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NOTES

Nomenclature for Tetracycline Resistance Determinants

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Tetracycline resistance determinants are widespread and distinguishable genetically and biochemically. The nomenclature for this increasing number of determinants has been varied and inconsistent. This communication suggests ways of naming these determinants and their genes and gene products consistent with current genetic terminology.

A tetracycline resistance determinant can be defined as a naturally occurring, generally contiguous genetic unit which includes all genes (both structural and regulatory) involved in resistance. Over the past decade, more than 12 classes of tetracycline resistance determinants have been identified in gram-negative and gram-positive aerobic and anaerobic bacterial species on the basis of DNA-DNA hybridization with regions from structural genes and, in some cases, on the basis of subsequent DNA sequencing (Table 1). Determinants which do not hybridize with these classes represent others yet to be described. Of the more common determinants, classes A through E have been described among members of the family *Enterobacteriaceae* (6, 7), and classes L, M, and N have been described among gram-positive organisms (3). To these have now been added class O, a class M-related determinant found in *Campylobacter* spp. as well as in *Streptococcus* spp. (9).

Nomenclature for these determinants and their genes and gene products has become confusing and is sometimes inconsistent with accepted bacterial genetic terminology. In the literature, the determinants have been designated not only as class A, B, etc., but also as TetA, TetB, etc., and as *tetA*, *tetB*, *tetL*, *tetM*, etc. This poses problems. While the determinants of classes L and M bear a single structural gene, classes A through E have both a structural and a regulatory gene (4, 6, 10). Future studies may reveal more than one structural gene in some determinants. Therefore, designation of an entire determinant by a symbol used for a single gene (e.g., *tetM*) could not be applied to all classes. Also, the designation *tetA* has been used for the structural gene for the tetracycline resistance structural protein encoded by class B (Tn*10*) (2). Use of the letter A for both a gene and a different class has been confusing.

We therefore suggest the following practice, which is consistent with accepted genetic terminology in bacteria, is flexible enough to cover both known and yet-to-be-characterized determinants, and is orthographically simple. The determinants would continue to be classified by DNA-DNA hybridization into the classes designated by letters. The first structural gene of any class would be designated *tetA* to distinguish it from the repressor gene (if any), which would continue to be designated *tetR*. Subsequent structural genes (if any) would be called *tetB*, *tetC*, etc. In order to distinguish the determinant class for the structural and repressor genes, we recommend that the letter of the class, not italicized, be put in parentheses immediately following the structural gene or repressor gene designation. For example, for the class X determinant, the designations would be *tetA*(X) and *tetR*(X). If only the structural gene is being discussed in a communication, the *tetA* designation could be shortened to *tet*, with the designation of the class given in parentheses if necessary. Thus, the class X structural gene *tetA*(X) could be shortened to *tet*(X).

If, for orthographic reasons, authors would prefer a subscript for the class designation, we would find that also acceptable; however, there is always the problem of "losing" subscripts, which is why we prefer the parentheses.

TABLE 1. Classification of tetracycline resistance determinants

Class	Representative family, genus, or species[a]
A	*Enterobacteriaceae*[b]; *Aeromonas*, *Pseudomonas*, *Vibrio*
B	*Enterobacteriaceae*[b]; *Yersinia*, *Haemophilus*, *Vibrio*
C	*Enterobacteriaceae*[b]; *Pseudomonas*, *Vibrio*
D	*Enterobacteriaceae*[b]; *Aeromonas*, *Pasteurella*, *Vibrio*
E	*Escherichia*, *Aeromonas*
F	*Bacteroides fragilis*
G	*Vibrio anguillarum*
K	*Staphylococcus*
L	*Bacillus*, *Staphylococcus*, *Streptococcus*, *Enterococcus*
M	*Clostridium*, *Enterococcus*, *Staphylococcus*, *Streptococcus*, *Gardnerella*, *Kingella*, *Neisseria*, *Mycoplasma*, *Ureaplasma*, *Eikenella*, *Veillonella*, *Fusobacterium*, *Peptostreptococcus*
N	*Streptococcus agalactiae*
O	*Campylobacter*, *Streptococcus*, *Enterococcus*
P	*Clostridium perfringens*

[a] References 1, 3, 5–9.
[b] Described in more than one member of this group.

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TABLE 2. Proposed nomenclature for tetracycline resistance determinants[a]

Class[b]	Determinant[c]	First structural:		Regulatory (repressor):	
		Gene[d]	Protein[e]	Gene[f]	Protein[g]
X	Tet X	*tetA*(X)	TetA(X)	*tetR*(X)	TetR(X)

[a] Subscripts are acceptable alternatives to parentheses, e.g., $tetA_X$, $TetA_X$, $tetR_X$, $TetR_X$.
[b] Class X used as an example.
[c] Note space between Tet and X.
[d] Short forms: *tet*, *tetA*, *tet*(X).
[e] Short forms: Tet, TetA, Tet(X).
[f] Short form: *tetR*.
[g] Short form: TetR.

The protein product of a gene would be designated as is traditional, by capitalizing the first letter of the gene designation; e.g., TetA(X) would be the product of the gene *tetA*(X). This could be shortened to TetA or just Tet in repeated usage in a communication.

For referring to the determinant, we recommend the designations Tet X determinant or, for variety, class X determinant. Thus, we would have Tet A, Tet B, Tet M, Tet O determinant, etc. We also recommend that in naming future classes, the letter R be avoided, since it already is used to mean repressor or regulator.

A summary of the recommended nomenclature is given in Table 2. We hope these guidelines will prevent further confusion and inconsistencies in the literature.

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