**Original Paper**

**Streptococcus anginosus (milleri) Group Strains Isolated in Poland (1996–2012) and their Antibiotic Resistance Patterns**

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Submitted 1 December 2015, accepted 21 December 2015

**Abstract**

*Streptococcus anginosus*, *Streptococcus intermedius* and *Streptococcus constellatus* form a group of related streptococcal species, namely the Streptococcus Anginosus Group (SAG). The group, previously called “milleri” had been rarely described until 1980/1990 as a source of infections. Nowadays SAG bacteria are often described as pathogens causing predominantly purulent infections. The number of infections is highly underestimated, as SAG strains are often classified in the microbiology laboratory as less virulent “viridans streptococci”. Epidemiological situation regarding SAG infections in Poland has been unrecognized, therefore we performed a retrospective analysis of strains isolated between 1996 and 2012. Strains suspected of belonging to SAG were re-identified using an automated biochemical approach (Vitek2) and MALDI-TOF MS. We performed first analysis of antibiotic resistance among SAG strains isolated in Poland using automated methods (Vitek2), disk diffusion tests and E-Tests. We also performed PCR detection of resistance determinants in antibiotic resistant strains. Clonal structure of analyzed strains was evaluated with PFGE and MLVF methods. All three species are difficult to distinguish using automated diagnostic methods and the same is true for automated MIC evaluation. Our analysis revealed SAG strains are rarely isolated in Poland, predominantly from purulent infections. All isolates are very diverse on the genomic level as estimated by PFGE and MLVF analyses. All analyzed strains are sensitive to penicillin, a substantial group of strains is resistant to macrolides and the majority of strains are resistant to tetracycline.

**Keywords:** *Streptococcus anginosus* group, *Streptococcus constellatus*, *Streptococcus intermedius*, *Streptococcus milleri*, antimicrobial resistance, MLVA, MLVF, PFGE

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**Introduction**

Streptococci are a diverse group of Gram positive bacteria divided into multiple clusters based on mixed and constantly changing criteria. Recent classification reflects genetic relationships between groups and separates them into six divisions: (i) pyogenic, (ii) anginosus (formerly milleri), (iii) mitis/oralis, (iv) salivarius, (v) mutans, (vi) bovis and species of unknown evolutionary position such as *Streptococcus suis*. The genus includes species belonging to physiological flora, human and animal pathogens and opportunistic pathogens (Kohler, 2007). In the past, classification of Streptococci was based mostly on phenotypic traits such as carbohydrate fermentation and later on 16S rDNA sequencing. Unfortunately, even with the use of 16S rDNA sequencing, some of the strains cannot be clearly classified to previously described streptococcal species (Olson et al., 2013; Thompson et al., 2013). There are some methods available to discriminate streptococcal strains to the species and sub-species level (Poyart et al., 1998; Picard et al., 2004; Glazunova et al., 2010; Zbinden et al., 2011; Obszanska et al., 2015a; Takao et al., 2004). However, sequencing methods are not often used in diagnostic laboratory as the routine species identification and not all microbiology diagnostic laboratories have PCR set up.

Streptococcal groups that include the most pathogenic species are predominantly pyogenic (*Streptococcus pyogenes*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae* subsps. *equisimilis* and *dysgalactiae*) and mitis (includes *Streptococcus pneumoniae*) divisions.
However, in recent years, an increasing number of streptococcal species is being considered as pathogenic to humans. Three of the species (Streptococcus anginosus, Streptococcus intermedius and Streptococcus constellatus, SAG – streptococcus anginosus group), described until 1980/1990 as rare sources of infections are currently described as pathogens causing predominantly purulent infections (Asam and Spellerberg, 2014).

The classification of S. anginosus, S. constellatus and S. intermedius is especially confusing as they are described in literature under multiple names. In 1991 Whiley and Bright proposed a revision of systematic relationships between SAG strains previously described mostly as Streptococcus milleri (Whiley and Bright, 1991). The proposed classification was recently confirmed by genome analysis using next generation sequencing (Olson et al., 2013) and tandem repeat analysis (Obszanska et al., 2015a).

Unfortunately, SAG are rarely considered as pathogens as they represent the natural flora of the upper respiratory, digestive and reproductive tracts, however, epidemiological data suggest the need to consider SAG an etiological factor of infections ranging from mild skin infections to severe purulent and life threatening infections (Giuliano et al., 2012; Whiley et al., 1992; Asam and Spellerberg, 2014). A correlation between S. intermedius and brain and liver abscesses and S. constellatus and infections of respiratory tract has been detected (Whiley et al., 1992). The majority of published material about SAG is closely related to case reports and suggests that the number of infections caused by SAG is underestimated (Reissmann et al., 2010). Case reports usually describe otherwise healthy patients without any previous medical history and describe the role of SAG in the formation of various kinds of abscesses, which are probably caused by high resistance to phagocytosis and inhibition of chemotaxis (Wanahita et al., 2002). Possible molecular mechanisms involved in that process may include production of hydrogen sulfide from L-cysteine by L-cysteine desulphhydrase (Takahashi et al., 1995). The other postulated possibility draws similarity from increased survival of bacteria upon phagocytosis (Wanahita et al., 2002; Hoe et al., 2002; Voyich et al., 2004).

On the contrary to other streptococcal pathogens, the pathogenicity mechanisms of SAG are often unknown or poorly described (Sitkiewicz and Hryniewicz, 2010; Szczyapa et al., 2012; Obszanska et al., 2014). Only recently genomic analyses of SAG genomes were published (Olson et al., 2013; Thompson et al., 2013). Experimental reports describing SAG virulence factors are scarce.

The epidemiological situation in Poland regarding infections with non β-hemolytic streptococci that are not Streptococcus pneumoniae has been not described so far. Therefore, we decided to investigate strains collected between 1996 and 2012 by reference centers (KORLD, KOROUN and Polmicro) in Poland and during nationwide viridans streptococci surveillance causing invasive infections (2008–2009).

**Experimental**

**Materials and Methods**

**Bacterial strains.** Bacterial strains were collected between 1996 and 2012 by KORLD, KOROUN and Polmicro reference centers during their routine performance and the data about infected patients was stripped from all identifiers, except age, sex and the source of isolation (i.e. blood, wound, pus etc.). Ethics approval was not required. The collected strains were analyzed retrospectively.

Collected strains were stored at –80°C and prior to all microbiological tests or DNA isolation were plated on Columbia agar plates (Becton Dickinson) with 5% sheep blood and incubated 24–48 h at 37°C, 5% CO₂. Prolonged incubation was required because of the slow growth of these bacteria.

**Strains re-identification.** To confirm species identification all strains sent to our reference centers were re-identified using Vitek2 (bioMerieux) automated system with GP card. For the identification we used higher initial inoculum (0.5 McFarland) than recommended by the manufacturer. All strains were also identified using IDStrep (bioMerieux) that allows to grow bacteria under optimal O₂/CO₂ conditions for time long enough to read the strip and MALDI-TOF MS (Brücker and bioMerieux) according to manufacturer’s instructions. All strains were also tested for Lancefield antigen using Strep Plus test (Oxoid).

**Antibiotic resistance.** Screen for antibiotic resistance was performed using ST101 card (bioMerieux) dedicated to streptococci on Vitek2 system. The card allows detection of ampicillin, benzylpenicillin, cefotaxime, ceftriaxone, clindamycin, erythromycin, levofloxacin, linezolid, tetracycline, trimethoprim/sulfamethoxazole and vancomycin resistance. In some cases only subset of assays from the ST101 card was assayed by the instrument, so to confirm MIC values, for erythromycin, clindamycin, tetracycline, penicillin and linezolid we used E-test (bioMerieux) or M.I.C. Evaluator (Oxoid) or microdilution reference method and applied interpreted according to EUCAST (EUCAST, 2014). For strains with detected resistance to erythromycin, we performed double disc synergy test with erythromycin (15 µg) and clindamycin (2 µg) according to EUCAST (EUCAST, 2014).

**Antibiotic resistance determinants.** Chromosomal DNA was isolated as described by Obszanska and co-workers (Obszanska et al., 2015a). Starters and reaction conditions used to detect antibiotic resistance determinants are presented in Table I.
**Results and Discussion**

During 16 years of surveillance by reference centers in Poland, we collected only 78 isolates (about 5 isolates a year) confirmed as SAG. Nationwide invasive viridans streptococci strain collection did not significantly increase the number of SAG strains sent to reference centers compared with previous years. It can demonstrate either low level of infections caused by SAG, or poor recognition of SAG as pathogens. It is more likely poor recognition of SAG by health personnel and/or authorities as surveillance reports published worldwide describe much higher incidence reaching 8.65/100,000 population for SAG invasive disease (Laupland et al., 2006; Siegman-Igra et al., 2012; Arinto-Garcia et al., 2015). One of the reports describes a higher incidence of invasive SAG infections than those caused by groups A or B streptococci (Laupland et al., 2006).

Unfortunately, in Poland recognition of etiological microbiological factors is rather poor. Epidemiological reports regarding streptococcal infections are usually

**Restriction Fragment Length Polymorphism – Pulsed Field Gel Electrophoresis.** RFLP-PFGE analysis and results interpretation were performed as described previously (Obszanska et al., 2015b).

**Multi Locus Variable Tandem Repeat Fingerprinting.** MLVF analysis and results interpretation were performed as described previously (Obszanska et al., 2015a).

<table>
<thead>
<tr>
<th>Gene</th>
<th>Starter name</th>
<th>Sequence (5’-3’)</th>
<th>Reaction</th>
<th>Expected product size</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ermA</code></td>
<td><code>ermA_F_IS3</code></td>
<td>TGGGTCAGGaaaaAAGGACATTTTACCAAGG</td>
<td>35 cycles, annealing 67°C, 25 sec.</td>
<td>551 bp</td>
<td>This work</td>
</tr>
<tr>
<td><code>ermB</code></td>
<td><code>ermB_F_IS3</code></td>
<td>CGACGAAAATCTGGCTAAAATAAGTAAACAGG</td>
<td>30 cycles, annealing 67°C, 25 sec.</td>
<td>600 bp</td>
<td>This work</td>
</tr>
<tr>
<td><code>ermB</code></td>
<td><code>ermB_R_IS2</code></td>
<td>ATTTGAAACAGGTAAACAGG</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><code>mefA</code></td>
<td><code>mef_F_IS</code></td>
<td>CTATTGGGTGCTGTGAT</td>
<td>30 cycles, annealing 65°C, 25 sec.</td>
<td>566 bp</td>
<td>This work</td>
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<tr>
<td><code>tetO</code></td>
<td><code>tetO_F_IS</code></td>
<td>CTATCCCATAGAAGTCTCCGGTGTCATATGGCAACCT</td>
<td>35 cycles, annealing 57°C, 25 sec.</td>
<td>616 bp</td>
<td>This work</td>
</tr>
<tr>
<td><code>tetO</code></td>
<td><code>tetO_R_IS</code></td>
<td>TTATCCCATAGAAGTCTCCGGTGTCATATGGCAACCT</td>
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<td></td>
<td></td>
</tr>
<tr>
<td><code>tetO</code></td>
<td><code>tetO_40_up</code></td>
<td>TCAUGGTCCTGTTCCGATTGTC</td>
<td>35 cycles, annealing 67°C, 25 sec.</td>
<td></td>
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</tr>
<tr>
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<td><code>tetO_40_dn</code></td>
<td>TCAUGGTCCTGTTCCGATTGTC</td>
<td></td>
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<tr>
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<td>ASTTGGGTGCTGTGAT</td>
<td>35 cycles, annealing 67°C, 25 sec.</td>
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<tr>
<td><code>tetM</code></td>
<td><code>tetM_40_dn</code></td>
<td>AGTATTGGGTGCTGTGAT</td>
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<tr>
<td><code>tetM</code></td>
<td><code>tetM_40_up</code></td>
<td>AGTATTGGGTGCTGTGAT</td>
<td>35 cycles, annealing 57°C, 25 sec.</td>
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</tbody>
</table>
based on the physician’s reports and strain collection is not mandatory, reports are then collected by epidemiological authorities and sent to the National Institute of Public Health (NIZP-PZH) and published as bi-weekly reports (NIZP-PZH, 2015). In case of streptococcal infections only S. pyogenes infections such as scarlet fever (Lp. 46 in the cited report (NIZP-PZH, 2015)) erysipelas (considered invasive disease, Lp. 55), STSS (Lp. 56), puerperal fever (Lp. 57) and undefined invasive infections (Lp. 58) are reported. Using this data, incidence of invasive S. pyogenes is estimated to be 0.03/100,000 population for STSS or 0.2/100,000 population for undefined S. pyogenes invasive infections, what can be an example of dramatically underestimated streptococcal infections. We receive streptococcal strains in reference centers usually in cases when diagnostic laboratories have problems with identification or there are problems with treatment.

Usually identification of non β-hemolytic streptococci such as anginosus group is quite a challenge; strains are often misidentified by automated systems because of their slow growth under oxygen conditions. On the other hand manual, and semi-automated system such as ID strips (bioMérieux) often identify species only to anginosus group. To verify systematic classification into species, all strains sent to reference centers as anginosus group, or either Lancefield group F or non β-hemolytic Lancefield C and G, were initially re-identified using Vitek2 automated system with GP card (bioMérieux). The results given by IDStrep and MALDI-TOF MS were usually consistent while results from Vitek2 system often misidentified strains as closely related Streptococcus gordonii or called 50%/50% identification either as S. anginosus/S. constellatus or S. anginosus/S. intermedius. The problems with identification of streptococci using MALDI-TOF MS have been also reported by other groups (Woods et al., 2014; Chen et al., 2015). So, even with advanced techniques used for strain identification, we experienced multiple problems with proper species identification. In laboratories that routinely perform identification using PCR methods, detection and differentiation of SAG can be performed using molecular methods (Takao et al., 2004). From the clinical point of view, identification to anginosus group is enough to consider an isolate as an etiological factor of infection, however, identification as S. gordonii, which is a natural oral flora, may lead to misdiagnosis and not considering the strain as source of the infection.

Of all strains collected during that time, 48 isolates were consistently identified as S. anginosus, 27 as S. constellatus and only one as S. intermedius. One isolate could not be identified to the species level using neither IDStrep, VITEK2 nor MALDI-TOF MS system, another isolate was identified as S. anginosus/constellatus. The most common Lancefield antigen detected among SAG isolates was C, followed by F and G. In case of 20 isolates, we did not detect any of the A, B, C, G and F Lancefield antigens, what is consistent with group classification (Kohler, 2007). Two isolates of S. constellatus carried antigen A.

Strains from the analyzed collection were isolated from patients of all age groups, from young children to elderly over 65 years. Of all strains with provided information about isolation source, thirteen strains were isolated from invasive infections (blood and cerebrospinal fluid), 23 from pharyngitis and lower respiratory tract infections and 33 from purulent soft tissue infections, including swabs taken during surgeries. Large number of soft tissue isolates is consistent with large number of described purulent infections caused by SAG bacteria (Asam and Spellerberg, 2014). Mean age of patients with blood/CNS infections vs soft tissue vs respiratory tract isolates was different (54 vs 44 vs 35 years of age, respectively), however, only the difference between age of patients with invasive and respiratory tract infections was statistically significant (p = 0.03).

Initial screening for resistance to antibiotics usually used against streptococcal infections was performed using automated Vitek2 system. Unfortunately, similarly to experiences with strain identification, automated minimal inhibitory concentration (MIC) evaluation failed for ~10% of strains and was performed manually for erythromycin, clindamycin, tetracycline, penicillin and linezolid using E-test (bioMérieux), M.I.C. Evaluator (Oxoid) or reference microdilution method and interpreted according to EUCAST criteria (EUCAST, 2014). In some cases only a subset of assays from the ST101 card was assayed by the instrument.

We did not detect any ampicillin/benzylpenicillin, cefotaxime, ceftriaxone, levofloxacin, linezolid, and vancomycin, resistance and MIC values for the population were still above the “sensitive” range (Fig. 1 and Table II). Unfortunately, clear interpretation criteria for anginosus streptococci cannot be easily applied. In case of some antibiotics such as benzylpenicillin, according to EUCAST (EUCAST, 2014), different breakpoints should be applied for β-hemolytic streptococci (such as S. pyogenes), different to S. pneumoniae and different to a large group of species named viridans streptococci (Fig. 1 and Table II). Based on the slowly increasing knowledge about anginosus streptococci, it is not clear which group of breakpoints should be applied for the analysis.

Among the analyzed strains, several of them were resistant to erythromycin and/or clindamycin, however MIC50 and MIC90 values for the population were still within “sensitive” range. In case of detected erythromycin resistance, double disc diffusion test was performed to determine inducible or constitutive mechanism of the resistance. Among 5 strains with detected erta gene, 3 strains exhibited inducible clindamycin resistance.
Contrary to detected sensitivity to the majority of tested antibiotics, over 50% of strains were resistant to tetracycline, with MIC<sub>50</sub> and MIC<sub>90</sub> values within "resistant" range according to Eucast (Fig. 1).

To identify genes responsible for the resistance phenotypes, we performed PCR detection of resistance determinants using chromosomal DNA isolated from all analyzed strains with starters that allow detection of genes responsible for tetracycline resistance.

### Table II

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>MIC&lt;sub&gt;50&lt;/sub&gt;</th>
<th>MIC&lt;sub&gt;90&lt;/sub&gt;</th>
<th>Breakpoints for sensitive S ≤</th>
<th>Breakpoints for resistant R &gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ampicillin</td>
<td>&lt;0.25</td>
<td>&lt;0.25</td>
<td>ND / 0.5/0.5</td>
<td>ND / 2/2</td>
</tr>
<tr>
<td>Benzylpenicillin</td>
<td>&lt;0.06</td>
<td>&lt;0.06</td>
<td>0.25/0.06/0.25</td>
<td>0.25/2/2</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>&lt;0.12</td>
<td>0.25</td>
<td>ND / 0.5/0.5</td>
<td>ND / 2/0.5</td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>0.25</td>
<td>0.25</td>
<td>0.5/0.5/0.5</td>
<td>0.5/0.5/0.5</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>&lt;0.25</td>
<td>0.25</td>
<td>0.25/0.25/–</td>
<td>0.5/0.5/–</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>&lt;0.12</td>
<td>0.25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>0.5</td>
<td>1</td>
<td>1/2–</td>
<td>2/2–</td>
</tr>
<tr>
<td>Linezolid</td>
<td>&lt;2</td>
<td>&lt;2</td>
<td>2/2–</td>
<td>4/4–</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>&gt;16</td>
<td></td>
<td>1/1–</td>
<td>2/2–</td>
</tr>
<tr>
<td>Trimethoprim/sulfamethoxazole</td>
<td>&lt;10 (0.5/9.5)</td>
<td>40 (2/38)</td>
<td>1/1–</td>
<td>2/2–</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>0.5</td>
<td>0.75</td>
<td>2/2–</td>
<td>2/2–</td>
</tr>
</tbody>
</table>

MIC values for sensitive (S) or resistant (R) classes are given for β-hemolytic streptococci / S. pneumoniae / viridans streptococci, respectively, according to EUCAST. *–* insufficient data supporting S vs R call or antibiotic not recommended for use, ND not determined and sensitivity for β-hemolytic streptococci inferred from sensitivity to benzylpenicillin. * EUCAST breakpoints for trimethoprim/sulfamethoxazole are expressed as trimethoprim concentration. trimethoprim/sulfamethoxazole tested with ST-101 card in the ratio 1:19.
Fig. 2. RFLP-PFGE analysis of SAG strains resistant to tetracycline or macrolide antibiotics. Analysis was performed as described in (Obszanska et al., 2015b), and DNA in plugs was digested with EagI. The similarity coefficient was calculated using Dice algorithm (optimization and tolerance parameters set to 1%), followed by clustering analysis using UPGMA method (BioNumerics). Numbers on the dendrogram show percent of similarity between branches.
S. anginosus group strains isolated in Poland

Fig. 3. MLVF analysis of SAG collection.

A. Unclustered patterns obtained using MLVF typing (Obszanska et al., 2015a), patterns in red represent strains resistant to tetracycline, erythromycin and clindamycin, patterns in green represent strains sensitive to all tested antibiotics.

B. Minimum spanning tree generated using MLVF patterns, similarity coefficient was calculated based on the number of different bands with optimization and tolerance set to 0.3%. Red circles represent strains resistant to tetracycline, erythromycin and clindamycin, green circles represent strains sensitive to all tested antibiotics.
strains isolated in Poland are diverse on the genetic level. Strains (Fig. 3) and MLVF analysis confirms that all SAG clustering of MLVF patterns for resistant or sensitive different sources. We did not observe any significant strains 4737/08 and 4734/08 with identical PFGE pat and 2218/00, confirming the common source. However, “resistant” group shows any unique traits in compari

ysis was performed for strains that belonged to both

number of tandem repeats (MLVF) (Fig. 3). The anal

To further investigate the relationships between strains, we performed multi locus analysis of variable number of tandem repeats (MLVF) (Fig. 3). The analysis was performed for strains that belonged to both “sensitive” and “resistant” groups to see whether the “resistant” group shows any unique traits in compari

son with the “sensitive” group. The analysis showed very similar patterns detected for 3 strains 2210/00, 2211/00 and 2218/00, confirming the common source. However, strains 4737/08 and 4734/08 with identical PFGE pat

tern, shown different MLVF profiles, consistent with two different sources. We did not observe any significant clustering of MLVF patterns for resistant or sensitive strains (Fig. 3) and MLVF analysis confirms that all SAG strains isolated in Poland are diverse on the genetic level.

Table III

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>Number of resistant strains</th>
<th>Number of strains</th>
<th>Resistance determinant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tetracycline</td>
<td>40/78 (51%)</td>
<td>30</td>
<td>tetM</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
<td>tetO</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
<td>tetW</td>
</tr>
<tr>
<td></td>
<td></td>
<td>8</td>
<td>Not found</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>7/78 (9%)</td>
<td>4</td>
<td>ermA</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
<td>ermB</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
<td>mefA</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
<td>mefA + ermA</td>
</tr>
</tbody>
</table>

erythromycin and tetracycline determinants in strepto-
cocci (Table III). For all strains resistant to erythromy-
cin, we were able to detect the gene responsible for the phenotype, however in case of tetracycline resistance we could not detect any resistance determinant in 8 strains with any of the starters listed above. This suggests the presence of a novel variant of the resistance gene/genes that cannot be amplified with the used starters.

To test whether resistant strains are similar to each other, we performed strain comparison on the genomic level using modified PFGE (Fig. 2). The analysis shows that the group of resistant strains is highly diverse, except for two small clusters that exhibit the same patterns. Strains 2210/00, 2211/00 and 2218/00 were sent to the reference center from the same hospital to confirm species identification. Unfortunately, we do not have any additional epidemiological records, nor access to them. The strains may be as well isolates from multiple patients or sequential isolates from the same person. Based on the PFGE pattern they can be consid-
ered almost identical. Two other strains (4737/08 and 4734/08) were sent to the reference center during the survey from the same hospital, but were isolated from two different patients and different infections (blood and lower respiratory tract, respectively).

To further investigate the relationships between strains, we performed multi locus analysis of variable number of tandem repeats (MLVF) (Fig. 3). The analysis was performed for strains that belonged to both “sensitive” and “resistant” groups to see whether the “resistant” group shows any unique traits in compari

son with the “sensitive” group. The analysis showed very similar patterns detected for 3 strains 2210/00, 2211/00 and 2218/00, confirming the common source. However, strains 4737/08 and 4734/08 with identical PFGE pat

tern, shown different MLVF profiles, consistent with two different sources. We did not observe any significant clustering of MLVF patterns for resistant or sensitive strains (Fig. 3) and MLVF analysis confirms that all SAG strains isolated in Poland are diverse on the genetic level.

Conclusions. Streptococci belonging to anginosus group are rarely isolated in Poland presumably because of poor recognition by epidemiological and health authorities, predominantly from purulent infections. All analyzed isolates are very diverse on the genomic level as estimated by PFGE and MLVF analyses. All analyzed strains are sensitive to penicillin, a substanc
group of strains is resistant to macrolides and the majority of strains are resistant to tetracycline.

Abbreviations

CNS – central nervous system; EUCAST – The European Committee on Antimicrobial Susceptibility Testing; KORLD – Krajowy Ośrodek Referencyjny d.s. Lekowrażliwości Drob

noustrojów (National Reference Center for Antimicrobial Resistance); KOROUN – Krajowy Ośrodek Referencyjny d.s. Zakazeni

osrodowowego Ukladu Nerwowego (National Reference Center for Central Nervous System Infections); MALDI-TOF MS – Matrix-Assisted Laser Desorption/Ionization-Time of Flight Mass Spec

trometer; MIC – Minimal Inhibitory Concentration, MLVF – Multi Locus Variable tandem repeats Fingerprinting; RFLP-PFGE, Restriction Fragment Length Polymorphism – Pulsed Field Gel Electrophoresis; SAG – Streptococcus anginosus group

Competing interests

The authors have no competing interests to declare.

Authors contribution

KO performed strain re-identification, MLVF and PFGE analyses and wrote the manuscript, IKZ performed PFGE analysis, AR performed MIC analysis, KM performed MIC analysis and detection of antibiotic resistance determinants, ES coordinated strain collection, performed strain re-identification, WH analyzed the data, IS coordinated the study, analyzed the data and wrote the manuscript

Acknowledgments

The study was financed from grant N401535940 from NCN (National Science Center), partially supported from NIL internal funding (DS 5.02), SPUB-Mikrobank2 and the National Programme of Antibiotic Protection (MODUL I NPOA).

We are thankful to members of KORLD, KOROUN and Polmicro for help with strain banking and maintenance.

Literature


