

Table 3. Distribution of tetracycline resistance genes among Gram-positive bacteria, *Mycobacterium*, *Mycoplasma*, *Nocardia*, *Streptomyces* and *Ureaplasma* Modified Sept. 27, 2021 [n=58 genera]

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One Determinant n=27		Two Determinants n=7		Three or More Determinants n=22	
<i>Abiotrophia</i>	<i>tet</i> (M)	<i>Arthrobacter</i>	<i>tet</i> (33)(M) ^k	<i>Actinomyces</i>	<i>tet</i> (L)(M)(W)
<i>Afipia</i>	<i>tet</i> (M)	<i>Gardnerella</i>	<i>tet</i> (M)(Q)	<i>Aerococcus</i>	<i>tet</i> (M)(O)(58)(61)
<i>Amycolatopsis</i>	<i>tet</i> (M) ^o	<i>Gemella</i>	<i>tet</i> (M)(O)	<i>Bacillus</i>	<i>tet</i> (K)(L)(M)(O) ^{ao} (T) ^{ao} (W)(39) ^m (42) ^l (45) ^{at} otr(A) ^L
<i>Anaerococcus</i>	<i>tet</i> (M) ^g	<i>Granulicatella</i>	<i>tet</i> (M)(O)	<i>Bifidobacterium</i> ^{a, w}	<i>tet</i> (L)(M)(O)(W)
<i>Bacterionema</i>	<i>tet</i> (M)	<i>Lactococcus</i>	<i>tet</i> (M)(S)	<i>Bhargavaea</i>	<i>tet</i> (L) ^{ac} (M)(45) ^{aa}
<i>Brachybacterium</i>	<i>tet</i> (M) ^k	<i>Mobiluncus</i> ^a	<i>tet</i> (O)(Q)	<i>Clostridium</i> ^{a, f}	<i>tet</i> (K)(L)(M)(O)(P)(Q)(W)(36)(40) ^j (44) ^p (X) ^{ar}
<i>Catenibacterium</i> ^a	<i>tet</i> (M)	<i>Savagea</i>	<i>tet</i> (L)(M)	<i>Clostridioides</i> ^{at}	<i>tet</i>(L)(P)(W)(40)
<i>Cellulosimicrobium</i>	<i>tet</i> (39) ^m			<i>Corynebacterium</i>	<i>tet</i> (M)(Z)(33)(W) ^q (39) ^{ak}
<i>Cottaibacterium</i>	<i>tet</i> (M)			<i>Enterococcus</i>	<i>tet</i> (K)(L)(M)(O)(S)(T)(U)(58) ^{ad} (61) ^{aq}
<i>Cutibacterium</i>	<i>tet</i> (W) ^{aq}			<i>Eubacterium</i> ^a	<i>tet</i> (K)(M)(O)(Q)(32)
<i>Erysipelothrix</i>	<i>tet</i> (M)			<i>Lactobacillus</i> ^f	<i>tet</i> (K)(L)(M)(O)(Q)(S)(W)(Z)(36) ^{am}
<i>Finegoldia</i>	<i>tet</i> (M) ^g			<i>Listeria</i>	<i>tet</i> (K)(L)(M)(S)AB(46) ^{ag}
<i>Geobacillus</i>	<i>tet</i> (L)			<i>Microbacterium</i>	<i>tet</i> (M)(O) ^{ae} (42) ^l
<i>Helcococcus</i>	<i>tet</i> (M) ^{ah}			<i>Mycobacterium</i> ^c	<i>tet</i> (K)(L)(M)(O) ^t (V) ^{ar} otr(A)(B)
<i>Leifsonia</i>	<i>tet</i> (O) ^t			<i>Nocardia</i>	<i>tet</i> (K)(L)(M) ^{ai} (O) ^{ai}
<i>Lysinibacillus</i>	<i>tet</i> (39) ^m			<i>Paenibacillus</i>	<i>tet</i> (L)(M)(O) ^t (42) ⁱ
<i>Micrococcus</i>	<i>tet</i> (42)			<i>Peptostreptococcus</i> ^a	<i>tet</i> (K)(L)(M)(O)(Q)
<i>Mycoplasma</i> ^b	<i>tet</i> (M)			<i>Sporosarcina</i>	<i>tet</i> (K)(L) ^{ac} (M) ⁿ
<i>Oceanobacillus</i>	<i>tet</i> (L)			<i>Staphylococcus</i>	<i>tet</i> (K)(L)(M)(O)(S)(U)(W)(38)(42)(43)(44)(45)(63)
<i>Paeniclostridium</i>	<i>tet</i>(P)			<i>Streptococcus</i>	<i>tet</i> (K)(L)(M)(O)(Q)(S)(T)(U)(W)(32)(40) ^{u, v} AB(46)
<i>Pediococcus</i>	<i>tet</i> (L)			<i>Streptomyces</i> ^d	<i>tet</i> (K)(L)(M)(W)otr(A)(B)(C), <i>tcr3</i> , <i>tet</i> ^e

<i>Rhodococcus</i>	<i>tet(O)</i> ^t	<i>Trueperella</i> ^{ap}	<i>tet(K)(L)(M)(W)(33)</i>
<i>Robinsoniella</i>	<i>tet(L)</i>		
<i>Roseburia</i>	<i>tet(W)</i>		
<i>Ruminococcus</i> ^a	<i>tet(Q)</i>		
<i>Ureaplasma</i> ^b	<i>tet(M)</i>		
<i>Vagococcus</i>	<i>tet(L)</i>		
<i>Virgibacillus</i>	<i>tet(L)</i>		
<i>Trueperella</i>	<i>tet(33)</i>		

Carrying Mosaic genes^X n=4 genera^{af}

Bifidobacterium tet(O/W/32/O/W/O), tet(W/32/O), tet(O/W)^w

Clostridium tet(O/32/O)

Lactobacillus tet(W/32/O/W/O)^w

Streptococcus tet(O/W/32/O)^u, *tet(O/32/O)*^v, *tet(S/M)*^{ab}

From pig manure *tet(W/N/W)*

Blue new genes since last update

^aAnaerobic genus; ^bCell-wall-free bacteria with a Gram-positive metabolism; ^cAcid-fast bacteria; ^dMulticellular bacteria;

^e*tet* and *tcr* have not been given number designations; ^g formerly *Peptostreptococcus* from whole genome sequence not clear if isolates are tetracycline resistant;

^h from whole genome sequence not clear if isolates are tetracycline resistant; ^lBrown *et al.* AAC 2008, 52:4518;

^j*tet(40)* Kazimierzak *et al.*, App En Mviro 2007; 73:2199; ^kRahman *et al.*, JAC 62:627, 2009; ^lLopez *et al.* Rev Argen Microbiol 40:231, 2008;

^mAdelowo & Fagade, 2009; Let App Microbiol 48:167-172; ⁿNonaka *et al.*, 2007, 4:355; ^oRossi-Fedele *et al.*, 2006 Oral Micro Immun. 21:218;

^p Abril, Broadard, Perreten. AAC 2010; 54:3052; ^q GenBank ADLJ01000017;

^s now called *Trueperella*, [<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1661>];

^tPopwska *et al.*, AAC 56:1434; ^uPalmieri *et al.*, 2012, AAC 56:4697; ^vHu *et al.*, 2011 J Bacteriol 193:2375; ^wvan Hoek *et al.*, 2008 52:248.;

^xfecal/oral microbiome samples have found *tet(O/W/O)*, *tet(O/W/32/O)*, *tet(O/32/O)*, *tet(O/W/32/O/W/O)* Patterson et al, 51:1115 AAC 2007, ^wMosaic ribosomal protection genes also in *Megasphaera* [Gram-negative] (Levy,McMurry & Roberts 2005, AAC 43:1523; Stanton & Humphrey, 2003 Appl Environ Microbiol, 69:3874 ; van Hoek *et al.*, 2008 52:248);

^{aa}GenBank JF837330, JF837331; ^{ab}Barile et al. Microbiol. 158:2353, 2012; ^{ac}You et al., Appl Environ Microb 78:3205-13, 2012; ^{ad}Kyselkova not published;

^{ae}Popowska et al., AAC 2012 56:1434; ^{af}Warburton, Amadeo, Roberts et al., JAC 2016, 17:3333-3339;

^{ag}Buschmann et al, PLOSOne 2012; 8:e42724; [two genes need for resistance *tetAB(46)*];

^{ah}Vergne et al., Eur J Clin Microbiol & Infect Dis 2015 doi: 10.1007/s10096-015-2451-5;

^{ai}Valdezate et al., Frontiers in Microbiol. April 2015 doi: 10.3389/fmicb.2015.00376; ^{aj}Dr. Kyselkova; ^{ak}Roberts et al., J. Antimicrob. Chemother. 2015; 70:619;

^{al}from Dr. Sebastien, Institut of Microbiology Chinese Academy of Sciences; ^{am}Whitehead et al., International J Systematic & Evo Microbiology submitted;

^{an}Whitehead personal communications; ^{ao}Gao et al, Water Reserach 2012; 46:2355;

^{ap}Zhang et al., Microbial Patho 2017; 105:51 [Note *Trueperella* was *Arcanobacterium*]; ^{aq}*tet(61)* on same plasmid as *tet(58)*Dr. Chrudimsky;

^{ar}Kyselkova et al., Microbes Environ. 2012; 413:422; ^{as}GenBank AY255627; ^{at}Zhu et al., Frontiers Microbiol 2016 doi 10.3389/fmicb.2016.00718;

^{aq}Aoki et al. in press 2019 doi:10.1128/AAC.01810-19 AAC ; ^{ar}GenBank, nonfunctional since requires oxygen from growth;

^{as}**Zhang, Dong, Shen et al., Nature communications 2020 11:4648 <https://doi.org/10.1038/s41467-020-18475-9>; ^{at}*Clostridioides* was *Clostridium difficile*;**

^{au}*Panenclostridium* was *Clostridium sordellii*;

^{av}**Yan, Zhu, Schwarz et al., Vet Microbiol 2021 252:109065 <https://doi.org/10.1016/j.vetmic.2021.109065>**