**Table S1.** Genes with most resistance to antimicrobials and hierarchical clustering.

| States | Antimicrobial-resistance genes |
|---|---|
| PA | *aadA*, *aph(3'')*, *aph(3'')-Ib*, *aph(6)-I*, *aph(6)-Id*, *bla*, *blaCMY*, *sul2*, *tet*, and *tet(A)* |
| NY | *aadA*, *aph(3'')*, *aph(3'')-Ib*, *aph(3')*, *aph(3')-Ia*, *aph(6)-I*, *aph(6)-Id*, *blaCMY*, *blaCMY-2*, *blaTEM*, *blaTEM-1*, *bla*, *sul2*, *tet*, and *tet(A)* |
| MD | *aadA*, *aph(3'')*, *aph(3'')-Ib*, *aph(6)-I*, *aph(6)-Id*, *blaCMY*, *sul2*, *tet*, and *tet(A)* |
| NM | *aadA*, *aph(3'')-Ib*, *aph(6)-I*, *aph(6)-Id*, *aac(3)*, *aadA1*, *aph(3')*, *aph(3')-Ia*, *blaCMY*, and *blaCMY-2*, *blaTEM*, *blaTEM-1*, *fos*, *fosA*, *qac*, *qacEdelta1*, *sul1*, *sul2*, *tet(A)*, and *tet(B)* |
| MN | *aadA*, *aadA1*, *aph(3')*, *aph(3')-I*, *aph(3'')*, *aph(3'')-Ib*, *aph(6)-I*, *aph(6)-Id*, *bla*, and *blaCMY*, *blaCMY-2*, *blaTEM*, *blaTEM-1*, *fosA*, *sul2*, *tet*, *tet(A)*, and *tet(B)* |
| CA | *aadA*, *aph(3'')*, *aph(3'')-Ib*, *aph(6)-I*, *aph(6)-Id*, *bla*, *fos*, *fosA*, and *oqxB* |

**Table S2.** Metabolic functions of the most common antimicrobial-resistance genes.

| Genes | Metabolic Functions |
|---|---|
| *aadA* | • Aminoglycoside resistance<br>• Integration of the plastome-specific *aadA* cassette into the nuclear genome for a fraction of the resistant cell lines |
| *aph(3')* | • Aminoglycoside resistance<br>• Catalysis of the addition of phosphate from ATP to the 3'-hydroxyl group of a 4,6-disubstituted aminoglycoside<br>• Origination from enzymes from the metabolic pathway for aminoglycosides and development in order to counteract the toxic effects of these antibiotics in the host bacterial cell<br>• Transferase |
| *aph(3')-Ia* | • Aminoglycoside resistance<br>• A transposon-encoded aminoglycoside phosphotransferase<br>• Conference of resistance to kanamycin and neomycin |
| *aph(3'')* | • Aminoglycoside resistance<br>• Phosphorylation of streptomycin on the hydroxyl group at position 3'' |
| *aph(3'')-Ib* | • Aminoglycoside resistance<br>• Catalysis of ATP-dependent phosphorylation of a hydroxyl group<br>• Aminoglycoside phosphotransferase encoding by plasmids, transposons, integrative conjugative elements, and chromosomes in *Enterobacteriaceae* and *Pseudomonas* spp |
| *aph(6)-I* | • Aminoglycoside resistance<br>• Catalysis of ATP-dependent phosphorylation of a hydroxyl group |
| *aph(6)-Id* | • Aminoglycoside resistance<br>• Streptomycin phosphotransferase<br>• Phosphotransferase activity, alcohol group as an acceptor |
| *bla* | • Hydrolysis of the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillin and cephalosporin |

| | |
|---|---|
| | • Beta-lactamase |
| *blaCMY* | • Hydrolysis of the beta-lactam bond in susceptible beta-lactam antibiotics<br>• ampC-related *bla* gene |
| *blaCMY-2* | • Hydrolysis of beta-lactam bond<br>• Beta-lactamase |
| *blaTEM, blaTEM-1* | • Hydrolysis of beta-lactam bond<br>• Responsibility of amino acid substitutions for the extended-spectrum beta lactamase (ESBL) phenotype cluster around the active site of the enzyme and change its configuration, allowing access to oxyimino-beta-lactam substrates. |
| *tet, tet(A), tet(B)* | • Tetracycline-resistant protein<br>• Active tetracycline efflux<br>• Decrease of the accumulation of the antibiotic in whole cells<br>• Metal-tetracycline/H+ antiporter |
| *fos, fos(A)* | • Fosfomycin-resistant genes<br>• Inactivation of fosfomycin by addition of a glutathione residue |
| *oqxB* | • Efflux pump membrane transporter<br>• Component of RND-type multidrug efflux pump that confers resistance to olaquindox |
| *sul2* | • Dihydropteroate synthase activity<br>• High-affinity sulfate permease<br>• Sulfate transmembrane transporter activity |