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The Gut as Reservoir of Antibiotic Resistance: Microbial Diversity of Tetracycline Resistance in Mother and Infant

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Abstract

The microbiota in the human gastrointestinal tract (GIT) is highly exposed to antibiotics, and may be an important reservoir of resistant strains and transferable resistance genes. Maternal GIT strains can be transmitted to the offspring, and resistances could be acquired from birth. This is a case study using a metagenomic approach to determine the diversity of microorganisms conferring tetracycline resistance (TcR) in the guts of a healthy mother-infant pair one month after childbirth, and to investigate the potential for horizontal transfer and maternal transmission of TcR genes. Fecal fosmid libraries were functionally screened for TcR, and further PCR-screened for specific TcR genes. TcR fosmid inserts were sequenced at both ends to establish bacterial diversity. Mother and infant libraries contained TcR, although encoded by different genes and organisms. TcR bacteria in the mother consisted mainly of Firmicutes and Bacteroidetes, and the main gene detected was tet(O), although tet(W) and tet(X) were also found. Identical TcR gene sequences were present in different bacterial families and even phyla, which may indicate horizontal transfer within the maternal GIT. In the infant library, TcR was present exclusively in streptococci carrying tet(M), tet(L) and erm(T) within a novel composite transposon, Tn6079. This transposon belongs to a family of broad host range conjugative elements, implying a potential for the joint spread of tetracycline and erythromycin resistance within the infant’s gut. In addition, although not found in the infant metagenomic library, tet(O) and tet(W) could be detected in the uncloned DNA purified from the infant fecal sample. This is the first study to reveal the diversity of TcR bacteria in the human gut, to detect a likely transmission of antibiotic resistance from mother to infant GITS and to indicate the possible occurrence of gene transfers among distantly related bacteria cohabiting the GIT of the same individual.

Introduction

The human gastrointestinal tract (GIT) is host to a very dense microbiota, harboring 10^{13}-10^{14} bacterial cells in adults and a broad diversity of bacterial species, of which a large proportion are not yet cultured. This microbiota is often exposed to a variety of antibiotics, both directly and indirectly, due to their routine use in clinical settings and in farm animals. Therefore, its many other fundamental roles in health notwithstanding [1–5], the GIT microbiota may serve as an important reservoir of antibiotic resistant strains that could act as opportunistic pathogens or as donors of resistance genes to other bacteria [6]. In infants, infections due to antibiotic resistant strains are on the rise and represent a major cause of mortality and morbidity worldwide. Although the infant’s gut is thought to be mostly germ-free at birth, it rapidly enters an extensive and complex process of colonization by a variety of microbes [7,8], and recent studies have firmly established that strains from the mother’s GIT can be transmitted to the infant and persist during the first weeks of life [9]. Consequently, antibiotic resistances could be vertically transmitted from the maternal GIT and bear on infant health from a very early age.

Tetracyclines are one of the most widely used groups of antibiotics worldwide and tetracycline resistance (TcR) is extremely common among bacteria [10]. Presently, 43 distinct TcR genes are known and they are usually associated with large mobile genetic elements (MGE) (http://faculty.washington.edu/marilynr/). The most common forms are the active efflux of tetracycline from the cell and the synthesis of ribosomal protection proteins that prevent the binding of tetracycline to the ribosomes [10,11]. Although its medical applications have decreased in the last decade and it is no longer used for treatment of pregnant women or children under...
the age of 8 years [12], tetracycline is still widely used for therapeutic treatment in animal production and in some countries it is also used as growth promoter in animal feed [11,13]. Therefore intestinal bacteria are still extensively exposed to this antibiotic.

A recent microarray-based study has found tet(M) and tet(W) to be the most prevalent Te(\textsuperscript{c}) genes for the oral and fecal metagenomes of healthy adults, respectively [14]. Furthermore, Te(\textsuperscript{c}) genes like tet(M), tet(O) and tet(W) have also been detected in fecal samples from healthy and exclusively breast-fed infants, suggesting that Te(\textsuperscript{c}) genes are common in the environment [15]. However, these studies have not revealed the types of bacteria that harbor these resistances in the GIT and have not addressed the potential origin of the Te(\textsuperscript{c}) genes and strains present in healthy infants. Here, we have used a culture-independent approach to characterize the diversity of microorganisms conferring Te(\textsuperscript{c}) in the gut of one healthy infant-mother pair. Two fecal metagenomic libraries, one from the mother and one from her exclusively breast-fed infant one month after birth [9], were screened for fosmid clones conferring Te(\textsuperscript{c}), which were further screened by PCR for a battery of Te(\textsuperscript{c}) genes. End-sequencing established the microbial diversity among the Te(\textsuperscript{c}) organisms. Finally we identified a novel Tn\textsubscript{916}-like conjugative transposon, Tn\textsubscript{6079} carrying Te(\textsuperscript{c}) resistance genes tet(M) and tet(L) and the erythromycin resistance gene emr(T) in the infant gut.

### Results

#### Screening metagenome libraries from infant and mother for clones conferring Te(\textsuperscript{c})

The metagenome libraries from the infant and the mother contained 44 and 272 fosmid Te(\textsuperscript{c}) clones respectively. In a first instance, we screened all obtained Te(\textsuperscript{c}) clones for the common ribosomal protection genes tet(M), tet(O), tet(W) and tet(S). Out of the 44 Te(\textsuperscript{c}) fosmid clones from the infant library, 43 were shown to be positive for tet(M) by PCR. One of the end-sequences (B04-U-PPC1R, 386 bp) from the fosmid clone negative for the tet(M) PCR was identical to a region in tet(M) downstream of one of the screening primers. Thus all 44 Te(\textsuperscript{c}) clones from the infant’s metagenomic library were tet(M) positive and negative for tet(S), tet(O) and tet(W). In contrast, out of the 272 Te(\textsuperscript{c}) clones from the mother library, 21 (7.7%) were only positive for tet(W) and 204 (75%) were only positive for tet(O); for 47 (17.3%) of the Te(\textsuperscript{c}) clones none of the assayed Te(\textsuperscript{c}) genes were detected, and all clones were negative for tet(M) and tet(S).

To further investigate what resistance genes might be present in the 47 maternal clones that were negative for tet(M), tet(O), tet(W) and tet(S), we performed a series of multiplex PCRs designed to detect tet(A), tet(B), tet(C), tet(D), tet(E), tet(G), tet(K), tet(L), tet(P), tet(Q) and tet(X). This second round of PCR screening detected tet(X), encoding a tetracycline-inactivating enzyme, in 17 of the tested clones and none of the other genes assayed. Overall, our PCR screens were able to account for the Te(\textsuperscript{c}) genes present in 242 (89%) of the Te(\textsuperscript{c}) clones from the mother’s metagenomic library.

Sequencing of all the PCR screening products for tet(M) detected in the infant library identified a single sequence type, tet(M)a, based on 505 bp out of the 1920 bp of the tet(M) gene (Table S1). All 21 tet(W) PCR screening products, 63 of the 204 products for tet(O) and 12 of the 17 tet(X) products from the maternal library were also sequenced (Table S2). Of the sequenced tet(O) products, 13 were selected to represent genes assigned to different families/genera (see later in the Results section) and the remaining 50 were randomly selected. Based on 609 bp and 499 bp out of the 1920 bp of tet(W) and tet(O) and 446 bp out of the 1161–1167 bp of tet(X), 2 (tet(W)a, b), 9 (tet(O)a–i) and 1 (tet(X)a) different sequence types were identified (Table S2). The sequenced PCR screening products, tet(M)a and tet(O)a–i could discriminate among the known variants of tet(M) and tet(O) (Fig. S1, S2). tet(W)a and tet(W)b could discriminate between groups with highly related tet(W) genes sharing 99.9–100% and 99.5–100% sequence identity, respectively (Fig. S3). tet(X)a could discriminate among most known variants (Fig. S4) and was identical to the corresponding fragments from two tet(X) genes identified in Bacteroides, including the tet(X) gene first detected in transposon Tn\textsubscript{931}/Tn\textsubscript{4400} [16].

#### Identification of a novel composite Tn\textsubscript{916}/1545-like conjugative transposon carrying tet(M), tet(L) and emr(T) in the infant library

In a sequenced fosmid from the infant library, tet(M) was found on a Tn\textsubscript{916}/1545-like transposon, a family of conjugative transposons that have an extremely broad host range [17,18]. The transposon was highly similar to a putative Tn\textsubscript{916}-like transposon identified in Streptococcus galactolycus subsp. galactolycus strain UCN34 (FN597254), isolated from an elderly endocarditis strain UCN34 (FN597254), isolated from an elderly endocarditis and colon cancer patient [19], although the infant transposon was located at the 3’end of tpmG (predicted to encode protein L33 from the ribosomal 50S subunit), whereas the transposon from strain UCN34 was located in a putative peptidoglycan-linked protein (Fig. 1). Both transposons contained a second Te(\textsuperscript{c}) gene, tet(L), predicted to encode an efflux protein, closely linked to plasmid recombination/mobilization (pre/mob) and replication (rep) genes. A DNA fragment containing the Tn\textsubscript{916}-like rep12 as well as tet(M), tet(L), pre/mob and most of rep12 (see Fig. 1) has also recently been deposited in GenBank (AEEL01000025, contig of 6541 bp) as part of the draft sequence of a Human Microbiome Project (HMP) strain characterized as S. bovis ATCC 700338 and isolated from the vagina. This fragment is 100% identical to the homologous region in the infant transposon. Additionally, another DNA fragment from the same S. bovis draft sequence (AEEL01000027, contig of 33283 bp) contained a region (1900 bp) with Tn\textsubscript{916}-like rep5, xis and int that was 100% identical with a homologous region in the infant transposon (Fig. 1). This Tn\textsubscript{916}-like region was located at the 3’end of putative transposase IS\textsubscript{Sf}y. The infant transposon also contained a 3026 bp sequence encoding an erythromycin rRNA methylase gene, emr(T),
surrounded by two putative IS\textsubscript{1216} transposase genes, not present in strain UCN34. This 3026 bp sequence was 100% identical, except for an additional 30 bp between the \textit{erm}(T) leader and the second IS\textsubscript{1216} element (overall DNA identity of 99%), to a corresponding fragment from \textit{S. galloyticus} subsp. \textit{pasteurianus} NTUH 7421 (AY894138) [20] (Fig. 1). A fragment from \textit{S. bovis} ATCC 700338 (AEEL01000026, contig of 1578 bp) containing \textit{erm}(T), leader and an IS\textsubscript{1216} was 100% identical with the homologous region in the infant transposon (Fig. 1).

At the genic level, the \textit{tet}(M) sequence in the infant library insert was also highly similar to previously identified \textit{tet}(M) genes from the composite transposons, CTn\textsubscript{6002}, identified in \textit{Staphylococcus epidermidis} (AY898750, 99.9% DNA identity), and Tn\textsubscript{1545}, first identified in \textit{Staphylococcus pneumoniae} BM120 (AM689142, 98.2% DNA identity) [21,22]. The infant \textit{tet}(L) gene was shown to share 98.1% DNA identity (1.4% gaps) with \textit{tet}(L) genes found on \textit{pre}/\textit{mob} and \textit{rep}-containing plasmids in \textit{Bacillus stearothermophilus} (M63091), \textit{Enterococcus faecalis} (AF503772) and \textit{Staphylococcus aureus} (M63091).

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**Figure 1.** Composite transposon Tn\textsubscript{6079} from the infant metagenome compared to corresponding sequences from \textit{S. galloyticus} strains. Part of the sequenced fosmid-insert in the infant Tc\textsuperscript{r} metagenome (GU951538; 1–3095) is compared with the most similar homologous sequences in current databases, from \textit{S. galloyticus} subsp. \textit{galloyticus} strain UCN34 (FN597254; minus strand 564709–589025 and 52545–55152), \textit{S. galloyticus} subsp. \textit{pasteurianus} NTUH7421 (AY894138; minus strand 1–4107, 4107–8428) and \textit{S. bovis} ATCC700338 (AEEL01000024; 1–6541, AEEL01000024; 1–1578, AEEL01000027; 1–3192, AEEL01000028; 37166–39101). The relationships between sequences are shown as percentage identity at nucleotide level, calculated with the EMBOSS program Needle (http://www.ebi.ac.uk/Tools/emboss/align/index.html). Light gray arrows represent ORFs with homology to ORFs from Tn\textsubscript{916}/Tn\textsubscript{1545}-like conjugative transposons: \textit{orf}\textsubscript{5–10}, \textit{orf}\textsubscript{12–24}, \textit{tet}(M), an excisionase (\textit{xis}) and an integrase (\textit{int}) of Tn\textsubscript{6079}. Dark gray arrows illustrate ORFs that may be of plasmid origin: \textit{tet}(L), \textit{pre}/\textit{mob} and \textit{rep}. Black arrows illustrate ORFs that appear to be inserted by the two identical IS\textsubscript{1216}-like elements: first IS\textsubscript{1216}, \textit{erm}(T), \textit{erm}(T) leader sequence and second IS\textsubscript{1216}. \textit{rpmG} and \textit{rpmF} were predicted to encode L33 and L32 of the 50S ribosomal subunit. The functions of the predicted ORFs, \textit{mid12}_1, \textit{mid12}_5 and \textit{mid12}_7 are unknown. \textit{hisS}: histidyl-tRNA synthetase. \textit{ISSdy1}: putative transposase.

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Tc' was conferred exclusively by tet(M) and/or tet(L) from streptococci in the infant metagenomic library

In the infant Tc' metagenomic library, 97.7% (43/44) of the fosmids had at least one of their end-reads assigned within bacteria and at the genus level 72.7% (32/44) of the fosmids were assigned within Streptococcus (Fig. 2A and Table 1). This was further supported by a comparison showing 100% DNA identity between the rpmG and rpmF ORFs from the sequenced infant fosmid, predicted to encode the 50S ribosomal subunit proteins L33 and L32, and the corresponding regions from the three Streptococcus strains in Fig. 1 containing similar MGE fragments (S. galolyticus subsp. pasteurianus strain NTUH 7421, S. galolyticus subsp. galolyticus strain UCN34 and S. bovis ATCC 700336).

Out of the 44 infant fosmids, 43 were positive for a PCR designed to amplify the rpmG and rpmF ORFs region from the sequenced fosmid (Fig. 1). The reverse primer used in this PCR was specifically designed to target a sequence just downstream of the rpmF ORF that was present in the sequenced fosmid and in S. galolyticus subsp. pasteurianus strain NTUH 7421 and S. bovis ATCC 700336 (AEEL10000028) but not in S. galolyticus subsp. galolyticus strain UCN34 and S. bovis ATCC 700336.

The reverse end-sequence from the only strain UCN34 and designed to amplify the rpmF region from the same S. galolyticus-like genomic region having different fragment-specific start and end points.

Thus we detected much fewer Tc' fosmid clones in the infant metagenome than in the mother metagenome. The Tc' genes detected in the infant metagenomic library did not represent a subset of those found in the mother, but rather a completely distinct set, belonging to a different gene class and encoded by a different species. However, total fecal DNA from the infant sample was shown to also contain specific Tc' genes that were present in the maternal library (tet(W) and tet(X),) suggesting that these may have been transmitted from mother to son. Given that this DNA was not cloned, we cannot determine the organisms that carried these genes in the infant, but phylogenetic assignment of maternal fosmids suggests that they may have been present in organisms belonging to the Clostridiales (and/or to Bacteroides in the case of tet(O)).

In the infant library, tet(M) and tet(W) were detected in all the Tc' fosmids whereas mainly tet(O) but also tet(W) and tet(X) were detected among the Tc' fosmids from the mother. Although the approach employed here can only detect Tc' genes that can be expressed in the E. coli library host, the prevalence of Tc' genes observed in this study is in general agreement with former culture-independent studies that analyzed Tc' in Europe directly by PCR or microarray hybridization [14,15]. These works detected the tet(M) genotype to be abundant in Finnish infant fecal samples [15] and tet(O) and tet(W) to be the most prevalent Tc' genes in fecal samples from adults in six different European countries as detected by microarray analysis [14]. In contrast, a functional metagenomic screen of antibiotic resistances in the gut of two adult individuals carried out in the USA (Boston, MA) recovered numerous tet(W) sequences but did not identify any tet(O) or tet(X) genes [24]. It is important to note that the screening approaches in this latter work and in our own study both require that Tc' can be expressed in the E. coli library host strains at a level sufficient to confer resistance in the presence of the antibiotic, although each employs a different cloning vector. Our fosmid-based study has the potential disadvantage that resistance genes located on smaller plasmids (<40 kb) may not be represented in the metagenomic libraries, but, on the other hand, the larger insert size increases the likelihood to clone complete resistance genes and enables the recovery of complex genetic elements. The different results obtained in the two USA studies could be due to the different...
Figure 2. Microbial diversity of Tc' fosmid clones in infant (A) and mother (B) metagenomes. Modified MEGAN tree (collapsed at Genus level) showing summarized number of reads assigned at different taxonomical levels. The size of each node is proportional to the number of reads assigned to the node. Beneath each node the number and percentage of Tc' genes detected in this study are noted. A. The "No hits & removed MGE hits" category contains 13 reads with no BLASTX hits (or hits that did not attain the min score/length of 0.15), 2 removed reads which were predicted to be located in MGE and were initially assigned below order level and 4 reads that mapped to ORFs in the sequenced transposon (Tn6079). B. The "No hits & removed MGE hits" category contains 138 reads with no BLASTX hits (or hits that did not attain the min score/length of 0.15) and 31 removed reads which were predicted to be located in MGE and were initially assigned below order level. The "Not assigned" category contains 2 reads that were assigned by BLASTX hits to uncultured bacteria.

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cloning systems and/or reflect the antibiotic concentrations used in the functional screenings [10 µg/ml tetracycline in our study versus 20 µg/ml tetracycline, oxytetracycline or minocycline in Sommer et al]. In addition, functional screenings performed at even lower tetracycline concentrations might reveal further TcR genes that are weakly expressed.

The previous culture-independent analyses that identified TcR in human fecal samples did not investigate the bacterial species in which such resistance was encoded [14,15,24]. In our fosmid-based study, end-sequencing of fosmid inserts allowed for taxonomic identification of the resistant organisms present in the GIT of the two individuals analyzed. All infant TcR clones appeared to represent the same Streptococcus genomic region containing tet(M), tet(L) and erm(T) within a novel composite Tn916-like transposon, Tn6079, located at the 3’ end of rpmG. The nucleotide sequences of both rpmG and its 5’ neighbor rpmF were 100% identical to those of S. gallolyticus subsp. pasteurianus strain NTUH 7421, S. gallolyticus subsp. galloolyticus strain UCN34 and S. bovis ATCC 700338 (Fig. 1). It is important to note that the heterogenous group of strains traditionally designated S. bovis has recently been split by modern taxonomic techniques into the sister species S. galloolyticus and S. infantarius [25]. Indeed, the 16S rRNA sequence of S. bovis ATCC 700338 shows 99 to 100% identity with the S. galloolyticus subsp. pasteurianus and S. galloolyticus subsp. galloolyticus 16S rRNA sequences currently available in GenBank. Therefore, the presence of rpmG and rpmF next to the Tn6079 transposon in the sequenced infant fosmid allows for identification of the TcR-carrying organism in the infant GIT to species level. The similarities in sequence and structure between Tn6079 and corresponding MGE sequences in the S. galloolyticus subsp. pasteurianus, S. galloolyticus subsp. galloolyticus and S. bovis ATCC 700338 strains (Fig. 1) strongly suggest that the infant’s composite transposon arose through a process involving intraspecific genetic exchange.

Regarding the origin of the S. galloolyticus-like strain carrying the transposon in the infant, this organism was probably not transmitted from the maternal GIT, since no streptococci were detected in the mother’s fecal samples, neither in the resistance screens performed here, nor in the previous random end sequencing of the library [9], even though this species is a normal inhabitant in the GIT of humans and animals and can be isolated in 5–16% of fecal samples from healthy adults [26]. Possible origins may include transmission from other maternal areas that are known to often harbor streptococci, such as the skin, the birth canal and the mouth, from breast milk, where streptococci have also recently been detected [27], or from other individuals handling the infant. The 100% identities recovered between the sequenced fosmid insert and the vaginal strain S. bovis ATCC 700338 (see Fig. 1) suggest that the infant may have acquired this strain or a closely related one during his passage through the birth canal.

In the maternal library, microorganisms conferring TcR consisted mainly of Firmicutes and Bacteroidetes, which commonly represent the two major Phyla of the human GIT [28,29] and were also the most represented in the fosmid library of the mother according to random end reads [9]. For 9.9% of the maternal TcR fosmids, neither of the end-reads had any BLASTX hits against the NCBI non-redundant protein database in spite of being of substantial length (>500 bp). These fosmids likely carry TcR genes, mainly tet(O), from microorganisms for which no close relatives have yet been cultured. tet(O) was the main gene conferring resistance and was detected both within the Clostridiales (Firmicutes) and also the Bacteroidales (Bacteroidetes), where it had not been reported previously. Similarly, tet(X) was detected within the Clostridiales and the Bacteroidales and fosmids carrying identical tet(O) or tet(X) sequences were assigned within both phyla/orders. tet(W) was present only within Clostridiales, but also for this order fosmids carrying 100% identical tet(W) sequences were assigned within three different families (Table S2). Sequence identity is not expected between genes that have been diverging as orthologs since the phylogenetic split between such distantly related bacteria and can therefore be interpreted as evidence of recent horizontal transfers among these organisms [30–32]. tet(W) genes and flanking sequences in different isolates of GIT bacteria from diverse hosts have also been shown to share a high degree of similarity in previous analyses [33]. However, this is the first time that exact sequences of an antibiotic resistance gene are shown to occur in distantly related bacteria naturally.

### Table 1. Assignment of end-reads and corresponding fosmids from the infant TcR metagenome at different taxonomical levels.

<table>
<thead>
<tr>
<th>Level of assignment</th>
<th>Assignment details</th>
<th>No. of reads (percentage of total reads: 88)</th>
<th>No. of fosmids (percentage of total fosmids: 44)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kingdom</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteria.</td>
<td>69 (78.4%)</td>
<td>43 (97.7%)</td>
</tr>
<tr>
<td>Phylum</td>
<td>Reads/fosmids of which at least one end-read was assigned within Firmicutes.</td>
<td>55 (63.5%)</td>
<td>39 (88.6%)</td>
</tr>
<tr>
<td>Order</td>
<td>Reads/fosmids of which at least one end-read was assigned within Lactobacillales.</td>
<td>38 (43.2%)</td>
<td>36 (81.8%)</td>
</tr>
<tr>
<td>Family</td>
<td>Reads/fosmids of which at least one end-read was assigned within Streptococcaceae.</td>
<td>38 (43.2%)</td>
<td>36 (81.8%)</td>
</tr>
<tr>
<td>Genus</td>
<td>Reads/fosmids of which at least one end-read was assigned within Streptococcus.</td>
<td>33 (38.6%)</td>
<td>32 (72.7%)</td>
</tr>
<tr>
<td>No hit &amp; removed MGE hits</td>
<td>Both forward and reverse fosmid end-reads in “No hit &amp; removed MGE hits”</td>
<td>2 (2.3%)</td>
<td>1 (2.3%)</td>
</tr>
<tr>
<td></td>
<td>Both forward and reverse fosmid end-reads with no blasts hits or hits below min cut off (0.15 bit score/length).</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Both forward and reverse fosmid end-reads with no blasts hits.</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

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coexisting in the gut of a single person at a particular point in time. Although their coexistence does not prove that the horizontal transfers occurred in the GIT of the infant’s mother, alternative explanations would still necessitate recent transfers, in the environment or in the GITs of other individuals, followed by colocalization of the bacteria in this individual’s GIT. These scenarios would imply a high frequency of these exact sequences in nature and/or a high likelihood of colocalization of the bacteria carrying them, and therefore seem less parsimonious than in situ transfer among bacteria coexisting closely in the dense microbiota of the adult GIT. In addition to fosmids containing \( \text{tet}(\text{O}), \text{tet}(\text{W}) \) and \( \text{tet}(\text{X}) \), there was also a fraction of \( \text{Tc}^r \) maternal fosmids in which none of the assayed genes were detected (11%, assigned within Firmicutes or Bacteroidetes), and where \( \text{Tc}^r \) must have been conferred by rare resistance genes.

This study showed strong indications of transmission of specific \( \text{Tc}^r \) genes (\( \text{tet}(\text{W})_a \) and \( \text{tet}(\text{O})_b \)) from the mother’s GIT to that of the infant. However, the third \( \text{Tc}^r \) gene present in the maternal genomic library, \( \text{tet}(\text{X})_c \), was not detected in the infant. \( \text{tet}(\text{W})_a \) and \( \text{tet}(\text{O})_b \) could be found in the infant’s uncloned fecal DNA but not in the infant metagenomic library, suggesting that they were only present in low numbers. This is supported by the fact that PCR with \( \text{tet}(\text{W}) \) screening primers produced only a very faint band, and by the detection of a single \( \text{tet}(\text{O}) \) sequence type in the infant out of the 9 different types detected in the mother (Fig. S2). The scarcity of maternal \( \text{Tc}^r \) genes in the infant could be partially explained by the fact that approximately half of the detected \( \text{Tc}^r \) in the mother library was encoded by clostridia, and previous analyses of random end sequences from these libraries showed that clostridia were not abundant in the mother and that they were not transmitted to the infant [9]. On the other hand, those analyses, as well as comparisons of fosmid sequences and \( \text{Bacteroides} \)-specific 16S PCR libraries, have shown transmission to the infant of the two \( \text{Bacteroides} \) phylotypes present in the mother [9].

### Table 2. Assignment of end-reads and corresponding fosmids from the mother \( \text{Tc}^r \) metagenome at different taxonomical levels.

<table>
<thead>
<tr>
<th>Level of assignment</th>
<th>Assignment details</th>
<th>No. of reads (percentage of total reads: 544)</th>
<th>No. of fosmids (percentage of total fosmids: 272)</th>
</tr>
</thead>
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<tr>
<td>Kingdom</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteria.</td>
<td>365 (67.1%)</td>
<td>226 (83.1%)</td>
</tr>
<tr>
<td>Phylum</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteroidetes.</td>
<td>27 (5.0%)</td>
<td>22 (8.1%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Firmicutes.</td>
<td>254 (46.7%)</td>
<td>180 (66.2%)</td>
</tr>
<tr>
<td>Order</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteroidales.</td>
<td>20 (3.7%)</td>
<td>19 (7.0%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Firmicutes.</td>
<td>182 (33.4%)</td>
<td>139 (51.1%)</td>
</tr>
<tr>
<td>Family</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteroidaceae.</td>
<td>9 (1.7%)</td>
<td>9 (3.3%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Lachnospiraceae.</td>
<td>35 (6.4%)</td>
<td>29 (10.7%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Clostridiaceae.</td>
<td>9 (1.7%)</td>
<td>9 (3.3%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Eubacteriaceae.</td>
<td>1 (0.2%)</td>
<td>1 (0.4%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within Ruminococcaceae.</td>
<td>10 (1.8%)</td>
<td>10 (3.7%)</td>
</tr>
<tr>
<td>Genus</td>
<td>Reads/fosmids of which at least one end-read was assigned within Bacteroides.</td>
<td>9 (1.7%)</td>
<td>9 (3.3%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within ( \text{Dorea} ).</td>
<td>16 (2.9%)</td>
<td>12 (4.4%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within ( \text{Clostridium} ).</td>
<td>9 (1.7%)</td>
<td>9 (3.3%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within ( \text{Eubacterium} ).</td>
<td>1 (0.2%)</td>
<td>1 (0.4%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within ( \text{Ruminococcus} ).</td>
<td>8 (1.5%)</td>
<td>8 (2.9%)</td>
</tr>
<tr>
<td></td>
<td>Reads/fosmids of which at least one end-read was assigned within ( \text{Faecalibacterium} ).</td>
<td>2 (0.4%)</td>
<td>2 (0.7%)</td>
</tr>
<tr>
<td>“No hit &amp; removed MGE hits”</td>
<td>Both forward and reverse fosmid end-reads in “No hit &amp; removed MGE hits”</td>
<td>92 (16.9%)</td>
<td>46 (16.9%)</td>
</tr>
<tr>
<td></td>
<td>Both forward and reverse fosmid end-reads with no blastx hits or hits below min cut off (0.15 bit score/length)</td>
<td>76 (13.9%)</td>
<td>38 (13.9%)</td>
</tr>
<tr>
<td></td>
<td>Both forward and reverse fosmid end-reads with no blastx hits.</td>
<td>54 (9.9%)</td>
<td>27 (9.9%)</td>
</tr>
</tbody>
</table>

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established phylotype transmission, the fact that Bacteroides were
amply represented in both the mother and infant libraries and the
presence of tet(O)h and tet(X)a genes in Bacteroides-assigned
maternal fosmid, the lack of Bacteroides-encoded Tc in the infant’s
library suggests that 1) tet(O)h and/or tet(X)a were present in only a
small fraction of the maternal Bacteroides population and/or that 2)
tet(O)h- and tet(X)a-encoding Bacteroides were selected against
during the transmission process or in the infant gut. In fact, the
first proposition is likely true, as according to previous random end
sequencing analyses, Bacteroides represent nearly 48% of the
maternal fosmid clones [9], and therefore hundreds of Tc-
encoding fosmids would be expected in a 69,000-clone library if
tet(O)h and/or tet(X)a were present in every Bacteroides cell (based
on a genome size of 6.5 Mbp) in contrast, only 3 and 18 end-reads
were assigned to Bacteroidetes among the mother clones containing
tet(O)h and tet(X)a, respectively (Fig. 2B and Table S2).

In summary, for the first time we have characterized the
microbial diversity of Tc bacteria in human gut samples, by
analyzing GIT fosmid libraries from a mother and her infant.
The maternal and infant libraries contained different resistant taxa
coding distinct sets of genes, but some of the specific Tc genes
present in the mother could be recovered from uncloned infant
cecal DNA. This indicates that transmission of Tc genes from the
mother’s GIT to the infant likely occurred, but that, due to the
complexity of the GIT microbiota, species and genes present in
low numbers were missed in the infant metagenomic library in
spite of its large size (>70,000 clones). The likely role of the human
gut as a privileged environment for HGT has been previously
recognized [8], but here we present the first documented cases of
identical resistance genes that could be directly linked to distantly
related bacteria coexisting in the GIT of the same individual.
The finding of a transposon in the infant carrying tet(M), tet(L) and
erm(T), belonging to a family of broad host-range transposons,
implied a strong potential for the joint transfer of tetracycline and
erthyromycin resistance within the infant’s gut. These findings
reinforce the notion that the human GIT is currently a relevant
environment for the spread of antibiotic resistances, even in the
case of young infants that solely ingest maternal milk. Further
analyses involving more mother-infant pairs will be required in
order to establish whether the trends observed in this case study
describe the general relationship between mother and infant
antibiotic resistomes.

Materials and Methods

Sample collection and ethics statement

The infant and mother metagenomic fosmid libraries analyzed
in this study were prepared from fecal samples obtained one
month after the infant’s birth [9]. The infant was a healthy male,
vaginally delivered at full term at the University Medical Center
of the University of Arizona in Tucson (USA). He was exclusively
breast-fed for 5 months. Samples were collected at the University
of Arizona, with informed written consent from the infant’s
parents, using protocols approved by the institutional review
boards of the Lawrence Berkeley National Laboratory and the
University of Arizona.

Metagenomic fosmid libraries and preparation of master
plates with pooled clones

The infant and mother metagenomic fosmid libraries analyzed
consisted of approximately 76000 and 69100 clones, respectively
[9]. Fosmid inserts were approximately 40 kb, thus the infant and
mother libraries represent roughly 3 Gb of DNA each. Clones
from the infant and mother metagenomic fosmid libraries were
pooled resulting in a reduction from 198 and 180 library (384
wells) plates to 14 and 12 (384 wells) master plates, respectively.
Each master plate was constructed by pooling 15 library plates
into one master plate using a Plate Mate Plus from Matrix. Each
well in the master plates contained 30–40 µL LB (Miller’s) broth
supplied with 7.5% Glycerol and 2 µL from each of the original
library plates.

Phenotypic screening of library master plates for Tc

All master plates were screened for clones conferring Tc in
growth plates (384 wells) containing 60 µL LB (Miller’s) broth with
10 µg/mL tetracycline per well. Growth or no growth was detected
after overnight incubation at 37°C. When growth was detected,
each of the 13 clones from the original fosmid libraries that could
be responsible for the observed resistance phenotype was tested for
Tc separately as described above.

Genotypic PCR screenings and sequencing

All Tc clones (44 infant and 272 mother clones) from the two
metagenomic libraries were screened for tet(M), tet(S), tet(O) and
tet(W) by PCR using primer pairs TetM-1D/TetM-2, TetW-1/
TetW-2, TetS-1/TetS-2 and TetO-1/TetO-2 (Table S3) [34]. To
detect other possible resistance genes in the maternal Tc clones
that were negative for these screening primers, we performed a
series of multiplex PCRs designed to detect tet(A), tet(B), tet(C),
tet(D), tet(E), tet(G), tet(K), tet(L), tet(X), tet(AP), tet(Q) and tet(N),
yielding previously reported primer combinations and protocols [35]. In
addition, purified DNA from the infant fecal sample from which
the infant fosmid library was constructed was screened for the Tc
genes detected in the mother (tet(W), tet(O) and tet(X)).

After characterization of transposon Tn6079, the 44 infant
cloned were also screened for tet(L) [36], for a region linking erm(T)
to an IS element (1010 bp) and for a region containing the rpmG
and rpmF ORFs (664 bp) using primer pairs TetrL-1/TetrL-2,
ermG-2/IS1216V3-1 and <rEO/rRNA_S (Table S3). The latter
PCR primer pair was designed to specifically target the region
starting just downstream of the int gene within Tn6079 and ending
downstream of the rpmF gene.

PCR screening products from both uncultured fecal DNA from
the infant (tet(W) and tet(O)) and from each metagenomic library
(tet(M), tet(W), tet(O) and tet(X)) were sequenced with the PCR
primers by Macrogen, Korea (http://www.macrogen.com/eng/
sequencing/sequence_main.jsp) (see Tables S1 and S2). In
addition, 5 randomly selected PCR screening products containing
the rpmG and rpmF ORFs (B04-M4, B04-M8, B04-M13, B04-M16
and B04-M18) were also sequenced. ClustalX [37] was used to
align sequences within the tet groups to determine different
sequence types (Tables S1 & S2) and to align the rpmG and rpmF
sequences. All together, 13 different Tc gene sequence types were
deposited in GenBank (accession no. HN150556–HN150563,
HR941095–HR941098 and JN104731). Neighbor Joining (NJ)
trees based on the total gene sequence of selected Tc genes (57
tet(M), 18 tet(O), 24 tet(W) and 26 tet(X)) from GenBank and NJ
trees based on the sequenced PCR screening products (505 bp,
499 bp, 609 bp and 446 bp, respectively) were constructed
in ClustalX [37]. The trees were compared in order to show to what
degree the sequenced PCR screening products were able to
discriminate among the known variants of tet(M), tet(O), tet(W)
and tet(X).

Sequencing a fosmid-insert carrying tet(M)

One fosmid carrying tet(M) from the infant library (B04-M2) was
sequenced as part of a mix of 12 fosmids pyrosequenced with
Multiple Sequence Identifiers (MIDs) in a Roche GS FLX

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instrument in the Sequencing Technology group of the DOE Joint Genome Institute (JGI), CA, USA [http://www.jgi.doe.gov/. Reads belonging to the B04-M2 fosmid were sorted out and assembled using the Roche 454 Newbler software. Seven contigs were generated of which five (lengths 23744 bp, 19061 bp, 6382 bp, 1570 bp and 809 bp) were used to assemble the fosmid sequence. The remaining two contigs (lengths 938 bp and 507 bp) were highly similar or identical to the E. coli host genome and therefore were not incorporated into the assembly. Ten sequencing primers, M1b, M2b, M3, M4, M5, M6, C340F, C01F and C01R were designed (Table S3) and Sanger reads, produced by Macrogen, Korea, were used to close the remaining five gaps. FosmidMAX™ DNA Purification Kit (EPICENTRE, USA) was used to prepare fosmid DNA template for the Sanger sequencing reactions. A finished 53499 bp circular fosmid containing a 45066 bp insert was assembled. The insert was annotated by NCBI ORF finder, visualized by Vector NTI 10 (Invitrogen) and deposited in GenBank (accession no. GU951538).

### End-Sequencing

Inserts from all Tc’ fosmid clones from the infant (44) and adult (272) library were sequenced at both ends using pEpIFOS forward (PGC1F) or T7 promoter sequencing (T7) primers and the pEpIFOS reverse primer (PGC1R) (Table S3). End-sequencing was performed by the Sanger method using BigDye Terminators in ABI 3730 sequencers at the JGI. Out of 632 end-reads, 543 high quality (Phred≥Q20) sequences [38,39], with a minimum length of 100 bp were retained after being trimmed by the program Trim at Greengenes [http://greengenes.lbl.gov] [40]. The remaining 89 end-reads were resequenced by Macrogen, Korea, and quality checking (≥Q20) and trimming were performed manually in Vector NTI. Vector contaminations were removed from 16 end-reads prior to Genome Survey Sequences (GSS) submission to GenBank. All together 632 end-reads with lengths ranging from 100 bp to 811 bp were deposited in Genbank (accession no. HN149924–HN150555). Read lengths ranged from 500 bp to 799 bp for 84.1% and 86.4% of infant and mother Tc’ end-reads, respectively.

### Assignment of end-sequences

All together 632 high quality sequences were used as queries to establish bacterial diversity through BLASTX searches against the NCBI non-redundant protein database (e-value<e^-15). End-sequencing has recently been validated as a reliable method of determining diversity in a metagenomic sample, as random sequence reads from fosmid libraries of human fecal samples provide results very similar to those obtained based on the analysis of 16S sequences [41]. Each of the two BLASTX results (mother and infant) were separately parsed and visualized using MEGAN (version 3.7.4) software (Min Score = 35, Min Score/Length = 0.15, Top Percent = 20, Min Support = 1) [42]. Min Score/Length = 0.15 was chosen in order to account for the different read lengths. Because end-sequences located in MGE could easily bias the bacterial assignment by MEGAN, the BLASTX results were parsed for reads with hits containing the regular expressions conjugative, transposon, in1916, integrase, recombinase, excisionase, mobilization and resistance, and if such reads were assigned below order-level they were manually removed (Tables S4 & S5). Additionally, 4 infant end-reads (B04-M19-PCC1F, B04-M20-PCC1F, B04-M29-PCC1R, B04-M33-PCC1R) that were not found by the parsing of the BLASTX result but mapped to ORFs in the sequenced transposon were also removed. The assignment of reads by MEGAN based only on one BLASTX hit is very sensitive to misclassified sequences in GenBank. Therefore the taxonomical classification of BLASTX hit sequences used by MEGAN to assign reads at species level was reviewed (Tables S6 & S7). Finally, it was checked that assignments of forward and reverse end-reads from the same fosmid did not contradict each other.

### Supporting Information

#### Figure S1 NJ tree based on 305 bp corresponding to the sequenced PCR screening products of tet(M). The tree includes 57 tet(M) genes from GenBank and sequence type tet(M)a (bold) found among Tc’ clones in the infant metagenomic library. tet(M)a differs from the 57 tet(M) genes present in GenBank at the time of screening. (TIF)

#### Figure S2 NJ tet(O) trees showing that tet(O)a–i can discriminate among the known variants of tet(O). A. Tree based on 499 bp corresponding to the sequenced PCR screening products of tet(O). tet(O)a–i represent the nine sequence types found among 63/204 tet(O) fosmids from the maternal metagenomic library and tet(O)_infant_plug represents the sequence type detected directly in uncloned DNA from the infant fecal sample. B. Tree based on the total tet(O) gene (1920 bp) of 18 GenBank sequences defined as tet(O) by sharing ≥80% identity at the amino acid level. However, NC_006134 is a mosaic combination of tet(O) and tet(M). (TIF)

#### Figure S3 NJ trees showing to what degree tet(W)a,b can discriminate among the known variants of tet(W). A. Tree based on 609 bp corresponding to the sequenced PCR screening products of tet(W). tet(W)a,b represent the two sequence types found among 21 tet(W) fosmids from the maternal metagenomic library and tet(W)_infant_plug represents the sequence type detected directly in uncloned DNA from the infant fecal sample. (DQ525023 is not included in group tet(W)b because the tet(W) screening primers are not specific for this gene). B. Tree based on the total tet(W) gene (1920 bp) of 24 GenBank sequences defined as tet(W) by sharing ≥80% identity at the amino acid level. However, AY485122, AY485126, AY196920, AY196921, and DQ525023 are different mosaic combinations of tet(W), tet(O) and tet(S) and the tet(W) screening primers are not specific for these genes. (TIF)

#### Figure S4 NJ trees showing to what degree tet(X)a can discriminate among the known variants of tet(X). A. Tree based on 447 bp corresponding to the sequenced PCR screening products of tet(X). tet(X)a represents the single sequence type found among 12 sequenced tet(X) PCR screening products from the maternal metagenomic library. B. Tree based on the total tet(X) gene (1167 bp) of 26 GenBank sequences of tet(X). (TIF)

### Table S1 Sequence type of 43 tet(M) genes detected in the infant metagenome.
(DOCX)

### Table S2 Sequence types among 21 tet(W) and 63 out of a total of 204 tet(O) genes detected in the mother metagenome.
(DOCX)

### Table S3 Primers used in this study.
(DOCX)

### Table S4 End-reads (17) from the infant Tc’ metagenome for which BLASTX hits contained the regular expressions conjugative, transposon, in1916, integrase, recombinase, excisionase, mobilization and resistance
and therefore were predicted to be located in MGE (2 end-reads in bold letters were assigned below order level and therefore removed from their initial assignments to the group with no hits in figure 2A).

(DoCX)

Table S5 End-reads (141) from the mother Te⁻ meta-genome for which BLASTX hits contained the regular expressions conjugative, transposon, tn916, integrase, recombinase, excisionase, mobilization and resistance and therefore were predicted to be located in MGE (31 end-reads in bold letters were assigned below order level and therefore removed from their initial assignments to the group with no hits in figure 2B).

(DoCX)

Table S6 Review of taxonomical classification of BLASTX hit sequences used by MEGAN to assign reads at species level in the infant Te⁺ metagenome.

(DoCX)

References


