Antibiotic Resistance in Acetic Acid Bacteria Originating from Vinegar

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**Supplementary files:**

**Table S1.** Microbiological MIC values (µg/mL) of Acetic acid bacteria against 10 antibiotics

**Table S2.** The putative proteins associated with antibiotic resistance mechanisms through the analysis of the *K. saccharivorans* CV1 genome using the COG database.

Supplementary Table 1. Microbiological MIC values (µg/mL) of acetic acid bacteria against 10 antibiotics.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Strain name** | **Microbiological MIC values (µg/mL) of Acetic acid bacteria against antibiotics (10 kinds)** | | | | | | | | | |
| **Ampicillin** | **Chlolamphenicol** | **Erythromycin** | **Gentamicin** | **Streptomycin** | **Kanamycin** | **Clindamycin** | **Tetracycline** | **Aztreonam** | **Ciprofloxacin** |
| **AM** | **CL** | **EM** | **GM** | **SM** | **KM** | **CM** | **TC** | **AT** | **CI** |
| 1 | *K. swingsii* YU19 | 4 | >256 | >256 | 2 | 1.0 | 0.75 | >256 | 0.50 | >256 | 16 |
| 2 | *K. xylinous* CV4 | 1.5 | >256 | >256 | 1.0 | 2 | 1.0 | >256 | 1.5 | >256 | >32 |
| 3 | *K. intermedius* CV2 | 0.75 | >256 | >256 | 6 | 1.0 | 1.0 | >256 | 0.25 | >256 | 3.0 |
| 4 | *K. saccharivorans* CV1 | 1.5 | >256 | >256 | 1.0 | 0.75 | 0.25 | >256 | 6 | >256 | >32 |
| 5 | *A. malorum* CV11 | 2 | >256 | >256 | 1.5 | 2 | 0.75 | >256 | 0.25 | >256 | >32 |
| 6 | *A. cerevisiae* KSO5 | 24 | 128 | >256 | 1.5 | 0.75 | 0.75 | >256 | 1.5 | >256 | >32 |
| 7 | *A. pasteurianus* A33 | 0.19 | >256 | 192 | 8 | 2 | 0.75 | >256 | 4 | >256 | >32 |
| 8 | *A. pasteurianus* A37 | 1.5 | >256 | >256 | 6 | 2 | 0.75 | >256 | 0.50 | >256 | >32 |
| 9 | *A. pasteurianus* JGB20-11 | 0.75 | >256 | >256 | 4 | 3 | 2 | >256 | 8 | >256 | >32 |
| 10 | *A. pasteurianus* JGB21-17 | 16 | 96 | >256 | 4 | 1.5 | 1.0 | >256 | 4 | >256 | >32 |
| 11 | *A. pasteurianus* JGB21-20 | 2 | 192 | >256 | 0.75 | 0.75 | 0.19 | >256 | 3 | >256 | >32 |
| 12 | *A. pasteurianus* GHA7 | 2 | 192 | 32 | 1.0 | 0.5 | 0.19 | >256 | 6 | >256 | >32 |
| 13 | *A. pasteurianus* GHA20 | 2 | 192 | 32 | 1.5 | 0.5 | 0.19 | >256 | 6 | >256 | 32 |
| 14 | *A. pasteurianus* GYA23 | 2 | 128 | >256 | 1.0 | 1.5 | 0.5 | >256 | 4 | >256 | 12 |
| 15 | *A. pasteurianus* GHG8 | 3 | >256 | >256 | 2 | 3 | 4 | >256 | 6 | >256 | 32 |
| 16 | *A. pasteurianus* GHG17 | 4 | >256 | 64 | 1.0 | 1.5 | 0.5 | >256 | 8 | >256 | >32 |
| 17 | *A. pasteurianus* A11-2 | 1.5 | >256 | 3 | 6 | 0.75 | 0.5 | >256 | 0.75 | >256 | >32 |
| 18 | *A. pasteurianus* GSR2 | 1.0 | >256 | 64 | 2 | 0.75 | 0.5 | >256 | 2 | >256 | 32 |
| 19 | *A. pasteurianus* CHR1 | 1.0 | >256 | 8 | 1.5 | 3 | 1.0 | >256 | 6 | >256 | 24 |
| 20 | *A. pasteurianus* GAR12 | 0.75 | 128 | 128 | 1.0 | 1.5 | 0.75 | >256 | 4 | >256 | 12 |
| 21 | *A. pasteurianus* GSB12 | 1.5 | 128 | 6 | 1.5 | 0.75 | 0.5 | >256 | 6 | >256 | >32 |
| 22 | *A. pasteurianus* GYO12 | 0.75 | 128 | >256 | 4 | 1.5 | 1.5 | >256 | 4 | >256 | 24 |
| 23 | *A. pasteurianus* A24 | 0.75 | >256 | 6 | 1.5 | 2 | 1.0 | >256 | 2 | >256 | 24 |
| 24 | *A. pasteurianus* JKR1 | 1.0 | >256 | >256 | 2 | 2 | 1.0 | >256 | 1.5 | >256 | 16 |
| 25 | *A. pasteurianus* GSB8 | 1.0 | 128 | 4 | 1.0 | 1.0 | 0.38 | >256 | 2 | >256 | 24 |
| 26 | *A. pasteurianus* GSB26 | 1.5 | 128 | 4 | 1.5 | 3 | 1.0 | >256 | 3 | >256 | 32 |

**Spplementary Table 2**. The putative proteins associated with antibiotic resistance mechanisms through the analysis of the *K. saccharivorans* CV1 genome using the COG database.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus\_Tag** | **Start** | **End** | **Strand** | **Type** | **Ref** | **GI** | **Product** | **COG\_blast** | **Identity** | **e-value** | **bitscore** |
| CV1\_1\_00438 | 473492 | 475054 | + | CDS | [162147862](http://www.ncbi.nlm.nih.gov/protein/162147862) | 2E+08 | multidrug transporter MurJ | Peptidoglycan biosynthesis protein MviN/MurJ, putative lipid II flippase | 66.14 | 0 | 614 |
| CV1\_1\_00646 | 710066 | 711985 | - | CDS | [162148117](http://www.ncbi.nlm.nih.gov/protein/162148117) | 2E+08 | penicillin-binding protein 2 | Cell division protein FtsI/penicillin-binding protein 2 | 80.31 | 0 | 1046 |
| CV1\_1\_00714 | 788591 | 791716 | - | CDS | [162147080](http://www.ncbi.nlm.nih.gov/protein/162147080) | 2E+08 | multidrug efflux RND transporter permease subunit | Multidrug efflux pump subunit AcrB | 82.8 | 0 | 1764 |
| CV1\_1\_00716 | 793056 | 793757 | + | CDS | [162147078](http://www.ncbi.nlm.nih.gov/protein/162147078) | 2E+08 | TetR family transcriptional regulator | DNA-binding transcriptional regulator, AcrR family | 43.19 | 1.00E-46 | 161 |
| CV1\_1\_00988 | 1064032 | 1066596 | - | CDS | [162147176](http://www.ncbi.nlm.nih.gov/protein/162147176) | 2E+08 | penicillin-binding protein 1A | Membrane carboxypeptidase/penicillin-binding protein | 71.1 | 0 | 1141 |
| CV1\_1\_01019 | 1100797 | 1102086 | - | CDS | [162147138](http://www.ncbi.nlm.nih.gov/protein/162147138) | 2E+08 | Bcr/CflA family drug resistance efflux transporter | Predicted arabinose efflux permease, MFS family | 75.82 | 0 | 625 |
| CV1\_1\_01110 | 1194198 | 1195631 | + | CDS | [162147077](http://www.ncbi.nlm.nih.gov/protein/162147077) | 2E+08 | multidrug transporter | Na+-driven multidrug efflux pump | 69.85 | 0 | 628 |
| CV1\_1\_01148 | 1229058 | 1230290 | + | CDS | [162146936](http://www.ncbi.nlm.nih.gov/protein/162146936) | 2E+08 | Bcr/CflA family drug resistance efflux transporter | Predicted arabinose efflux permease, MFS family | 63.04 | 8.00E-168 | 485 |
| CV1\_1\_01285 | 1364599 | 1364931 | + | CDS | [560142401](http://www.ncbi.nlm.nih.gov/protein/560142401) | 6E+08 | multidrug transporter | Multidrug transporter EmrE and related cation transporters | 60.55 | 3.00E-37 | 129 |
| CV1\_1\_01353 | 1425805 | 1426791 | + | CDS | [258542396](http://www.ncbi.nlm.nih.gov/protein/258542396) | 3E+08 | multidrug export protein EmrA | Multidrug resistance efflux pump | 53.25 | 1.00E-101 | 310 |
| CV1\_1\_01354 | 1426788 | 1429568 | + | CDS | [258542397](http://www.ncbi.nlm.nih.gov/protein/258542397) | 3E+08 | multidrug ABC transporter ATP-binding protein | ABC-type sugar transport system, ATPase component | 66.96 | 0 | 1244 |
| CV1\_1\_01527 | 1616539 | 1617129 | + | CDS | [15597776](http://www.ncbi.nlm.nih.gov/protein/15597776) | 2E+07 | Modulator of drug activity B | Putative NADPH-quinone reductase (modulator of drug activity B) | 64.8 | 3.00E-93 | 278 |
| CV1\_1\_01529 | 1618799 | 1619986 | - | CDS | [162149611](http://www.ncbi.nlm.nih.gov/protein/162149611) | 2E+08 | multidrug transporter | Multidrug efflux pump subunit AcrA (membrane-fusion protein) | 60.88 | 3.00E-171 | 492 |
| CV1\_1\_01812 | 1937261 | 1938547 | + | CDS | [258542015](http://www.ncbi.nlm.nih.gov/protein/258542015) | 3E+08 | multidrug transporter | Multidrug efflux pump subunit AcrA (membrane-fusion protein) | 62.87 | 0 | 553 |
| CV1\_1\_01856 | 1973431 | 1976727 | - | CDS | [162149137](http://www.ncbi.nlm.nih.gov/protein/162149137) | 2E+08 | acriflavine resistance protein B | Multidrug efflux pump subunit AcrB | 76.86 | 0 | 1608 |
| CV1\_1\_01857 | 1976724 | 1979900 | - | CDS | [162149136](http://www.ncbi.nlm.nih.gov/protein/162149136) | 2E+08 | multidrug transporter | Multidrug efflux pump subunit AcrB | 83.38 | 0 | 1744 |
| CV1\_1\_01858 | 1979971 | 1981275 | - | CDS | [162149135](http://www.ncbi.nlm.nih.gov/protein/162149135) | 2E+08 | multidrug transporter | Multidrug efflux pump subunit AcrA (membrane-fusion protein) | 72.68 | 0 | 535 |
| CV1\_1\_01859 | 1981394 | 1982869 | - | CDS | [158422726](http://www.ncbi.nlm.nih.gov/protein/158422726) | 2E+08 | multidrug transporter | Predicted arabinose efflux permease, MFS family | 48.48 | 1.00E-135 | 409 |
| CV1\_1\_01872 | 1998233 | 1999342 | + | CDS | [162149123](http://www.ncbi.nlm.nih.gov/protein/162149123) | 2E+08 | multidrug export protein EmrA | Multidrug resistance efflux pump | 69.34 | 2.00E-171 | 491 |
| CV1\_1\_02411 | 2543795 | 2545162 | - | CDS | [162147982](http://www.ncbi.nlm.nih.gov/protein/162147982) | 2E+08 | Multidrug resistance protein NorM | Na+-driven multidrug efflux pump | 48.15 | 2.00E-104 | 326 |
| CV1\_1\_02500 | 2648682 | 2649878 | + | CDS | [162149135](http://www.ncbi.nlm.nih.gov/protein/162149135) | 2E+08 | multidrug transporter | Multidrug efflux pump subunit AcrA (membrane-fusion protein) | 65.3 | 7.00E-165 | 478 |
| CV1\_1\_02501 | 2649878 | 2653048 | + | CDS | [162149136](http://www.ncbi.nlm.nih.gov/protein/162149136) | 2E+08 | multidrug transporter | Multidrug efflux pump subunit AcrB | 72.74 | 0 | 1507 |
| CV1\_2\_00024 | 33155 | 34360 | - | CDS | [260752743](http://www.ncbi.nlm.nih.gov/protein/260752743) | 3E+08 | multidrug transporter | Multidrug efflux pump subunit AcrA (membrane-fusion protein) | 48.35 | 9.00E-111 | 338 |
| CV1\_2\_00090 | 116619 | 117953 | - | CDS | [162149599](http://www.ncbi.nlm.nih.gov/protein/162149599) | 2E+08 | Erythromycin esterase | Erythromycin esterase homolog | 71.97 | 0 | 619 |