Table 3. Distribution of tetracycline resistance genes among Gram-positive bacteria, *Mycobacterium*, *Mycoplasma*, *Nocardia*, *Streptomyces* and *Ureaplasma* Modified **Feb. 5, 2024** [n=58 genera]

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One Determinant n=27		Two Determinants n=7		Three or More Determinants n=22	
Abiotrophia	*tet*(M)	*Arthrobacter*	*tet*(33)(M)[k]	*Actinomyces*	*tet*(L)(M)(W)
Afipia	*tet*(M)	*Gardnerella*	*tet*(M)(Q)	*Aerococcus*	*tet*(M)(O)(58)(61)
Amycolatopsis	*tet*(M)[o]	*Gemella*	*tet*(M)(O)	*Bacillus*	*tet*(K)(L)(M)(O)[ao](T)[ao](W)(39)[m](42)[I] (45)[at]otr(A)[L]
Anaerococcus	*tet*(M)[g]	*Granulicatella*	*tet*(M)(O)	*Bifidobacterium* [a, w]	*tet*(L)(M)(O)(W)
Bacterionema	*tet*(M)	*Lactococcus*	*tet*(M)(S)	*Bhargavaea*	*tet*(L)[ac](M)(45)[aa]
Brachybacterium	*tet*(M)[k]	*Mobiluncus*[a]	*tet*(O)(Q)	*Clostridium*[a,f]	*tet*(K)(L)(M)(O)(P)(Q)(W)(36)(40)[j](44)[p](X)[ar]
Catenibacterium[a]	*tet*(M)	*Savagea*	*tet*(L)(M)	*Clostridioides*[at]	*tet*(L)(P)(W)(40)
Cellulosimicrobium	*tet*(39)[m]			*Corynebacterium*	*tet*(M)(Z)(33)(W)[q] (39)[ak]***tet*(65)**[aw]
Cottaibacterium	*tet*(M)			*Enterococcus*	*tet*(K)(L)(M)(O)(S)(T)(U)(58)[ad](61)[aq]
Cutibacterium	*tet*(W)[aq]			*Eubacterium*[a]	*tet*(K)(M)(O)(Q)(32)
Erysipelothrix	*tet*(M)			*Lactobacillus*[f]	*tet*(K)(L)(M)(O)(Q)(S)(W)(Z)(36)[am]
Finegoldia	*tet*(M)[g]			*Listeria*	*tet*(K)(L)(M)(S)AB(46)[ag]
Geobacillus	*tet*(L)			*Microbacterium*	*tet*(M)(O)[ae](42)[I]
Helcococcus	*tet*(M)[ah]			*Mycobacterium*[c]	*tet*(K)(L)(M)(O)[t](V)[ar]*otr*(A)(B)
Leifsonia	*tet*(O)[t]			*Nocardia*	*tet*(K)(L)(M)[ai] (O) [ai]
Lysinibacillus	*tet*(39)[m]			*Paenibacillus*	*tet*(L)(M)(O)[t](42)[i]
Micrococcus	*tet*(42)			*Peptostreptococcus*[a]	*tet*(K)(L)(M)(O)(Q)
Mycoplasma[b]	*tet*(M)			*Sporosarcina*	*tet*(K)(L)[ac](M)[n]
Oceanobacillus	*tet*(L)			*Staphylococcus*	*tet*(K)(L)(M)(O)(S)(U)(W)(38)(42)(43)(44)(45)(63)
Paeniclostridius	*tet*(P)			*Streptococcus*	*tet*(K)(L)(M)(O)(Q)(S)(T)(U)(W)(32)(40)[u,v]AB(46)
Pediococcus	*tet*(L)			*Streptomyces*[d]	*tet*(K)(L)(M)(W) *otr*(A)(B)(C), *tcr3*, *tet*[e]

Rhodococcus	*tet*(O)[t]
Robinsoniella	*tet*(L)
Roseburia	*tet*(W)
Ruminococcus[a]	*tet*(Q)
Ureaplasma[b]	*tet*(M)
Vagococcus	*tet*(L)
Virgibacillus	*tet*(L)
Trueperella	*tet*(33)
Trueperella [ap]	*tet*(K)(L)(M)(W)(33)

Carrying Mosaic genes[x] n=4 genera[af]

Bifidobacerium 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

[a]Anaerobic genus; [b]Cell-wall-free bacteria with a Gram-positive metabolism; [c]Acid-fast bacteria; [d]Multicellular 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; [I] Brown *et al*. AAC 2008, 52:4518;

[j] *tet*(40) Kazimierczak *et al*., App En Mvicro 2007; 73:2199; [k]Rahman et al., JAC 62:627, 2009; [L]Lopez et al. Rev Argen Microbiol 40:231, 2008;

[m]Adelowo & Fagade, 2009; Let App Microbiol 48:167-172; [n]Nonaka et al, 2007, 4:355; [o] Rossi-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];

[t]Popwska et al, AAC 56:1434; [u]Palmieri et al, 2012, AAC 56:4697; [v] Hu et al., 2011J Bacteriol 193:2375; [w] van Hoek *et al.*, 2008 52:248.;

[x]fecal/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, [w]Mosaic 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 *tet*AB(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, Institue of Microbiology Chinese Academy of Scinences; [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] *Paneniclostridius* was *Clostridium sordellii*;

[av] Yan, Zhu, Schwarz et al., Vet Microbiol 2021 252:109065 https://doi.org/10.1016/j.vetmic.2021.109065;

[aw] Kitt, Brodard, Tresch, Perreten, submitted