

MOLECULAR EPIDEMIOLOGY OF *STREPTOCOCCUS AGALACTIAE* (GROUP B *STREPTOCOCCUS*)

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1. ABSTRACT

Group B *Streptococcus* (GBS) is a common cause of sepsis and meningitis in newborns, and causes disease in pregnant women and non-pregnant adults. The incidence of disease among non-pregnant adults, particularly those with underlying conditions, is increasing. In addition, many individuals are asymptomatically colonized with GBS. When compared to group A *Streptococcus* and *Streptococcus pneumoniae*, however, little is known about the pathogenesis, natural history and transmission dynamics of GBS. Various molecular tools have been utilized to study this organism, including both phenotypic techniques, such as serotyping and multilocus enzyme electrophoresis, and genotypic techniques such as plasmid analysis and pulsed-field gel electrophoresis. This review outlines the contributions of these methods to our current understanding of GBS infections.

2. INTRODUCTION

In recent years, the application of molecular tools to epidemiologic problems, or 'molecular epidemiology', has become increasingly more popular and important for health care providers, scientists, public health officials, and researchers in many different fields. Molecular epidemiology can be used to examine disease patterns, investigate outbreaks, describe transmission and population dynamics, understand evolution and disease pathogenesis, and identify uncultivable organisms (1, 2).

Little is known about the epidemiology, transmission and pathogenesis of Group B *Streptococcus* (GBS), or *Streptococcus agalactiae* when compared to other members of the *Streptococcus* family including *Streptococcus pneumoniae* and group A *Streptococcus*. This review will discuss the epidemiology of GBS; outline

specific GBS characteristics; examine various molecular methods used to study GBS and discuss the knowledge gained from them; highlight limitations associated with these methods; and emphasize specific GBS research areas that require further study.

3. EPIDEMIOLOGY OF GROUP B STREPTOCOCCUS

3.1. Disease presentation and incidence

GBS, a facultative gram-positive diplococcus with an ultrastructure similar to other gram-positive cocci (3, 4), was originally known for causing bovine mastitis (5-7) and was not demonstrated to be a human pathogen until 1938 (8). Currently, GBS remains a common cause of sepsis and meningitis in newborns despite prevention efforts (9), and can cause urosepsis, pneumonia, and skin and soft tissue infections, among non-pregnant adults with underlying medical conditions (10). During pregnancy, the primary clinical manifestation is bacteremia, but chorioamnionitis, endometritis and septic abortion also occur (11).

The incidence of early-onset newborn disease attributable to GBS has decreased from 1.7 to 0.6 cases per 1000 live births between 1993 and 1998, while the incidence among pregnant girls and women decreased from 0.29 in 1993 to 0.23 cases per 1000 deliveries in 1998 (11). In contrast, the number of GBS-attributable conditions among non-pregnant adults, particularly the elderly with underlying conditions, is increasing (10), ranging from 4.1 to 7.2 cases per 100,000 adults over the past decade (12-15).

3.2. Asymptomatic colonization

Many individuals are asymptotically colonized with GBS. Depending on the characteristics of the study population and the detection methods utilized, 10 to 40% of individuals are colonized (16-18). Newborns over 48 hours old are most commonly colonized in the throat and rectum (19) and can remain colonized throughout childhood; little is known, however, about the duration of colonization. At the onset of sexual activity, colonization generally shifts to the genitourinary tract (5, 20-31).

3.3. Transmission and pathogenesis

Among newborns presenting with early-onset disease, GBS is generally acquired from the mother during labor and delivery (32), yet transmission can occur nosocomially (33-39) or via direct contact from other individuals (34, 35). Newborns with early-onset invasive disease have an increased density of epithelial cell surface receptors specific for GBS, (40) and some GBS strains can replicate more readily in amniotic fluid (41); both facilitate colonization, the first step in disease pathogenesis. Among adults, transmission is hypothesized to occur by the fecal-oral route or by person-to-person direct contact (30, 42). Few studies, however, have been conducted to directly assess this. The primary site of asymptomatic GBS colonization is the rectum, or the gastrointestinal tract (43, 44), with secondary spread to the genitourinary tract occurring frequently (16, 33).

The ability of certain GBS strains to move from a colonizing state to a disease-causing state is unclear, but many risk factors have been identified that may affect this process. Host factors, such as low type-specific maternal antibody levels at delivery (45-49), genetic predisposition (50-55), a compromised immune system or faulty immune response (20, 56), race/ethnicity (19, 31, 57, 58), and specific behavioral factors (e.g. sexual (30, 31, 57, 59)) in conjunction with different bacterial characteristics, such as virulence capacity (e.g., polysaccharide type (60)), adherence capabilities (61, 62, 63-71), host evasion mechanisms (72, 73), and inoculum density (32, 74) contribute to GBS colonization and subsequent disease. Like most infectious diseases, GBS disease pathogenesis is a multifactorial process in which colonization leads to invasion and clinical manifestations in certain individuals.

3.4. Risk factors

Maternal risk factors associated with the development of neonatal GBS disease, such as GBS colonization, premature delivery, prolonged rupture of membranes, intrapartum fever, GBS urinary tract infection, age less than 20 years, multiple pregnancies, history of GBS infection in a previous child, and African American ethnicity, have been identified (16, 19, 43, 57, 58, 74-76). Low birth weight, African American ethnicity, prematurity, low Apgar scores, and decreased level of maternal antibodies are examples of neonatal factors found to be associated with GBS disease (43, 75, 77). Among non-pregnant adults, most invasive disease occurs in the setting of underlying conditions including diabetes mellitus, cirrhosis, arteriosclerosis, malignancy or advanced age (10, 13, 32, 78). Further, those adults residing in a nursing home facility are 4 times more likely to have GBS disease when compared to age-matched individuals living in the community (79).

Only a few studies have been conducted on healthy, non-pregnant GBS carriers to identify risk factors associated with colonization. Ever engaging in sexual activity appears to be a common behavior associated with GBS colonization (25, 29, 31), as well as age less than 20 years, presence of an intrauterine device, time since last menses (25), tampon use, milk consumption, infrequent handwashing (29), use of yeast medication, and African American ethnicity (31). Sexual behaviors associated with colonization include: increased frequency of sexual intercourse, fewer days since last sex, acquiring a new sex partner, and having multiple sex partners (31). In a recent study conducted on heterosexual college couples, male-to-female oral sex, having four or more lifetime sex partners, and first sex at age 20 years or older were associated with co-colonization, or carriage of the genetically identical GBS strain among sex partners (30). Among pregnant women, diabetes mellitus (56, 80), age younger than 20 years (81, 82), and having fewer than three pregnancies (57, 81, 82) are associated with higher colonization rates. Others include: multiple sex partners, increased frequency of sexual activity, concurrent colonization with *Candida* sp., older age with lower parity, less education, and cohabitation with sex partners (57).

4. PREVENTION EFFORTS

In order to decrease the morbidity and mortality associated with GBS disease in newborns, the Centers for Disease Control and Prevention (CDC) and other organizations developed guidelines to provide women at risk of delivering a GBS-diseased infant with intrapartum prophylaxis (9, 16, 83, 84). As a result, at least 24% of women receive antibiotics during labor and delivery (9). Penicillin or ampicillin are the primary agents used to treat GBS infections. Clindamycin and erythromycin were recommended for use among penicillin-allergic women (16) until recently; resistance to both agents is increasing (85-90). Since the development of the GBS prevention program, the incidence of GBS neonatal sepsis has decreased significantly (11, 91), but the incidence of sepsis caused by *Escherichia coli* among very-low-birth-weight infants has increased by four percent. In addition, the majority of these *E. coli* were resistant to ampicillin (91).

Because antibiotic resistance is a major public health concern, alternative prevention protocols must be evaluated and implemented. For GBS, a good alternative to intrapartum prophylaxis is a vaccine, (92, 93) which should significantly reduce the number of women receiving antibiotics. This vaccine is under development, but is not available for use yet. In the interim, the threat of GBS acquiring resistance to penicillin is real and, therefore, it is imperative to gain a better understanding of the pathogenesis of GBS infections and identify host and bacterial characteristics important for disease progression.

5. OVERVIEW OF MOLECULAR METHODS

In the past, molecular epidemiologic approaches have been less critical for GBS when compared to other organisms since the source of adult and neonatal infection was generally known (32). Although this is true, recent studies conducted on GBS demonstrate that more molecular epidemiologic information will be useful to better understand the natural history of GBS and design alternative prevention strategies. For instance, comparing strains that cause disease with those that do not is important to identify other bacterial factors that may be important in disease pathogenesis. Also, examining strains that are shared among sex partners may reveal information regarding the transmission mode of GBS among nonpregnant adults.

Traditionally, phenotypic molecular techniques, such as serotyping, have been used to study GBS. Differentiating GBS strains by serotype enabled the earliest molecular epidemiologic studies to be conducted. More recently, genotypic techniques, such as pulsed-field gel electrophoresis and nucleotide sequence analyses, have been utilized to better characterize the GBS strains in circulation, and to gain a better understanding of disease pathogenesis, strain-to-strain variation, and possible transmission modes.

6. PHENOTYPIC CHARACTERISTICS

For GBS, serotyping is the most commonly used phenotypic assessment. Other systems that examine the bacterial proteins produced by GBS, such as the polysaccharide capsule, and evaluate their effect on the host, such as the immunologic response, also have been utilized. These phenotypic methods have contributed to our understanding of GBS infections, but they are limited since they do not reveal information regarding genetic identity, and they are often unable to differentiate between a large number of strains (94). Because of this, many investigators now use genotypic techniques alone or in conjunction with certain phenotypic techniques.

6.1. Serotype

The discovery of a group B-specific "C" substance and type-specific "S" substance led to the identification of four serotypes (Ia, Ib, II and III) (20, 95-101). Differences in the polysaccharide capsule are the basis for serotyping and since 1979, five more serotypes (IV-VIII) have been identified (102-108). To date, it has proven to be an extremely useful tool to study the epidemiology of GBS infections.

In the 1970's and 1980's GBS serotypes I, II and III predominated among asymptomatic newborns, newborns with early-onset disease, children, and adults (109-115). This serotype distribution has changed over time (19, 103, 116, 117). Serotype III still causes most cases of neonatal meningitis (20), yet serotype V has emerged to cause approximately 55% of all cases in the United States (14) with 10% to 15% targeting neonates (117-119). Serotypes VI-VIII are not frequently found in the United States and rarely contribute to disease (20) though the prevalence of serotype VIII is high in Japan (120, 121).

A similar distribution of serotypes has been observed among healthy, asymptomatic individuals: types Ia, III and V predominate in the United States (19). In a study of a random sample of male and female college students in Michigan conducted in 1998, serotype V (29%) and serotype III (20%) predominated (29).

In addition to determining which serotypes are responsible for disease, several researchers compared serotypes, as well as biochemical and biologic characteristics of GBS strains causing perinatal disease with strains causing bovine mastitis to determine if zoonotic transmission occurs (20, 122-126). In general, the virulence factors associated with bovine mastitis differ from those associated with human GBS strains (127) and there is no additional evidence supporting GBS transmission from cows to humans (20).

Serotyping does, however, have limitations in that it groups isolates into a few large categories and, when used alone, it may not be sensitive enough to detect important differences among epidemiologically unrelated strains (128). In fact, GBS serotypes are not homogenous groupings (14, 129-132) as considerable genetic variation

within each type has been found when assessed by various techniques, (118, 129, 131-134) with the exception of serotype V (14, 135, 136).

Another limitation associated with serotyping is that it requires specific reagents that may not be readily available and are too expensive for routine use in many research and clinical laboratories (137, 138). As discussed by Chaffin *et al.*, developing a PCR-based serotyping system using specific primers that distinguish among the capsular types may alleviate this problem (139). Despite these limitations, serotyping is informative to use in conjunction with other molecular methods as it creates a means to compare strain distributions among distinct populations.

6.2. Antibiotic susceptibility profiles

Antibiograms have been used to characterize epidemiologically related GBS strains in several earlier studies. For example, Band *et al.* used antibiotic susceptibility testing in conjunction with bacteriophage typing to determine that GBS strains isolated from three infants were related and acquired nosocomially (36). Antibiograms, however, are not useful for most epidemiologic studies since the expression of resistance can vary in one strain at different points in time. Because plasmids and mobile genetic elements often carry resistance genes, acquisition or loss of these elements can rapidly change the phenotype of any strain (140). Therefore, genetically different strains can have the same resistance patterns and visa versa. Furthermore, the development of resistance in many organisms is attributable to selective pressures, which usually varies depending on an individual's previous exposure to antibiotics; previous history of antibiotic use is the primary factor influencing resistance in many organisms (141). Because of this, some epidemiologically related strains might have different antibiograms.

6.3. Expressed virulence factors

Evaluating the expression of specific virulence factors *in vitro* or in animal models has been performed by many GBS investigators and has contributed greatly to our understanding of disease pathogenesis. The main problem with these studies, however, is that some virulence factors are only expressed in the host and not in the laboratory, thus the expression levels measured may not accurately reflect *in vivo* levels. This variable expression often decreases the reproducibility of the results (142).

6.3.1. Polysaccharide capsule

Similar to *S. pneumoniae*, the polysaccharide capsule, which is the basis for serotyping, is the major known virulence factor among GBS (41, 143, 144). Serotype III strains with increased capsule production are more resistant to opsonophagocytic killing (72, 73) by interfering with host complement factor C3b (72), and are more virulent (145). Therefore, a multivalent GBS vaccine targeting the more virulent GBS serotypes in circulation is under development (93). In general, many technical challenges must be overcome in order to make an effective capsule-containing vaccine, such as the inclusion of

multiple capsular types, the identification and validation of a protein conjugate that enhances the immunogenicity, and the assessment of any cross-reactivity with human tissues (146). Those investigators working on the multivalent GBS vaccine, however, have made significant progress (93).

6.3.2. Alpha and beta C proteins

The cell surface antigens, particularly the C protein components, have been studied extensively. The C protein is common among many GBS strains and can contain a trypsin-sensitive (beta antigen) or trypsin-resistant (alpha antigen) component (147, 148). Both are independently expressed on the bacterial cell surface (149, 150). The C proteins are analogous to the variety of M-protein types found in group A streptococci (151), which are thought to play a role in virulence and immunity (127). Furthermore, organisms with C proteins have enhanced *in vitro* resistance to opsonophagocytosis (152, 153) and killing (154).

The alpha antigen is present in 50% (150) to 90% (73) of human GBS strains, yet there is considerable variation in the quantity of the alpha antigen produced by each strain (73), which may be related to virulence. In contrast, the beta antigen has been identified in only about 8% (19) to 42% (73) of human GBS strains. Several studies have demonstrated that the beta antigen acts as a receptor that binds human IgA via the Fc portion (155-160), thereby suggesting that it may inactivate the host immune response. This is functionally analogous to the Arp protein receptor found among group A streptococci (159), yet these two receptors show no homology at the protein level.

Several studies have demonstrated that antibodies directed against both the alpha and beta antigens offer protection from infection (73, 101, 148, 149, 161-165). Therefore, both may be useful vaccine candidates (164-166). In fact, it was estimated that a vaccine containing an alpha antigen and serotype III component would protect against at least 90% of GBS infections (167).

6.3.3. Other cell surface proteins

Some GBS strains also contain X and R antigens, which are immunologically cross-reactive cell surface proteins (4, 124, 168). Of the streptococcal R-proteins, R4 appears to be the most prevalent (169). Another surface protein designated Rib, confers protective immunity in mice (165, 170) and offers cross-protection in group A *Streptococcus* (171). It is also found in most serotype III strains (170), which are commonly associated with disease (20).

Two alpha-like proteins (172, 173) and a Rib-like protein (174) have been described, which suggests the existence of a family of GBS cell surface antigens (127, 172). Additionally, a cell surface protein designated Fbs (174) and a R-like protein named BPS (175) were identified as well as a glutamine synthetase (176), α -enolase (177), Hsp70 (178), and surface immunogenic protein (Sip) (179).

Unfortunately, the roles most of these proteins play in the disease process are unclear. For instance, two research teams observed no differential expression of alpha and beta proteins between pathogenic and colonizing GBS strains (180, 181). As with all assays that measure protein expression, however, it is possible that *in vitro* expression is altered and thus, the expression levels detected may not reflect the true levels *in vivo*. Furthermore, some researchers have reported that the GBS capsule may undergo phase variation (182-184) that may allow the organism to shift from a colonizing state to a disease-causing state (182). Because of the difficulties associated with expression assays, many investigators are now turning to genotypic assays that screen for the presence of genes that encode these proteins. This approach, however, also has limitations that will be discussed further.

6.4. Allelic variation at enzyme loci

It has been suggested that virulence determinants among many pathogenic species are not randomly distributed among different phylogenetic lineages (185). Therefore, several investigators have used multilocus enzyme electrophoresis (MLEE), which analyzes variations in protein mobility via starch gel electrophoresis to type GBS strains. The protein variations are due to charge differences that reflect amino acid substitutions in the chromosomal genes encoding them (138).

Musser *et al* demonstrated that serotype III GBS strains recovered from 18 states separated into two distantly related phylogenetic lines that differed in their ability to invade. They also identified a single serotype III clone that was associated with most invasive disease cases. Further characterization of isolates closely related to this highly virulent clone demonstrated that when compared to the less virulent strains they produced more extracellular hyaluronidase, an extracellular protein that cleaves hyaluronic acid present in the extracellular matrix of many tissues (133, 186). Other investigators, with the exception of Hauge *et al* (187), also have identified distinct groups of serotype III strains with enhanced virulence using this method (188-190).

These findings are important because they suggest that those GBS strains that cause disease may be unique and that identifying strains based on specific MLEE profiles might be an appropriate way to track virulence. Despite this, the few enzyme loci analyzed only represent a limited segment of the GBS genome, and thus, epidemiologically related and unrelated strains could have similar profiles. Additionally, MLEE is technically demanding and expensive and therefore, is difficult to perform outside of research and reference laboratories (191). In general, it should only be used to type GBS in conjunction with another molecular technique. Using MLEE alone, however, may be an appropriate tool to study phylogeny, or to define a group of strains that need further characterization.

7. GENOTYPIC CHARACTERISTICS

Genotypic techniques examine DNA differences between microorganisms of the same family, and are

considered superior to phenotypic techniques in that they can more accurately identify epidemiologically related strains (128, 192). Further, phenotypic techniques often lack the typeability, reproducibility, and discriminatory power that genotypic methods have (138). For example, because many GBS strains within a serotype can be genetically similar (118, 131, 133, 189, 190) and most disease-causing microorganisms are relatively homogeneous when compared to other lineages (193), genotypic techniques are extremely helpful to identify subtle genetic differences between strains.

7.1. Plasmids

Decades ago, researchers recognized that the study of GBS was limited by the lack of a discriminatory molecular typing system. Plasmid analysis was the earliest molecular epidemiologic tool used to study genotypic characteristics of GBS to describe the relatedness between R plasmids isolated from groups B and D streptococci (194). Plasmids, however, are found infrequently among GBS (129), thereby limiting their usefulness as a typing system.

7.2. Bacteriophage

Bacteriophage typing was utilized in the early 1980's with serotyping data to study epidemiologically related GBS strains. The primary purpose was to determine whether several neonatal infections were acquired nosocomially or via the mother (37, 195), and to identify the source of infection in various nurseries (36, 196-198). Because bacteriophage typing requires the availability of specific reagents (130, 138), is labor-intensive (138), and has low discriminatory power when used alone (195), it is rarely used to study GBS.

7.3. Nucleotide sequences

Although sequencing the entire genome of various GBS disease-causing strains would be helpful for identifying important virulence gene combinations, this task has not been completed to date. In the interim, several investigators have focused their work on identifying and assessing the function of specific bacterial genes that may be important in disease pathogenesis. Describing the distribution of genes or gene sequences encoding putative virulence factors among a wide variety of disease-causing and colonizing isolates is critical to fully evaluate the role they play, and to assess their potential as vaccine candidates.

There are, however, limitations associated with screening strains for the presence or absence of nucleotide sequences. Primarily, strains containing the genes of interest may not be expressing the proteins and therefore, can be falsely classified. However, if the overall goal is to determine whether invasive strains are more likely to carry a specific gene when compared to colonizing strains, then screening for specific nucleotide sequences may be an easy first step. Genes found in fewer than 10% of invasive strains, for example, are likely not to be important in invasive disease, while those found in 60% of invasive strains may be important. Further studies, such as protein expression analyses, could then be conducted to better characterize each factor.

7.3.1. Putative virulence genes

Virulence factors other than capsule have been described and many are found in virtually all GBS isolates (e.g., hemolysin, CAMP, proteases, and LTA) (68, 117, 144, 199, 200). Although these most likely contribute to disease pathogenesis, they are generally expressed by both strains that cause disease and those that asymptomatically colonize the host. Consequently, the focus of this section will be on those factors with varying distributions in different human populations, at both the protein and gene level.

Because several studies have identified more virulent subgroups of GBS strains using different molecular typing methods (133, 189, 190), many investigators are concentrating on the identification of virulence factors that contribute to GBS pathogenicity. Currently, several putative virulence genes have been identified, cloned and sequenced. Three of these encode for the cell surface proteins alpha and beta antigen and Rib discussed earlier.

The gene encoding the alpha antigen, *bca*, was sequenced by Michel *et al* (162, 201), and is homologous to the antiphagocytic M-proteins of group A streptococci (201). The *bca* gene contains nine identical tandem repeats (201); the antigenicity (163, 202, 203) and pathogenicity (204) of strains containing the alpha antigen is dependant on the number of repeats expressed (73, 202). Furthermore, *bca* mutants have reduced virulence in neonatal mice (127).

The beta antigen is encoded by the *bac* gene (158, 159), which is present in 19% of strains from asymptomatically colonized newborns (205) to 46% of GBS strains from adult and newborn cases (206). Rib, encoded by the *rib* gene, also contains numerous repeats. It has 47% identity at the amino acid level to the alpha antigen repeat region, but has no immunologic cross-reactivity (207). Additionally, it is expressed in most serotype III strains (170), which are more commonly associated with invasive neonatal infections (20).

Although these reports strongly support a role for these antigens in disease pathogenesis, the gene distributions are confusing. For instance, no difference in the frequency of *bca* was identified between newborns with sepsis, and asymptomatic newborns and pregnant women from Germany (205). There is a possibility, however, that the proteins are differentially expressed as described previously (208).

Other putative virulence genes identified by a variety of methods encode a surface immunogenic protein (*sip*) (179), a placental laminin binding protein (*lmb*) (70), an R-like protein antigen (*alp4*) (209), a glutamine synthetase (*glnA*) (176), a protein important for cell division and antibiotic tolerance (*pcsB*) (210), a superoxide dismutase (*sodA*) (211), a glutamine transport gene (*glnQ*) (212), an adhesin and C5a protease (*cpB*) (71), a two-component signal transduction system (*rgfBDAC*) (213), and numerous outer surface proteins with homology to *Streptococcus pneumoniae* (214). Most of these have been

discovered only recently and, thus, have not been studied enough to fully evaluate their role in disease pathogenesis.

7.3.2. Mobile genetic elements

Several interesting insertion elements that may be important for GBS disease have been identified and sequenced. Hyaluronidase, demonstrated to be an important virulence factor in various studies (133, 215), is thought to play a role in bacterial dissemination (216). Granlund *et al* identified an insertion element (*IS1548*) present in 9 of 13 isolates originating from the blood of endocarditis patients and in only 3 of 22 asymptomatically colonized women. The insertion was located within the hyaluronidase gene (*hyB*) in most cases and therefore, prevented expression. The authors speculate that *IS1548* may be associated with GBS strains that specifically cause endocarditis but not neonatal infections (186).

The insertion element *ISSa4*, which belongs to the *IS982* family, also was present in GBS, yet only in those strains isolated after 1996 suggesting it was recently acquired (217). The role of *ISSa4* in GBS disease has not been elucidated. Another insertion sequence *IS1381*, previously found in multiple copies in *Streptococcus pneumoniae* strains (218), also was identified in GBS. Screening for the presence of *IS1381* proved to be a useful subtyping tool to identify epidemiologically linked GBS isolates (219).

7.4. DNA fingerprinting

7.4.1. Restriction endonuclease analyses

Several techniques involving restriction endonucleases, enzymes that cleave DNA at specific nucleotide sequences, have been used for DNA fingerprinting to type GBS. Restriction endonuclease analysis (REA) of chromosomal DNA digested with restriction enzymes and resolved by linear gel electrophoresis has answered several important epidemiologic questions (129, 132, 134, 220). First, Denning *et al* used REA to determine that two GBS-associated relapses in an infant were due to the originally infecting GBS strain (221) suggesting that reinfection does occur. In another study by Denning *et al* on 54 human and animal GBS strains conducted to assess the geographic distribution of specific strains, 28 REA patterns from six different serotype groups and one nontypable group were identified. All epidemiologically related isolates matched by REA analysis, and genetically identical strains were recovered from different geographic locations suggesting that specific clones were in circulation (129). Additionally, Ellis and colleagues found that GBS strains isolated from mother/baby pairs had similar restriction patterns, which provided additional evidence for vertical transmission (134).

REA also has been used to study the population structure of GBS. Takahashi *et al* subclassified serotype III strains from Tokyo and Utah into three distinct phylogenetic lineages using REA with two different enzymes (*HindIII* and *Sse8387I*). One lineage was composed of 91% of the invasive neonatal GBS isolates tested, which suggests that strains in this lineage may be

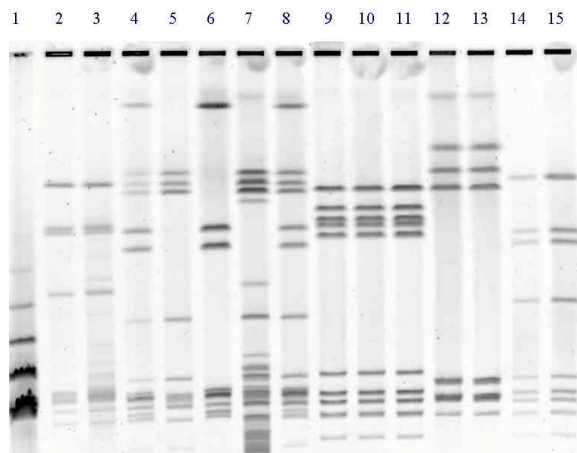


Figure 1. Pulsed-field gel electrophoresis (PFGE) of group B *Streptococcus* (GBS) strains isolated from college women with urinary tract infections and their most recent sex partner. Lane 1 is a DNA ladder. Lanes 2-3 and 14-15 represent rectal and vaginal GBS isolates from two different women. Lanes 4-6 are two urine isolates and one rectal isolate from one woman and lanes 7 and 8 are the urine and rectal isolate from her sex partner, respectively. Lanes 9-11 represent a female vaginal isolate and her sex partner's urine and rectal isolate.

more virulent (220). Further characterization of these strains using genomic subtractive hybridization revealed nine unique DNA sequences that were not found in other serotypes or type III lineages (222). Six of these nine sequences mapped to a fragment that contained or was located near known GBS virulence genes (223).

Although REA has enabled researchers to differentiate epidemiologically related strains and to identify a subset of more virulent strains, the complex banding patterns that result are often difficult to interpret. In order to avoid the problems associated with interpreting REA results, DNA or rRNA hybridization procedures have been used. This technique highlights specific fragments that vary in length between strains (restriction fragment length polymorphisms (RFLPs)). For GBS, this method was first used by Bingen and colleagues on total chromosomal DNA and ribosomal DNA (ribotyping) to determine whether GBS was transmitted to infants via maternal breast milk (130). When total GBS DNA was assessed, strains from mother-infant pairs produced 10 unique RFLP patterns, and those strains shared by the mother and infant within each pair were genetically identical. This is consistent with other findings among different mother-infant pairs and twin-twin strains (118). The ribotyping analysis was less discriminatory and yielded fewer patterns in this analysis (130) as well as another study (224); therefore, few investigators currently use it to characterize epidemiologically related GBS strains. Because ribosomal sequences are relatively stable within bacterial species, different strains can have identical ribotype patterns (138, 225, 226). Consequently, ribotyping is useful to study the phylogeny of GBS, but when used for typing, it should be performed in

conjunction with another typing method to enhance the discriminatory power (224, 227-229).

7.4.2. Pulsed-field gel electrophoresis

Digestion of chromosomal DNA with a rare-cutting enzyme and pulsed-field gel electrophoresis (PFGE) also will produce fewer DNA fragments, thereby making interpretations easier (Figure 1). PFGE, which is considered the method of choice for outbreak investigations (230), is extremely reproducible, has high discriminatory power (231), and thus, appears to be a good typing technique for GBS (20, 232) and most other bacteria (191).

Green *et al* first used PFGE to demonstrate that recurring GBS disease in infants could be attributed to either the original infecting strain or a newly acquired strain (233). Ellis and colleagues identified a single clone associated with neonatal infections within serotype III strains from two geographically distinct populations in Australia. They concluded that a highly virulent clone may be widely distributed and more likely to contribute to neonatal disease (134). This is consistent with previous reports using alternative typing methods (133, 188-190, 220, 234, 235). In other studies, PFGE was used to demonstrate that individuals can be colonized with more than one genetically distinct strain at different sites and time points (29), and to illustrate that sex partners frequently share genetically identical GBS strains (30).

In addition to being expensive and laborious, the primary limitation associated with PFGE is that it may be too sensitive in some instances since minor genetic events are often reflected by the gain or loss of a restriction site (236). However, this does not apply to GBS. For example, most serotype V strains have identical banding patterns [unpublished data], which suggests the dissemination of a single clone. Utilizing more sensitive techniques to study these strains may reveal subtle genetic differences that cannot be detected by PFGE. This approach, however, may not be epidemiologically useful.

7.4.3. Polymerase chain reaction (PCR)-based methods

Random amplified polymorphic DNA (RAPD) analysis, a PCR-based typing method, uses short arbitrary nucleotide sequences as primers to discriminate between strains (237, 238). Chatellier *et al* examined a GBS collection that was previously characterized by MLEE and found that both methods were in agreement with regard to the groupings obtained, yet this occurred only when all four PCR primers were used together. Interestingly, RAPD subdivided the strains further than MLEE, and therefore, they concluded that RAPD was more sensitive to type GBS for epidemiologic investigations, particularly when combined with serotyping (235). This was demonstrated previously by Limansky *et al* (239) and for other pathogens as well (240). RAPD has also been utilized to type GBS strains with resistance to erythromycin. Culebras *et al* determined that resistance was not attributable to the dissemination of a single clone since 35 RAPD patterns were observed from the 54 resistant GBS strains studied (241).

Although RAPD represents a quick, easy and inexpensive way to group GBS isolates, there are also limitations associated with its use. PCR products are easily contaminated and it is often challenging to identify suitable primers that yield consistent results. Also, the technique is susceptible to variations in PCR conditions, and thus, the results can be difficult to reproduce (138, 231).

8. SUMMARY

Because GBS contributes to substantial morbidity and mortality in many individuals, it is surprising that our knowledge of the GBS genome and the genetic factors that enhance pathogenicity is so limited. Further, epidemiologic research is still lacking in key areas, such as understanding the GBS transmission modes and the duration of colonization.

Recent advances in molecular analyses, particularly the genotypic techniques, have been applied to GBS and have revealed important information regarding the pathogenesis of disease. For example, several studies have demonstrated that strains causing certain types of invasive disease represent a unique, but relatively homogeneous group (133, 188-190, 220, 234, 235), which is consistent with findings from other human pathogens (193). Because of these studies and others that have utilized molecular epidemiologic approaches, we now have a more detailed understanding of the genetic differences between disease-causing and colonizing strains. When compared to other microorganisms including *Streptococcus pneumoniae* and group A *Streptococcus*, however, our knowledge is still relatively limited.

9. FUTURE WORK

Since GBS has acquired resistance to several of the commonly used antibiotics, such as erythromycin and clindamycin, (10, 86) and the emergence of penicillin resistance is a possibility, prevention protocols other than intrapartum chemoprophylaxis must be utilized to prevent neonatal disease. Further, the incidence of adult disease is increasing (10), and currently, there is no established prevention protocol for this population. Therefore, future work should focus on gaining a better understanding of the genetic profiles of the more virulent GBS strains in circulation nationwide. This could facilitate the development of a screening program. For instance, Chatellier and colleagues suggest that RAPD-PCR could be used to identify GBS isolated from individuals that yield specific RAPD banding patterns indicative of enhanced virulence (235). These patterns could represent a marker for high disease risk and could aid in the implementation of prevention strategies. In general, establishing convenient phenotypic or genotypic criteria for strains with enhanced virulence would help health care providers identify individuals with a high risk of infection.

More work should also concentrate on identifying and analyzing novel bacterial characteristics that may be important in GBS disease via cloning, sequencing, mutagenesis, subtractive hybridization techniques, or

microarray-based expression profiling analyses. Further epidemiologic studies should be conducted to assess whether those bacterial factors identified are more frequently found in disease-causing strains. If relevant, putative virulence factor components could be incorporated into the multivalent GBS vaccine that will be comprised of the most virulent polysaccharide capsular types (242). This would provide added protection in case the serotype distribution changes over the next few decades as was demonstrated previously (19, 103, 116, 117). If this vaccine was administered to pregnant women today, eradication of GBS disease, at least among neonates, pregnant women receiving the vaccine, and future elderly female populations could be realized given that the non-vaccine serotypes do not change in their ability to cause disease.

Because the GBS vaccine is currently not ready for clinical use, more knowledge on the natural history of GBS is critical. For instance, little is known about the GBS transmission dynamics in non-pregnant and pregnant adults. Preventing colonization, the initial step in disease pathogenesis, also could have an impact on the incidence of GBS disease in various populations, as well as gaining a better understanding of the complex interactions between the host and bacterium.

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