**Supplementary information**

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

**Cheng-Han Liu1,2, Yi-Lynne Chuang1, Revathi Gurunathan1,4, Chi-Ying Hsieh5\*\*, Hans-Uwe Dahms1,4,6\***

1 Department of Biomedical Science and Environmental Biology, College of Life science, Kaohsiung Medical University, Kaohsiung City, 80708, Taiwan (R.O.C.)

2 Green Energy and Biotechnology Industry Research Center, Feng Chia University, Taichung City, 40724, Taiwan (R.O.C.)

3 Department of Medicinal and Applied Chemistry, College of Life science, Kaohsiung Medical University, Kaohsiung City, 80708, Taiwan (R.O.C.)

4 Research Center for Environmental Medicine, Kaohsiung Medical University, Kaohsiung City, 80708, Taiwan (R.O.C.)

5 Department of Environmental Science and Engineering, College of Engineering, National Pingtung University of Science and Technology, Pingtung County, 91201, Taiwan (R.O.C.)

6 Department of Marine Biotechnology and Resources, College of Marine sciences, National Sun Yat-sen University, Kaohsiung City, 80424, Taiwan (R.O.C.)

**\*** Corresponding author: Hans-Uwe Dahms [hudahms11@gmail.com](mailto:hudahms11@gmail.com)

**\*\*** Corresponding author: Chi-Ying Hsieh [chiying@mail.npust.edu.tw](mailto:chiying@mail.npust.edu.tw)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 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 | ─ | ─ | ─ | ─ | ─ | ─ |