

LIST OF ABBREVIATIONS	IV
LIST OF TABLES	VI
LIST OF FIGURES	VI
1 INTRODUCTION	1
2 LITERATURE	3
2.1 Genus <i>Staphylococcus</i>	3
2.2 Staphylococci of the intermedius-group (SIG)	4
2.3 <i>Staphylococcus pseudintermedius</i>	5
2.3.1 Virulence factors of <i>S. pseudintermedius</i>	6
2.3.1.1 Excreted virulence-associated factors	6
2.3.1.2 Surface-associated factors	8
2.3.1.3 Global regulation of gene expression in SIG	8
2.3.2 Phenotypic identification of <i>S. pseudintermedius</i>	9
2.3.3 Molecular identification techniques for <i>S. pseudintermedius</i>	10
2.3.4 Genotypic typing techniques of <i>S. pseudintermedius</i>	11
2.3.4.1 Pulsed-Field Gel Electrophoresis (PFGE)	11
2.3.4.2 Staphylococcus protein A (<i>spa</i>) typing	12
2.3.4.3 Multi-Locus Sequence Typing (MLST)	13
2.3.4.4 Staphylococcal Cassette Chromosome (SCC <i>mec</i>) typing	14
2.3.4.5 Dru-typing	15
2.3.4.6 Whole genome sequence analyses (WGS)	15
2.4 Antibiotic resistance in bacteria: General aspects	16
2.4.1 Antibiotic resistance in <i>Staphylococcus pseudintermedius</i>	17
2.4.2 Resistance towards beta-lactam antibiotics	17
2.4.3 Further antibiotic resistances described for <i>S. pseudintermedius</i>	18
2.5 Epidemiology of <i>S. pseudintermedius</i>	21
2.5.1 Molecular epidemiology of <i>S. pseudintermedius</i>	22

3	MATERIALS	25
3.1	Bacterial isolates, reference-strains, Polymerase chain reaction components	25
4	METHODS	34
4.1	Bacterial cultivation, strain storage and disc diffusion antibiotic sensitivity testing	34
4.2	Molecular genetic methods	34
4.2.1	DNA extraction	34
4.2.2	Polymerase chain reaction (PCR)	34
4.2.3	Gel electrophoresis	35
4.2.4	Triplex PCR	35
4.2.5	Verification of <i>S. pseudintermedius</i> among SIG isolates	36
4.2.6	Detection for virulence-associated genes in <i>S. pseudintermedius</i>	37
4.2.7	Pulsed-field gelelectrophoresis (PFGE)	38
4.2.8	Analysis of PFGE pattern using Bionumerics	39
4.2.9	Multi-locus sequence typing (MLST)	40
4.2.10	MLST data analysis and generation of a minimum spanning tree	41
4.3	Statistical Analysis	41
5	RESULTS	42
5.1	Characterisation of <i>S. pseudintermedius</i> isolates with respect to origin, methicillin resistance and virulence factors	42
5.2	Virulence-associated factors among <i>S. pseudintermedius</i> isolates	44
5.3	Results of multi-locus sequence typing	46
5.4	Results of PFGE analysis	49
5.4.1	Detailed description of five major PFGE clades	49
5.4.1.1	Description of major PFGE clade 1	49
5.4.1.2	Description of major PFGE clade 2	50
5.4.1.3	Description of major PFGE clade 8	50
5.4.1.4	Description of major PFGE clade 12	51
5.4.1.5	Description of major PFGE clade 16	51
5.4.2	Comparison of PFGE clades with genomic background of MRSP and MSSP isolates	55

6	DISCUSSION	57
6.1	Characteristics of <i>S. pseudintermedius</i> isolates in Germany	57
6.2	Proportion and distribution of virulence factors among MRSP and MSSP	58
6.3	Current genotypes of <i>S. pseudintermedius</i> from different regions in Germany	60
6.4	Genetic relationship of <i>S. pseudintermedius</i> circulating in Germany: Comparison of PFGE- and MLST results	61
7	SUMMARY	63
8	ZUSAMMENFASSUNG	65
9	REFERENCES	67
10	APPENDIX 1	78
11	LIST OF PUBLICATIONS	87
12	ACKNOWLEDGEMENTS	90
13	SELBSTSTÄNDIGKEITSERKLÄRUNG	92