | 1.15 | 0.58 | 0.58 |  |  |
| Gen | Mean | 16.67 a | 16.00 ab | 15.33 b | 16.00 ab | 5.3333 | 0.0260 |
|  | SD | 0.58 | 0.00 | 0.58 | 0.00 |  |  |
| Sxt | Mean | 19.00 a | 18.33 a | 18.67 a | 18.67 a | 0.8889 | 0.4872 |
|  | SD | 0.00 | 0.58 | 0.58 | 0.58 |  |  |
| Tet | Mean | 22.33 a | 20.67 b | 17.00 c  | 17.67 c | 75.8889 | <0.0001 |
|  | SD | 0.58 | 0.58 | 0.00 | 0.58 |  |  |
| Tmp | Mean | 18.00 a | 18.00 a | 18.00 a | 17.67 a | 1.0000 | 0.4411 |
|  | SD | 0.00 | 0.00 | 0.00 | 0.58 |  |  |
| Van | Mean | 17.00 a | 17.00 a | 13.33 b | 13.33 b | 20.1667 | 0.0004 |
|   | SD | 0.00 | 1.00 | 0.58 | 1.15 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S5J** Results of growth zone diameters (GIDs) for *B. subtilis*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | GID (mm) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 34.33 a | 33.67 a | 33.67 a | 32.00 a | 2.3778 | 0.1456 |
|  | SD | 1.15 | 0.58 | 1.53 | 1.00 |  |  |
| Chl | Mean | 23.67 a | 22.33 a | 19.67 b | 20.00 b | 21.9440 | 0.0003 |
|  | SD | 0.58 | 0.58 | 0.58 | 1.00 |  |  |
| Cip | Mean | 27.33 a | 25.67 a | 26.67 a | 24.67 b | 3.7692 | 0.0592 |
|  | SD | 1.15 | 1.53 | 0.58 | 0.58 |  |  |
| Ctx | Mean | 24.67 a | 23.33 a | 24.33 a | 23.67 a | 3.3333 | 0.0770 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.58 |  |  |
| Ery | Mean | 26.33 a | 25.33 a | 17.33 b | 17.67 b | 84.0000 | <0.0001 |
|  | SD | 0.58 | 0.58 | 1.53 | 0.58 |  |  |
| Gen | Mean | 18.67 a | 18.33 a | 17.67 a | 18.00 a | 2.2222 | 0.1631 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.00 |  |  |
| Sxt | Mean | 19.00 a | 19.33 a | 19.00 a | 18.67 a | 0.1905 | 0.9000 |
|  | SD | 1.00 | 1.15 | 1.00 | 1.15 |  |  |
| Tet | Mean | 22.67 a | 21.00 a | 16.67 b | 17.00 b | 63.4670 | <0.0001 |
|  | SD | 0.58 | 0.00 | 0.58 | 1.00 |  |  |
| Tmp | Mean | 19.33 a | 18.33 a | 18.67 a | 19.00 a | 2.2222 | 0.1631 |
|  | SD | 0.58 | 0.58 | 0.58 | 0.00 |  |  |
| Van | Mean | 16.33 a | 16.00 ac | 14.00 b | 14.33 bc | 9.8667 | 0.0046 |
|   | SD | 0.58 | 0.00 | 1.00 | 0.58 |   |   |

Different alphabet among the mean values of the zone diameters indicates significant at 5% level using Tukey tests.

**Table S6A** Results of minimum inhibitory concentrations (MICs) for*E. coli*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 2.52 a | 4.00 a | 16.00 b | 25.40 b | 45.3333 | <0.0001 |
|  | SD | 0.974 | 0.000 | 0.000 | 9.815 |  |  |
| Chl | Mean | 8.00 a | 16.00 b  | 32.00 c | 25.40 bc | 28.0000 | 0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 9.815 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 1.00 b | 1.00 b | ∞ | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ctx | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Gen | Mean | 0.40 a | 0.40 a | 0.40 a | 0.50 a | 0.3333 | 0.8018 |
|  | SD | 0.153 | 0.153 | 0.153 | 0.000 |  |  |
| Sxt | Mean | 2.00 a | 2.00 a | 2.00 a | 2.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tet | Mean | 2.00 a | 8.00 b | 32.00 c | 32.00 c | ∞ | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 8.00 a | 8.00 a | 8.00 a | 8.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|   | SD | 0.000 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6B** Results of minimum inhibitory concentrations (MICs) for*K. pneumonia*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 4.00 a | 5.04 ab | 8.00 b | 16.00 c | 28.0000 | 0.0001 |
|  | SD | 0.000 | 1.948 | 0.000 | 0.000 |  |  |
| Chl | Mean | 6.35 a | 8.00 a | 16.00 b | 25.40 b | 15.1667 | 0.0012 |
|  | SD | 2.454 | 0.000 | 0.000 | 9.815 |  |  |
| Cip | Mean | 0.79 a | 0.79 a | 1.00 a | 2.00 a | 7.1667 | 0.0118 |
|  | SD | 0.307 | 0.307 | 0.000 | 0.000 |  |  |
| Ctx | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Gen | Mean | 0.25 a | 0.25 a | 0.25 a | 0.25 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tet | Mean | 4.00 a | 8.00 b | 16.00 c | 12.70 bc | 28.0000 | 0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 4.908 |  |  |
| Tmp | Mean | 6.35 a | 6.35 a | 8.00 a | 8.00 a | 0.6667 | 0.5957 |
|  | SD | 2.454 | 2.454 | 0.000 | 0.000 |  |  |
| Van | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|   | SD | 0.000 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6C** Results of minimum inhibitory concentrations (MICs) for *Enterobacter* sp.; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 5 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 4.00 a | 4.00 a | 8.00 b | 8.00 b | ∞ | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Chl | Mean | 2.00 a | 6.35 b | 32.00 c | 25.40 c | 62.6667 | <0.0001 |
|  | SD | 0.000 | 2.454 | 0.000 | 9.815 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 1.00 b | 2.52 c | 44.0000 | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.974 |  |  |
| Ctx | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Gen | Mean | 0.25 a | 0.25 a | 0.25 a | 0.25 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tet | Mean | 2.00 a | 2.52 a | 16.00 b | 10.08 b | 39.1667 | <0.0001 |
|  | SD | 0.000 | 0.974 | 0.000 | 3.895 |  |  |
| Tmp | Mean | 6.35 a | 8.00 a | 8.00 a | 8.00 a | 1.0000 | 0.4411 |
|  | SD | 2.454 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|   | SD | 0.000 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6D** Results of minimum inhibitory concentrations (MICs) for*S. marcescens*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 2.00 a | 2.00 a | 2.52 a | 6.35 b | 11.3333 | 0.0030 |
|  | SD | 0.000 | 0.000 | 0.974 | 2.454 |  |  |
| Chl | Mean | 4.00 a | 4.00 a | 16.00 b | 16.00 b | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 1.00 b | 2.00 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ctx | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Gen | Mean | 0.25 a | 0.25 a | 0.25 a | 0.25 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 1.59 a | 2.00 a | 2.00 a | 2.00 a | 1.0000 | 0.4411 |
|  | SD | 0.613 | 0.000 | 0.000 | 0.000 |  |  |
| Tet | Mean | 4.00 a | 8.00 ab | 12.70 b | 10.08 b | 9.3333 | 0.0054 |
|  | SD | 0.000 | 0.000 | 4.908 | 3.895 |  |  |
| Tmp | Mean | 8.00 a | 8.00 a | 8.00 a | 8.00 a | 0.0000 | 1.0000 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|   | SD | 0.000 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6E** Results of minimum inhibitory concentrations (MICs) for*Acinetobacter* sp.; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 16.00 a | 16.00 a | 16.00 a | 16.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Chl | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 0.50 a | 0.79 a | 4.0000 | 0.0519 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.307 |  |  |
| Ctx | Mean | 4.00 a | 4.00 a | 5.04 a | 4.00 a | 1.0000 | 0.4411 |
|  | SD | 0.000 | 0.000 | 1.948 | 0.000 |  |  |
| Ery | Mean | 32.00 a | 32.00 a | 32.00 a | 32.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Gen | Mean | 2.00 a | 2.52 a | 2.52 a | 2.52 a | 0.3333 | 0.8018 |
|  | SD | 0.000 | 0.974 | 0.974 | 0.974 |  |  |
| Sxt | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tet | Mean | 1.00 a | 4.00 b | 8.00 c | 8.00 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 0.25 a | 0.25 a | 0.31 a | 0.31 a | 0.6667 | 0.5957 |
|  | SD | 0.000 | 0.000 | 0.122 | 0.122 |  |  |
| Van | Mean | 32.00 a | 32.00 a  | 32.00 a | 32.00 a | ─ | ─ |
|   | SD | 0.000 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6F** Results of minimum inhibitory concentrations (MICs) for*S. aureus*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 3 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.13 a | 0.13 a | 0.13 a | 0.13 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Chl | Mean | 4.00 a | 16.00 b | 16.00 b | 25.40 b | 48.0000 | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 9.815 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 0.63 ab | 1.00 b | 8.0000 | 0.0086 |
|  | SD | 0.000 | 0.000 | 0.243 | 0.000 |  |  |
| Ctx | Mean | 2.00 a | 2.00 a | 2.00 a | 2.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 0.50 a | 1.26 b | 8.00 c | 12.70 c | 87.3333 | <0.0001 |
|  | SD | 0.000 | 0.487 | 0.000 | 4.908 |  |  |
| Gen | Mean | 0.79 a | 0.79 a | 0.79 a | 1.00 a  | 0.3333 | 0.8018 |
|  | SD | 0.307 | 0.307 | 0.307 | 0.000 |  |  |
| Sxt | Mean | 0.50 a | 0.50 a | 0.63 a | 0.63 a | 0.6667 | 0.5957 |
|  | SD | 0.000 | 0.000 | 0.243 | 0.243 |  |  |
| Tet | Mean | 2.00 a | 8.00 b | 8.00 b | 16.00 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 1.00 a | 1.00 a | 6.35 b | 8.00 b | 97.0000 | <0.0001 |
|   | SD | 0.000 | 0.000 | 2.454 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6G** Results of minimum inhibitory concentrations (MICs) for*S. epidermidis*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 4 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.13 a | 0.13 a | 0.13 a | 0.13 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Chl | Mean | 5.04 a | 25.40 b | 32.00 b | 25.40 b | 18.2220 | 0.0006 |
|  | SD | 1.948 | 9.815 | 0.000 | 9.815 |  |  |
| Cip | Mean | 0.50 a | 0.50 a | 0.63 ab | 1.00 b | 8.0000 | 0.0086 |
|  | SD | 0.000 | 0.000 | 0.243 | 0.000 |  |  |
| Ctx | Mean | 2.00 a | 2.00 a | 2.00 a | 2.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 0.25 a | 2.52 b | 8.00 b | 8.00 b | 200.0000 | <0.0001 |
|  | SD | 0.000 | 0.974 | 0.000 | 0.000 |  |  |
| Gen | Mean | 1.00 a | 1.00 a | 1.00 a | 1.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 0.50 a | 0.50 a | 0.63 a | 0.63 a | 0.6667 | 0.5957 |
|  | SD | 0.000 | 0.000 | 0.243 | 0.243 |  |  |
| Tet | Mean | 2.00 a | 4.00 b  | 8.00 c | 8.00 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 0.79 a | 0.79 a | 1.00 a | 1.00 a | 0.6667 | 0.5957 |
|  | SD | 0.307 | 0.307 | 0.000 | 0.000 |  |  |
| Van | Mean | 0.63 a | 2.00 b | 8.00 c | 8.00 c | 113.0000 | <0.0001 |
|   | SD | 0.243 | 0.000 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6H** Results of minimum inhibitory concentrations (MICs) for*B. megatium*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.13 a | 0.13 a | 0.16 ab | 0.25 b | 8.0000 | 0.0086 |
|  | SD | 0.000 | 0.000 | 0.061 | 0.000 |  |  |
| Chl | Mean | 2.52 a | 6.35 b | 8.00 b | 8.00 b | 11.1667 | 0.0031 |
|  | SD | 0.974 | 2.454 | 0.000 | 0.000 |  |  |
| Cip | Mean | 0.25 a | 0.25 a | 0.50 b | 0.50 b | 0.6667 | 0.5957 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Ctx | Mean | 1.00 a | 1.00 a | 1.26 a | 1.26 a | 15.1667 | 0.0012 |
|  | SD | 0.000 | 0.000 | 0.487 | 0.487 |  |  |
| Ery | Mean | 0.50 a | 0.50 a | 2.00 b | 1.59 b | 41.0000 | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.613 |  |  |
| Gen | Mean | 2.00 a | 2.00 a | 2.00 a | 2.00 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 0.25 a | 0.25 a | 0.25 a | 0.31 a | 1.0000 | 0.4411 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.122 |  |  |
| Tet | Mean | 2.00 a | 4.00 b | 8.00 c | 8.00 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 0.50 a | 0.50 a | 0.50 a | 0.50 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 2.00 a | 2.52 b | 4.00 b | 4.00 b | 11.1667 | 0.0031 |
|   | SD | 0.000 | 0.974 | 0.000 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6I** Results of minimum inhibitory concentrations (MICs) for*B. cereus*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.13 a | 0.13 a | 0.16 ab | 0.25 b | 8.0000 | 0.0086 |
|  | SD | 0.000 | 0.000 | 0.061 | 0.000 |  |  |
| Chl | Mean | 2.00 a | 5.04 b | 8.00 b | 8.00 b | 32.0000 | 0.0001 |
|  | SD | 0.000 | 1.948 | 0.000 | 0.000 |  |  |
| Cip | Mean | 0.25 a | 0.25 a | 0.63 b | 1.00 b | 8.0000 | 0.0086 |
|  | SD | 0.000 | 0.000 | 0.243 | 0.000 |  |  |
| Ctx | Mean | 0.79 a | 0.79 a | 0.79 a | 1.00 a | 0.0833 | 0.8018 |
|  | SD | 0.307 | 0.307 | 0.307 | 0.000 |  |  |
| Ery | Mean | 0.31 a | 1.00 b | 1.26 b | 1.00 b | 14.6667 | 0.0013 |
|  | SD | 0.122 | 0.000 | 0.487 | 0.000 |  |  |
| Gen | Mean | 1.59 a | 2.00 a | 2.00 a | 2.00 a | 1.0000 | 0.4411 |
|  | SD | 0.613 | 0.000 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 0.25 a | 0.25 a | 0.31 a | 0.31 a | 0.6667 | 0.5957 |
|  | SD | 0.000 | 0.000 | 0.122 | 0.122 |  |  |
| Tet | Mean | 1.00 a | 2.52 b | 2.52 b | 4.00 b | 12.6667 | 0.0021 |
|  | SD | 0.000 | 0.974 | 0.974 | 0.000 |  |  |
| Tmp | Mean | 0.40 a | 0.50 a | 0.50 a | 0.50 a | 1.0000 | 0.4411 |
|  | SD | 0.153 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 1.00 a | 2.00 b | 2.52 b | 2.00 b | 12.0000 | 0.0025 |
|   | SD | 0.000 | 0.000 | 0.974 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S6J** Results of minimum inhibitory concentrations (MICs) for*B. subtilis*; *F*critical = 4.0662, *α* = 0.05

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibacterial | MIC (μg mL-1) |   |   |   |
|   |   | Site 1 | Site 7 | Site 8 | Site 9 | *F* | *p* |
| Amp | Mean | 0.125 a | 0.125 a | 0.125 a | 0.198 a | 4.0000 | 0.0519 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.077 |  |  |
| Chl | Mean | 2.000 a | 2.000 a | 8.000 b | 8.000 b | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Cip | Mean | 0.250 a | 0.250 a | 0.500 b | 0.794 b | 24.0000 | 0.0002 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.307 |  |  |
| Ctx | Mean | 0.794 a | 1.000 a | 1.000 a | 1.000 a | 1.0000 | 0.4411 |
|  | SD | 0.307 | 0.000 | 0.000 | 0.000 |  |  |
| Ery | Mean | 0.500 a | 0.500 a | 2.000 b | 1.587 b | 41.0000 | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.613 |  |  |
| Gen | Mean | 1.587 a | 1.587 a | 2.000 a | 2.000 a | 0.6667 | 0.5957 |
|  | SD | 0.613 | 0.613 | 0.000 | 0.000 |  |  |
| Sxt | Mean | 0.250 a | 0.250 a | 0.315 a | 0.250 a | 1.0000 | 0.4411 |
|  | SD | 0.000 | 0.000 | 0.122 | 0.000 |  |  |
| Tet | Mean | 1.000 a | 2.000 b | 4.000 c | 4.000 c | ∞  | <0.0001 |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Tmp | Mean | 0.500 a | 0.500 a | 0.500 a | 0.500 a | ─ | ─ |
|  | SD | 0.000 | 0.000 | 0.000 | 0.000 |  |  |
| Van | Mean | 1.000 a | 1.260 ab | 2.520 b | 2.000 ab | 6.6667 | 0.0144 |
|   | SD | 0.000 | 0.487 | 0.974 | 0.000 |   |   |

Different alphabet among the mean values of the MICs indicates significant at 5% level using Tukey tests.

**Table S7A** Intensity of antibiotic action on *Enterobacteriaceae* recommended by CLSI (*S*=susceptible, *I*=intermediate, *R*=resistant)

|  |  |  |
| --- | --- | --- |
| Antibiotic | Zone diameter breakpoints (mm) | MIC breakpoints (μg mL-1) |
|   |   | Disk content | *S* | *I* | *R* | *S* | *I* | *R* |
| Ampicillin | 10μg | ≥17 | 14─16 | ≤13 | 8≤ | 16 | ≥32 |
| Chloramphenicol | 30μg | ≥18 | 13─17 | ≤12 | 8≤ | 16 | ≥32 |
| Ciprofloxacin | 5μg | ≥21 | 16─20 | ≤15 | 1≤ | 2 | ≥4 |
| Cefotaxime | 30μg | ≥26 | 23─25 | ≤22 | 1≤ | 2 | ≥4 |
| Erythromycin | 15μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Gentamicin | 10μg | ≥15 | 13─14 | ≤12 | 4≤ | 8 | ≥16 |
| Trimethoprin-sulfamethoxazole | 1.25/23.75μg | ≥16 | 11─15 | ≤10 | 2≤ | ─ | ≥4 |
| Tetracycline | 30μg | ≥15 | 12─14 | ≤11 | 4≤ | 8 | ≥16 |
| Trimethoprin | 5μg | ≥16 | 11─15 | ≤10 | 8≤ | ─ | ≥16 |
| Vancomycin | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |

**Table S7B** Intensity of antibiotic actionon *Acinetobacter* spp. recommended by CLSI (*S*=susceptible, *I*=intermediate, *R*=resistant)

|  |  |  |
| --- | --- | --- |
| Antibiotic | Zone diameter breakpoints (mm) | MIC breakpoints (μg mL-1) |
|   |   | Disk content | *S* | *I* | *R* | *S* | *I* | *R* |
| Ampicillin | 10μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Chloramphenicol | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Ciprofloxacin | 5μg | ≥21 | 16─20 | ≤15 | 1≤ | 2 | ≥4 |
| Cefotaxime | 30μg | ≥23 | 15─22 | ≤14 | 8≤ | 16─32 | ≥64 |
| Erythromycin | 15μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Gentamicin | 10μg | ≥15 | 13─14 | ≤12 | 4≤ | 8 | ≥16 |
| Trimethoprin-sulfamethoxazole | 1.25/23.75μg | ≥16 | 11─15 | ≤10 | 2≤ | ─ | ≥4 |
| Tetracycline | 30μg | ≥15 | 12─14 | ≤11 | 4≤ | 8 | ≥16 |
| Trimethoprin | 5μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Vancomycin | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |

**Table S7C** Intensity of antibiotic actionon *Staphylococcus* spp. recommended by CLSI (*S*=susceptible, *I*=intermediate, *R*=resistant)

|  |  |  |
| --- | --- | --- |
| Antibiotic | Zone diameter breakpoints (mm) | MIC breakpoints (μg mL-1) |
|   |   | Disk content | *S* | *I* | *R* | *S* | *I* | *R* |
| Ampicillin | 10μg | ≥29 | ─ | ≤28 | 0.125≤ | ─ | ≥0.25 |
| Chloramphenicol | 30μg | ≥18 | 13─17 | ≤12 | 8≤ | 16 | ≥32 |
| Ciprofloxacin | 5μg | ≥21 | 16─20 | ≤15 | 1≤ | 2 | ≥4 |
| Cefotaxime | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Erythromycin | 15μg | ≥23 | 14─22 | ≤13 | 0.5≤ | 1─4 | ≥8 |
| Gentamicin | 10μg | ≥15 | 13─14 | ≤12 | 4≤ | 8 | ≥16 |
| Trimethoprin-sulfamethoxazole | 1.25/23.75μg | ≥16 | 11─15 | ≤10 | 2≤ | ─ | ≥4 |
| Tetracycline | 30μg | ≥19 | 15─18 | ≤14 | 4≤ | 8 | ≥16 |
| Trimethoprin | 5μg | ≥16 | 11─15 | ≤10 | 8≤ | ─ | ≥16 |
| Vancomycin | 30μg | ─ | ─ | ─ | 2≤ | 4─8 | ≥16 |

**Table S7D** Intensity of antibiotic actionon *Bacillus* spp. recommended by CLSI (*S*=susceptible, *I*=intermediate, *R*=resistant)

|  |  |  |
| --- | --- | --- |
| Antibiotic | Zone diameter breakpoints (mm) | MIC breakpoints (μg mL-1) |
|   |   | Disk content | *S* | *I* | *R* | *S* | *I* | *R* |
| Ampicillin | 10μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Chloramphenicol | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Ciprofloxacin | 5μg | ≥21 | 16─20 | ≤15 | 1≤ | 2 | ≥4 |
| Cefotaxime | 30μg | ≥23 | 15─22 | ≤14 | 8≤ | 16─32 | ≥64 |
| Erythromycin | 15μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Gentamicin | 10μg | ≥15 | 13─14 | ≤12 | 4≤ | 8 | ≥16 |
| Trimethoprin-sulfamethoxazole | 1.25/23.75μg | ≥16 | 11─15 | ≤10 | 2≤ | ─ | ≥4 |
| Tetracycline | 30μg | ≥15 | 12─14 | ≤11 | 4≤ | 8 | ≥16 |
| Trimethoprin | 5μg | ─ | ─ | ─ | ─ | ─ | ─ |
| Vancomycin | 30μg | ─ | ─ | ─ | ─ | ─ | ─ |