

## Multiple Alleles of *Treponema pallidum* Repeat Gene D in *Treponema pallidum* Isolates

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**Two new *tprD* alleles have been identified in *Treponema pallidum*: *tprD2* is found in 7 of 12 *T. pallidum* subsp. *pallidum* isolates and 7 of 8 non-*pallidum* isolates, and *tprD3* is found in one *T. pallidum* subsp. *pertenue* isolate. Antibodies against TprD2 are found in persons with syphilis, demonstrating that *tprD2* is expressed during infection.**

Syphilis, caused by *Treponema pallidum* subsp. *pallidum*, is a chronic disease characterized by periods of activity and latency, with clearance of early lesions but persistence of infection. The mechanisms *T. pallidum* uses to persist in humans are still not known, but it is possible that alterations in surface proteins will be involved because of their interaction with the host and their visibility to the immune response.

A family of 12 *tpr* genes is contained in the *T. pallidum* subsp. *pallidum* Nichols strain genome (7), some of which code for candidate surface-exposed proteins (3, 7, 12, 13). The *tpr* genes of *T. pallidum* are of interest for a variety of reasons. Their gene products are homologous to the Msp proteins of *Treponema denticola*, which have been implicated in cell attachment and porin function (6, 11). Anti-TprK antibody has been shown to opsonize *T. pallidum* Nichols strain for phagocytosis (3); thus, TprK may be exposed at the cell surface. Immunization with TprK is partially protective against challenge with *T. pallidum* Nichols strain (3), suggesting some *tpr* gene products are a focus of the protective immune response. Finally, the variable nature of the *tpr* genes suggests a role in immune evasion and persistence if different *tpr* genes are sequentially expressed. The 12 *tpr* gene products can be categorized into three subfamilies (3). Subfamilies I (TprCDFI) and II (TprEGJ) have conserved amino- and carboxyl-terminal sequences, but variable central amino acid sequences (3). Subfamily III Tpr proteins (TprABHKL) have scattered variable and conserved sequences throughout their length (3).

**A novel *tpr* gene was discovered.** Multiple *tprK* alleles have been found in recent isolates of *T. pallidum* (5), in contrast to the single *tprK* allele identified in the laboratory-adapted Nichols strain (7). Because of our interest in *tpr* heterogeneity, we compared *tpr* gene sequences from other *T. pallidum* isolates to those from the Nichols strain. For example, genomic DNA from the *T. pallidum* subsp. *pallidum* Mexico A isolate was used as a template for PCR with primers A and B (Table 1), which are complementary to conserved regions flanking the central variable domains of *tpr* subfamilies I and II. The rabbit propagation, sources of the treponeme isolates, extraction of genomic DNA, and PCR conditions have been described previously (2–5). One of the amplicons was homologous to subfamily I (*tprCDFI*) at the conserved 5' and 3' ends, yet distinct

from all of the subfamily I genes in much of the variable region (GenBank accession no. AF187953). This novel *tpr* was also found in the *T. pallidum* subsp. *pallidum* Bal-3 isolate (GenBank accession no. AF187952).

**The novel *tpr* gene occupies the *tprD* locus, and thus was termed *tprD2*.** In order to localize the novel *tpr* gene in the genome, inverse PCR was used to amplify a fragment of genomic DNA containing the 5' portion of the novel *tpr* gene and the 5' flanking DNA. Genomic Bal-3 DNA (100 ng) was digested with *Sau3A1* and ligated with T4 DNA ligase (New England Biolabs, Beverly, Mass.) in a 120- $\mu$ l volume, such that circles were likely to be formed. This was used as a template in a PCR with primers C and G (Table 1 and Fig. 1) and yielded a 1.7-kb amplicon. Sequencing of this amplicon demonstrated that the novel *tpr* gene is flanked at the 5' end by DNA with almost complete identity to the TP0132 and TP0133 genes, which are at the 5' flanking end of *tprD* in the *T. pallidum* Nichols genome (Fig. 1).

The entire *tprD* locus and flanking regions (Fig. 1, primers H and I) were amplified from *T. pallidum* subsp. *pallidum* isolates Bal-3, Mexico A, Sea 81-3, Sea 81-4, and Bal-7 and from the Gauthier strain of *T. pallidum* subsp. *pertenue*. The sequence of these amplicons demonstrated that a novel sequence is found in the *tprD* locus of the Bal-3, Mexico A, Sea 81-4, and Sea 81-3 isolates (GenBank accession no. AF187952, AF217539, AF217540, and AF217541, respectively), and this allele was termed *tprD2* (Fig. 1). The sequences of the *tprD2* allele and flanking regions were identical in all four of these isolates. The amplicon from Bal-7 (GenBank accession no. AF217537) was identical to the *tprD* gene found in the Nichols strain, and the amplicon from the Gauthier strain (GenBank accession no. AF217538) was different from both *tprD* and *tprD2* and was termed *tprD3*.

There are four regions of heterogeneity between *tprD2* and *tprD*: a 330-bp central variable region and three smaller variable regions to the 3' end of the open reading frames. No significant homology (>18-bp identity) to these four variable regions of *tprD2* is present anywhere in the *T. pallidum* Nichols genome. These four variable regions are also reflected by differences in the predicted amino acid sequences of *tprD2* and *tprD* (Fig. 2). Both TprD and TprD2 have predicted cleavable signal sequences (at amino acid 17), but TprD2 is highly predicted to be in the outer membrane, while TprD is predicted to localize in the inner membrane by PSORT analysis (<http://psort.nibb.ac.jp/>). Outer membrane expression of TprD2 could increase the repertoire of variable Tpr proteins on the surface

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TABLE 1. Oligonucleotides used in this study

Primer	Characteristic	Sequence
A	<i>tpr</i> conserved sense	CGACTCACCTCGAACCA
B	<i>tpr</i> conserved antisense	GGTGAGCAGGTGGGTGTAG
C	<i>tprD2</i> -specific sense	CACTAGTCTTGGGGACACGC
D	<i>tprD2</i> -specific antisense	TACGTGAATTGCAACCAGGA
E	<i>tprA</i> -specific sense	TACCTACCGGATACGAACAGT
F	<i>tprA</i> -specific antisense	TGCAAGGCATGGGTGTAATCAT
G	<i>tprD2</i> antisense 2	TGACTTCATGGACCCTCTGTG
H	Tp0130 antisense bp 45–66	CATGGCATTGGTGAGAAAAGACG
I	Tp0132 sense bp 137–157	CGCGTACCGCTTTCAGTTC

for antigenic variation or to change the functionality of the protein. TprD3 is 95% identical to TprD, with the major region of heterogeneity located between amino acid residues 285 and 304, but with scattered amino acid differences found throughout the sequence. Like TprD, TprD3 is predicted by PSORT analysis to have a cleavable signal sequence, but to be located in the inner membrane. It is noteworthy that, while the 5' conserved region (amino acids 1 to 284) of TprD2 is identical to the genome sequence for TprD, the same region in TprD3 has the signature at amino acids 234 to 245 (EQHYRKGTE DST) that characterizes TprF and TprI predicted from the genome sequence (7).

***tprD2* was identified in about half of the *Treponema* isolates.** Primers C and D (Table 1) were designed to amplify a *tprD2*-specific 273-bp amplicon (Fig. 1) to test for the presence of *tprD2* in a variety of *Treponema* isolates. We examined 12 isolates of *T. pallidum* subsp. *pallidum*, 4 isolates of *T. pallidum* subsp. *pertenue* (yaws spirochetes), 1 isolate of *T. pallidum* subsp. *endemicum* (endemic syphilis spirochete), the Simian isolate (primate spirochete [8]), and 2 isolates of *Treponema paraluisancuniculi* (rabbit venereal spirochetes) (Table 2). *tprD2* was detected in 7 of 12 *T. pallidum* subsp. *pallidum* genomes

and in 7 of 8 of the non-syphilis treponeme genomes (Table 2). Primers specific for *tprA* (primers E and F, Table 1) gave the predicted 315-bp amplicon with each of these isolates, demonstrating that the DNA from each treponeme isolate was intact and amplifiable (not shown). Rabbit DNA, a likely contaminant, did not give an amplicon with these sets of primers. Thus, it appears that the *tprD2* allele is present in about half of the *T. pallidum* subsp. *pallidum* isolates tested, but not the Nichols strain that was used for the genome sequencing project (7).

**Humans with syphilis make antibodies to TprD2-specific peptide.** An amplicon encoding a 90-amino-acid peptide (amino acids 301 to 391 in Fig. 2) unique to the predicted TprD2 protein was amplified (primers C and D, Table 1 and Fig. 1), expressed as a six-histidine fusion protein, and purified (TprD2-specific peptide) (3). This TprD2-specific peptide had no homology to any of the other predicted *tpr* gene products or homology to any of the predicted open reading frames of the *T. pallidum* Nichols strain genome.

To test for immunoreactivity to the TprD2-specific peptide, human sera (obtained with informed consent as approved by the University of Washington Institutional Review Board for human subjects) were preabsorbed overnight with 5% *Escherichia coli* lysate containing an irrelevant recombinant *Trypanosoma cruzi* SA85-1.1-III protein in pRSET (9). Western blotting with 100 ng of recombinant TprD2-specific peptide, 1:100 diluted human sera, and 1:3,000 alkaline phosphatase-conjugated goat anti-human immunoglobulin G (Sigma, St. Louis, Mo.) was performed as previously described (1). Antibodies in sera from five of seven persons with secondary syphilis were reactive with the TprD2-specific peptide, while no anti-TprD2 activity was detected in sera from seven uninfected persons, two persons with primary syphilis, and three persons with late latent syphilis. Representative immunoblots are shown in Fig. 3. The antibodies to TprD2-specific peptide that were generated during syphilis infection demonstrate that TprD2 is expressed by *T. pallidum* subsp. *pallidum* in humans. The pro-

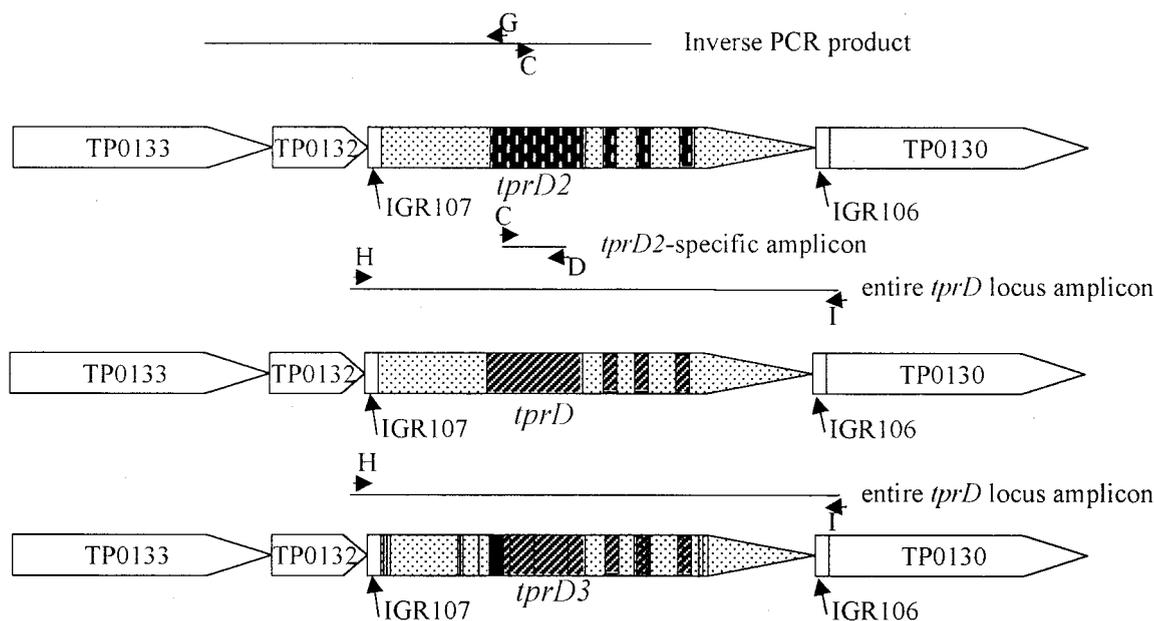


FIG. 1. Diagram of the *tprD* locus. Three different alleles of *tprD* (*tprD*, *tprD2*, and *tprD3*) are present in the *tprD* locus in the strains examined. The regions denoted as arrows and with TP or *tpr* are predicted coding regions with putative start codons at the beginning of the arrow and putative stop codons at the point of the arrow. IGR, intergenic region. PCR products are shown as thin lines, and the primers used to produce the products are shown as arrowheads. The different shading patterns and lines within the *tprD*, *tprD2*, and *tprD3* alleles demonstrate the differences between the alleles.

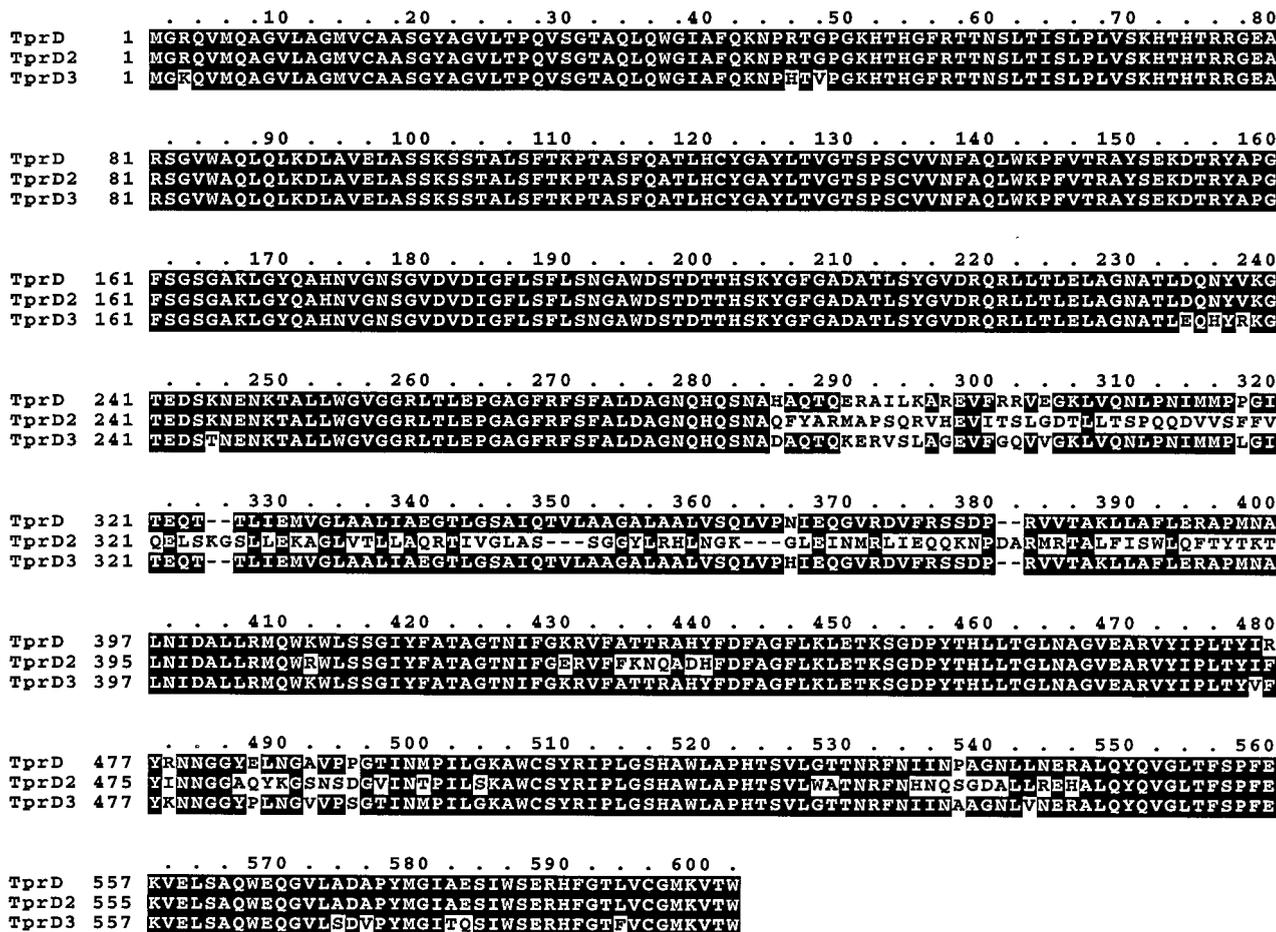


FIG. 2. Amino acid sequence alignments of *tprD*, *tprD2*, and *tprD3*. The alignments of the predicted amino acid sequences of the *tprD*, *tprD2*, and *tprD3* alleles are shown.

TABLE 2. *tpr* variable region amplification of genomic DNA from *Treponema* isolates

Isolate or sample	Designation	<i>tprD2</i> amplicon
<i>T. pallidum</i> subsp. <i>pallidum</i>	Nichols, Bal 73-1, Bal-7, Sea 83-1, Chicago	-
	Bal-2, Bal-3, Bal-8, Sea 81-3, Sea 81-4, Sea 84-2, Mexico A	+
<i>T. pallidum</i> subsp. <i>pernetue</i>	Gauthier	-
	Haiti B, <sup>a</sup> Samoa D, Samoa F	+
<i>T. pallidum</i> subsp. <i>endemicum</i>	Iraq B	+
Unnamed subspecies	Simian	+
<i>T. paraluisuniculi</i>	Cuniculi A, Cuniculi M	+
Rabbit DNA		-

<sup>a</sup> Molecular analysis suggests that the Haiti B isolate may be a *T. pallidum* subsp. *pallidum* isolate (3a).

portion of syphilitic sera reactive with TprD2-specific peptide (5 of 12 tested) is about the same proportion of *T. pallidum* subsp. *pallidum* isolates carrying the *tprD2* allele (7 of 12 tested). This suggests that most isolates containing the *tprD2* allele also express it.

We have demonstrated that 7 of 12 of the *T. pallidum* subsp.

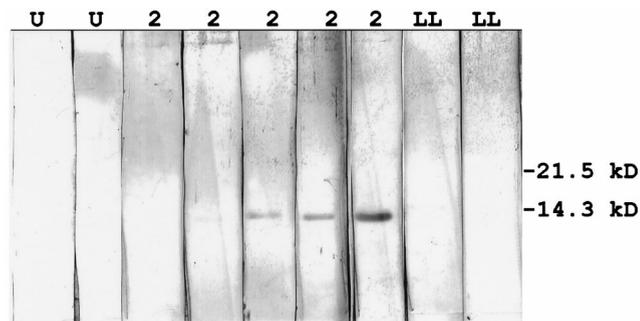


FIG. 3. Western blots demonstrating antibodies in sera from persons with secondary syphilis react with the TprD2-specific peptide. Shown are immunoblots with the 14-kDa TprD2-specific recombinant peptide from a representative experiment. The immunoblots were reacted with sera from two uninfected controls (U), five persons with secondary syphilis (noted by no. 2), and two persons with late latent syphilis (LL). Antibody reactivity to the *tprD2*-specific peptide is seen with the sera from three of five persons with secondary syphilis. Shown to the right are the positions of the molecular mass markers.

*pallidum* isolates and most of the non-syphilis treponemes tested have a novel *tprD2* allele. The one non-syphilis treponeme that did not contain *tprD2*, the Gauthier strain of *T. pallidum* subsp. *pertenue*, contains another variant of *tprD*, termed *tprD3*. In the four *tprD2*-containing isolates examined, the *tprD2* gene occupies the position of the *tprD* gene, as defined in the Nichols strain; similarly, *tprD3* occupies the same position in the Gauthier genome. Substitution of *tprD2* and *tprD3* for *tprD* generates additional diversity of the *tpr* genes in some strains. The differences in the predicted amino acid sequences of *tprD* and *tprD2* are localized to a 110-amino-acid central variable region and three smaller variable regions toward the carboxyl terminus of TprD2. If these differences are in the immunodominant or exposed regions of these molecules, this could help to explain why immunity from heterologous challenge is not as complete as it is with homologous challenge (10). Alternatively, these variable domains may provide a functional capacity, like cell binding, and the sequence variation may extend the functional capacity of individual isolates. It is notable that TprD2, but not TprD or TprD3, is predicted to be in the outer membrane, suggesting a different functional role for TprD2.

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