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Mobile genetic elements provide evidence for a bovine origin of clonal complex 17 of

_Streptococcus agalactiae_

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This work was presented in part at the XVIth Lancefield International Symposium on
We sought an explanation for epidemiological changes in *Streptococcus agalactiae* infections, by investigating the link between ecological niches of the bacterium, by determining the prevalence of 11 mobile genetic elements. The prevalence of nine of these elements differed significantly according to the human or bovine origin of the isolate. Correlating this distribution with the phylogeny obtained by multilocus sequence analysis, we observed that human isolates harboring GBSi1, a clear marker of the bovine niche, clustered in clonal complex 17. Our results are thus consistent with the emergence of this virulent human clone from a bovine ancestor.
Epidemiological changes in the pattern of *Streptococcus agalactiae* infections over the last six decades, from predominantly bovine infections (13), to a leading cause of neonatal infections (25, 26) and, more recently, a cause of invasive disease in elderly adults (6), requires explanation. Genomic lineages grouping the most invasive isolates have been described by multilocus enzyme electrophoresis (17, 23), by pulsed-field gel electrophoresis (1, 24) and more recently by the analysis of the polymorphism in the allelic profiles of housekeeping genes (11), but are insufficient to account for the emergence of *S. agalactiae* from such diverse ecosystems. A link between the bovine and human niches has been proposed (8, 19), but remains a matter of debate. Indeed, it was recently suggested that human and bovine *S. agalactiae* isolates are largely unrelated (3) and represent distinct populations or subtypes (5, 27). Conversely, another study provided evidence to suggest that the major hyperinvasive ST-17 clone implicated in neonatal invasive diseases had arisen from bovine lineage ST-61 (2), whereas others suggested that the genome of the common ancestor was closer to that of human ST-17 strains than to that of the ST-61 strains of bovine origin (4). We hypothesized that mobile genetic elements (MGEs), such as insertion sequences (ISs) or group II introns, which drive bacterial evolution (12, 30), might provide insight into changes in the epidemiology of *S. agalactiae* infections.

We tested this hypothesis by analyzing a collection of 98 epidemiologically unrelated isolates, mostly collected in France (3 isolates from Germany and 1 from Malaysia) between 1966 and 2003: 63 human isolates from colonized individuals, adults with invasive diseases and neonates with meningitis (52 of which were previously typed by MLST and studied for the prevalence of IS1548, IS861, IS1381, ISSa4 and GBSi1) (10), and 35 bovine isolates obtained from cows with clinical evidence of udder infection.
The prevalence of 11 MGEs [one group II intron (GBSi1), and ten IS elements
corresponding to six insertion sequences (IS\textsubscript{1548}, IS\textsubscript{861}, IS\textsubscript{1381}, ISSa4, ISSag1 and
ISSag2), and four transposase genes corresponding to remnants of IS elements (ISSag9,
sag0448, sag1241, and sag0610, relating to the identification of the ORFs in strains
A909 and 2605V/R) (28, 29)], was evaluated by PCR. IS\textsubscript{1548}, IS\textsubscript{861}, IS\textsubscript{1381}, ISSa4,
ISSag1, ISSag2 and GBSi1 were detected as previously described (10). Other
transposase genes were detected with the primers listed in Table 1. The prevalence of all
the MGEs except IS\textsubscript{861} and ISSag2 differed significantly as a function of the original
reservoir (Fig. 1). This was particularly true for IS\textsubscript{1381}, IS\textsubscript{1548}, ISSag1 and ISSag9,
which were mostly present in human isolates, and for GBSi1 and ISSa4, which were
mostly present in bovine isolates (Fig. 1).

Multilocus sequence analysis, carried out with the standard multilocus sequence
typing (MLST) scheme described by Jones \textit{et al.} (11), resolved the 98 isolates into 47
STs. A phylogenetic tree was generated, based on the nucleotide sequences of the
supergene obtained by concatenation of the seven loci for the 98 isolates, using MEGA
software version 3.1 (www.megasoftware.net/) with the neighbor joining (NJ) method
(14). Clonal complexes (CCs) (isolates sharing six or seven identical alleles) were
defined by eBURST analysis (http://eburst.mlst.net/) (7). Seven main NJ phylogenetic
divisions were identified, closely matching the seven main CCs identified by eBURST
analysis (Fig. 2): subCC19 (n=21), subCC2 (n=11), CC10 (n=12), CC7 (n=6), CC17
(n=13), CC67 (n=15) and CC23 (n=10). Three of these CCs were “host-specific”: CC17
and subCC19 consisted almost exclusively of human isolates (100\% and 95\% of the
isolates, respectively), whereas CC67 was almost exclusively composed of bovine
isolates (93.8\% of the isolates). Moreover, the NJ dendrogram shows that human
lineage CC17 arose from bovine lineage CC67 (Fig. 2), consistent with the assertions of Bisharat et al. (2).

A factorial analysis of correspondence (FAC) was performed on the whole data set, with the 11 MGEs as active variables and the three main clonal complexes (CC19, CC17 and CC67) and the bovine or human origins of the strains as illustrative variables. Computations were performed with SPAD.N software (Centre International de Statistiques et Informatique Appliquées, St Mandé, France), as previously described (22). The projections of the active and illustrative variables and of the strains on the F1/F2 plane accounting for 40.97 % of the total variance (Fig. 3), separated two groups of variables and of strains. GBSi1 and ISSa4 (and to a lesser degree sag0448 and sag1241), bovine origin, CC17 and CC67 and 94.3% of bovine isolates were projected onto the negative values of F1. IS1548, IS1381, ISSag9 and ISSag1 (and to a lesser degree sag0610), human origin, CC19 and 79.4% of human isolates were projected onto the positive values of F1. These findings confirm those of Luan et al. in that the two major human S. agalactiae lineages are each marked by one MGE: subCC19 (defined as CC19 by Luan et al.) (16), is characterized by IS1548, whereas CC17 is characterized by GBSi1. All but one of the human isolates projected with the bovine isolates and variable CC67 onto the negative values of F1 belonged to CC17, highlighting the stronger linkage of CC17 with the bovine lineage CC67 than with any of the other human lineages (Fig. 3). Moreover, our data also suggest that the presence of GBSi1 in the bovine reservoir predates its presence in the human reservoir because (1) all our bovine isolates harbored GBSi1 whereas this element was present in less than one third of human isolates (almost all of which belonged to CC17) and (2) the bovine isolates had higher copy numbers and more complex patterns for GBSi1 than the human isolates (data not shown), consistent with an increase in IS pattern complexity over time (18).
MGEs therefore provide evidence for a bovine ancestor of the human clonal lineage CC17, all the isolates of which harbor GBSi1. This statement is consistent with the proposed evolutionary scheme of MGE acquisition, in which GBSi1 is thought to have been acquired recently by human isolates (10).

The particular distribution of MGEs among bovine and human isolates (Fig. 3) is also consistent with a physical barrier reducing the exchange of genetic material between the bovine and human reservoirs. The human isolate H14, which occupies a prominent position on the NJ dendrogram, between the bovine CC67 and the human CC17 (Fig. 2), displayed two particular features. First, the copy number of GBSi1 in this isolate was much higher than that in other isolates (human isolates had a median of 3 GBSi1, whereas H14 harbored 12 copies — data not shown). Parkhill et al. suggested that IS expansion occurs during evolutionary bottlenecks (20, 21). They argued that in *Yersinia*, IS expansion coincided with a change in the ecological niche of the species, from commensal organism of the gut to systemic pathogen (21). Second, isolate H14 harbored both IS1548 and GBSi1. In our study, as in previous studies (9, 15), very few isolates harbored both GBSi1 and IS1548 (see Fig. 2). Granlund et al. explained this mutually exclusive distribution by the presence of a closed insertion site for the two MGEs on the bacterial chromosome (9), but this distribution could also be explained by IS1548 and GBSi1 originating from two different ecological niches. Thus, human clone CC17 seems to have evolved from the bovine lineage containing GBSi1, and has retained the GBSi1 genetic marker from its bovine donor.

In conclusion, our results provide at least a partial explanation of the emergence of *S. agalactiae* as a major cause of neonatal meningitis, despite its original identification as the causal agent of bovine mastitis. Assuming that CC17 evolved from a bovine ancestor, as shown both by MLST analysis and by the presence of the bovine
marker GBSi1, the isolates of this clonal complex may have genetic features different from those of other *S. agalactiae* isolates that have adapted to their human hosts over a longer period of time. These features probably concern genes not present in the core genome, as recently defined by Tettelin *et al.*, but that have been acquired by horizontal exchange due to the environmental gene pool available in other ecosystems (28). Indeed, we recently reported a link between prophage DNA fragments and *S. agalactiae* isolates from neonatal cases of meningitis, suggesting the presence of additional genetic material in these strains (10).

**ACKNOWLEDGMENTS**

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REFERENCES


15. **Luan, S. L., M. Granlund, and M. Norgren.** 2003. An inserted DNA fragment with plasmid features is uniquely associated with the presence of the GBSi1 group II intron in *Streptococcus agalactiae*. Gene **312**:305-12.


TABLE 1. Primers used for the amplification of transposase genes from the 
*S. agalactiae* isolates.

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<th>Target</th>
<th>Genbank accession no.</th>
<th>Forward primer (5’-3’)</th>
<th>Reverse primer (5’-3’)</th>
<th>Tm (°C)</th>
<th>Amplicon (bp)</th>
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<td>50</td>
<td>994</td>
</tr>
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<td>394</td>
</tr>
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</table>

a NC_004116 refers to strain 2603 V/R (29)
FIG. 1. Prevalence of the mobile genetic elements within the human (filled bars) and the bovine (open bars) *S. agalactiae* isolates. Significant differences (without correction for bias due to multiple comparisons) are indicated by one asterisk for p values below 0.05 and two asterisks for p values below 0.001.
FIG. 2. Relatedness of the 98 isolates of *S. agalactiae* analyzed by the NJ method, using MEGA v3.1 software and the Kimura 2-parameter mutation model of genetic distance. The nucleotide differences between the supergene sequences obtained in multilocus sequence analysis, as described by Jones *et al.* (11), were used to infer phylogenetic relationships between isolates. We used eBURST v3 software to group the 98 isolates into clonal complexes (CC). For each isolate, sequence type (ST), ß-hemolysis, serotype and presence/absence of the 11 mobile genetic elements (MGEs) are indicated. Clonal complexes are also indicated on the right of the figure (several isolates were not attributed a CC number by the Start software and are considered “Singletons”).

The particular position of isolate H14 is indicated by a black arrowhead.

The human isolates are named L or LJ (meningocerebral fluid), H (adult), V or VV (vaginal carriage) or G (gastric fluid); the bovine isolates are named N (bovine isolates are underlined).

NT: non typable
FIG. 3. Factorial analysis of correspondence of 98 *S. agalactiae* isolates based on the mobile genetic element (MGE) data. Eleven active variables [the MGEs (▲) *IS1381*, *IS861*, *IS1548*, GBSi1, ISSa4, ISSag2, ISSag1, *sag0448*, *sag1241*, *sag0610* and ISSag9], and five illustrative variables [the main clonal complexes CC19 (♦), CC17 (♣) and CC67 (♦), and the human (●) and bovine (■) origins of the isolates], and the 98 isolates are projected onto the F1/F2 plane. This plane, obtained by computation, is defined by the two principal axes of the analysis; the first axis, F1, explains most of the variance, and the second axis, F2 (orthogonal to F1), explains most of the variance not explained by F1. Together, F1 and F2 accounted for 40.97% of the total variance. Isolates of CC17 (n=13) are shown in red, isolates of CC67 (n=15) in green, and isolates of subCC19 (n=21) in pink.
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**Type**

- +
- -

**Subtypes**

- CC2
- CC7
- CC10
- CC67
- CC17
- CC23