Supplementary Materials: Prevalence and Genetic Characteristics of *Staphylococcus aureus* and *Staphylococcus argenteus* Isolates Harboring Panton-Valentine Leukocidin, Enterotoxins, and TSST-1 Genes from Food Handlers in Myanmar

Meiji Soe Aung, Thida San, Mya Mya Aye, San Mya, Win Win Maw, Khin Nyein Zan, Wut Hmone Win Htut, Mitsuyo Kawaguchiya, Noriko Urushibara and Nobumichi Kobayashi

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                                     30                            60
COL       TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD112     TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD188     TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD8       TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD3       TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD110     TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD7       TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
N315      TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD15      TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD44      TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD97      TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD191     TCAAATGTAAATTAATAATTGTTTTGGGG-AGTTTGAAGTTAAATATTTAACAGGATTTA
TD21      TCAAATGTAAATTAATAATTGTTTTGGGG-AGTTTGAAGTTAAATATTTAACAGGATTTA
TD160     TCAAATGTAAATTAATAATTGTTTTGGGG-AGTTTGAAGTTAAATATTTAACAGGATTTA
TD115     TCAAATGTAAATTAATAATTGTTTTGGGG-AGTTTGAAGTTAAATATTTAACAGGATTTA
TD123     TCAAATGTAAATTAATAATTGTTTTGGGGGAGTTTGAAGTTAAATATTTAACAGGATTTA
TD158     TCAAATGTAAATTAATAATTGTTTTGGGGGAGCTTGAAGTTAAATATTTAACAGGATTTA
TD101     TCAAATGTAAATTAATAATTGTTTTGGGG-AGTTTGAAGTTAAATATTTAACAGGATTTA
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                                                                  120
COL       TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD112     TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD188     TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD8       TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD3       TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD110     TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD7       TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
N315      TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD15      TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD44      TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD97      TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCGAGTGCAATCGAATATTCAG
TD191     TTTTAATATTATTGTTAGAAGAAATTTTGACAAATTCAGCAAGTGCAATCGAATATTCAG
TD21      TTTTAATATTATTGTTAGAAGAAATTTTGACAAATTCAGCAAGTGCAATCGAATATTCAG
TD160     TTTTAATATTATTGTTAGAAGAAATTTTGACAAATTCAGCAAGTGCAATCGAATATTCAG
TD115     TTTTAATATTATTGTTAGAAGAAATTTTGACAAATTCAGCAAGTGCAATCGAATATTCAG
TD123     TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCAAGTGCAATCGAATATTCAG
TD158     TTTTAATATTATTGTTAGAAGGAATTTTTACAAATTCAGCAAGTGCAATCGAATATTCAG
TD101     TTTTAATATTATTGTTAGAAGAAATTTTGACAAATTCAGTAAGTGCAATCGAATATTCAG
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                                                                         180
COL             ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD112           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD188           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD8             ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD3             ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD110           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD7             ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
N315            ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD15            ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD44            ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD97            ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD191           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD21            ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD160           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD115           ACTTACATCATAAAAGTAAGTTTGATTCAAAGCGTCTAAGTAATGCTAAGATGTCATTCA
TD123           ACTTACATCATAAAAGTAAACTTGATTCAAAGCGTCTATATAATGCTAAGGTGTCATTTG
TD158           ACTTACATCATAAAAGTAAACTTGATTCAAAGCGTCTATATAATGCTAAGGTGTCATTTG
TD101           ACTTACATCATAAAAGTAAACTAAATTCAAAGCGTCTATATAATGCTAAGGTGTCATTTG
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                                                                         240
COL             TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD112           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD188           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD8             TCAATCCAACTCAGCTTGAAAATAAAAACACAAAAGATAGACTGTTGAAGCATGATTTGT
TD3             TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD110           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD7             TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
N315            TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD15            TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD44            TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD97            TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD191           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD21            TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD160           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD115           TCAATCCAACTCAGCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
TD123           CTAATCCAACTGATCTTGAAAATAAAAAAACAAACGATAGACTGTTGAAGCATGATTTGT
TD158           CTAATCCAACTGATCTTGAAAATAAAAAAACAAACGATAGACTGTTGAAGCATGATTTGT
TD101           CTAATCCAACTGATCTTGAAAATAAAAACACAAACGATAGACTGTTGAAGCATGATTTGT
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                                                                         300
COL             TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTTGAAA
TD112           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTTGAAA
TD188           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTTGAAA
TD8             TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTTGAAA
TD3             TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD110           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD7             TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAGGATTTTAAAGTTGAATTCGAAA
N315            TATTTCATGACATGTTCGTAAATGTTGCTTCGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD15            TATTTCATGACATGTTCGTAAATGTTGCTTCGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD44            TATTTCATGACATGTTCGTAAATGTTGCTTCGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD97            TATTTCATGACATGTTCGTAAATGTTGCTTCGAAAAAGGATTTTAAAGTTGAATTCGAAA
TD191           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD21            TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD160           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD115           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD123           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD158           TATTTCATGACATGTTCGTAAATGATGATTGGAAAAAAGATTTTAAAGTTGAATTCGAAA
TD101           TATTTCATGACATGTTCGTAAATGTTGCTTCGAAAAAGGATTTTAAAGTTGAATTCGAAA
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                                                                     360
COL        ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD112      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD188      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD8        ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD3        ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD110      ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD7        ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
N315       ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD15       ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD44       ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD97       ATGAGGCACTTTCAAAGAAATTTATAAATAAGAATATCGATATATATGCTGGAAGCTATA
TD191      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD21       ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD160      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD115      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD123      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD158      ATGAGGCACTTTCAAAGAAATTTATAAATAAGGATATCGATATATTTGCTGGAAATTATG
TD101      ATGAGGCACTTTCAAATGAATTTATAAATAAGAATATCGATATATATGCTGGAAATTATG
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                                                                     420
COL        GATACGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD112      GATACGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD188      GATACGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD8        GATACGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD3        GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD110      GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD7        GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
N315       GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD15       GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD44       GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD97       GCTATGAATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD191      GATATGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD21       GATATGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD160      GATATGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD115      GATATGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
TD123      GATACGGATGTCATGGGGGAGAAACCAATAAAACGCAATGTAGTTATGGAGGGGTTACTT
TD158      GATACGGATGTCATGGGGGAGAAACCAATAAAACGCAATGTAGTTATGGAGGGGTTACTT
TD101      GATACGGATGTCATGGGGGAGCAACCAATAAAACGCAATGTAGTTATGGTGGTGTTACTT
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                                                                     480
COL        TAAGTGACAATAATAAATACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD112      TAAGTGACAATAATAAATACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD188      TAAGTGACAATAATAAATACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD8        TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD3        TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD110      TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD7        TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
N315       TAAGTGACAATAATAAATAAGATGATTATAAGAATATACCTTCTAATTTATGGATTGACG
TD15       TAAGTGACAATAATAAATAAGATGATTATAAGAATATACCTTCTAATTTATGGATTGACG
TD44       TAAGTGACAATAATAAATAAGATGATTATAAGAATATACCTTCTAATTTATGGATTGACG
TD97       TAAGTGACAATAATAAATAAGATGATTATAAGAATATACCTTCTAATTTATGGATTGACG
TD191      TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD21       TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD160      TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD115      TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
TD123      TAAGTGACAATAATAAGTACGATAATGATAAGAATATACCTTGTAATTTATGGATTGACG
TD158      TAAGTGACAATAATAAGTACGATAATGATAAGAATATACCTTGTAATTTATGGATTGACG
TD101      TAAGTGACAATAATAAGTACGATGATTATAAGAATATACCTTGTAATTTATGGATTGACG
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                                                                         540
COL         GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACTATT
TD112       GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACTATT
TD188       GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD8         GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD3         GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD110       GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD7         GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
N315        GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAAAGAAAATTGTTACCATT
TD15        GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAAAGAAAATTGTTACCATT
TD44        GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAAAGAAAATTGTTACCATT
TD97        GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAAAGAAAATTGTTACCATT
TD191       GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD21        GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD160       GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD115       GACATCAAGCAGAAATAGAATTAACAGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD123       GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD158       GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACCATT
TD101       GACATCAAACAGAAATAGAACTAACTGCAGTAAAAACGAAAAA-GAAAATTGTTACTATT
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                                                                         600
COL         CAAGAATTAGAGGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD112       CAAGAATTAGAGGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD188       CAAGAATTAGAGGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD8         CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD3         CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD110       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD7         CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
N315        CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD15        CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD44        CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD97        CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD191       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD21        CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD160       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD115       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD123       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD158       CAAGAATTAGATGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
TD101       CAAGAATTAGAGGTTCAATTAAGAAATTATTTGAATGAGAAGTATAAGTTGTACGAACAA
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                                                                         660
COL         GGTGGCGACATTGTTAAAGGGTATGTTAAATATTATAATGATGATGAACAAAATGTAGAA
TD112       GGTGGCGACATTGTTAAAGGGTATGTTAAATATTATAATGATGATGAACAAAATGTAGAA
TD188       GGTGGCGACATTGTTAAAGGGTATGTTAAATATTATAATGATGATGAACAAAATGTAGAA
TD8         GGTGGCGACATTGTTAAAGGGTATGTTAAATATTATAATGATGATGAACAAAATGTAGAA
TD3         GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD110       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD7         GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
N315        GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATGTAGAA
TD15        GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATGTAGAA
TD44        GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATGTAGAA
TD97        GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATGTAGAA
TD191       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD21        GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD160       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD115       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAACAAAATATAGAA
TD123       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGA---AAAAAATGTAGAA
TD158       GGTGGCGACATTGTTAAAGGGTATGTTAAATATCATAATGATGATGAAAAAAATGTAGAA
TD101       GGTGGCGACATTGTTAAAGGGTATGTTAAATATTATAATGATGATGAACAAAATGTAGAA
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                                                                     720
COL       TATGATTTTTATAATTTAAATGGTGAGTATGGTCGTGAGGTATTAAAAATGTATGCTGAT
TD112     TATGATTTTTATAATTTAAATGGTGAGTATGGTCGTGAGGTATTAAAAATGTATGCTGAT
TD188     TATGATTTTTATAATTTAAATGGTGAGTATGGTCGTGAGGTATTAAAAATGTATGCTGAT
TD8       TATGATTTTTATAATTTAAATGGTGAGTATGGTCGTGAGGTATTAAAAATGTATGCTGAT
TD3       TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD110     TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD7       TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
N315      TATGATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD15      TATGATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD44      TATGATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD97      TATGATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD191     TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGATATTAAAAATGTATGCTGAT
TD21      TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGATATTAAAAATGTATGCTGAT
TD160     TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD115     TATAATTTTTATAATTTAAATGGTGAGTATGGTTATGAGGTATTAAAAATGTATGCTGAT
TD123     TATGATTTTTATAATTTAAATGGTGAGTATGGTCATGAGGTATTAAAAATGTATGCTGAT
TD158     TATGATTTTTATAATTTAAATGGTGAGTATGGTCATGAGGTATTAAAAATGTATGCTGAT
TD101     TATGATTTTTATAATTTAAATGGTGAGTATGGTCGTGAGGTATTAAAAATGTATGCTGAT
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                                                                     780
COL       AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD112     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD188     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD8       AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD3       AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD110     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD7       AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
N315      AATAAAACTATCAATAGAGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD15      AATAAAACTATCAATAGAGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD44      AATAAAACTATCAATAGAGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD97      AATAAAACTATCAATAGAGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD191     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD21      AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD160     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD115     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD123     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD158     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
TD101     AATAAAACTATCAATAGTGACAAATTGCATTTAGATATCTATTTATTCAAATCATAATTT
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COL       AATTAAG
TD112     AATTAAG
TD188     AATTAAG
TD8       AATTAAG
TD3       AATTAAG
TD110     AATTAAG
TD7       AATTAAG
N315      AATTAAG
TD15      AATTAAG
TD44      AATTAAG
TD97      AATTAAG
TD191     AATTAAG
TD21      AATTAAG
TD160     AATTAAG
TD115     AATTAAG
TD123     AAGTGAG
TD158     AAGTGAG
TD101     AATTAAG
          ** * **
```

Figure S1. Alignment of nucleotide sequences of intact *selw* genes and pseudogenes encoding truncated SElW. Sequences of strains COL and N315 represent intact and truncated *selw* genes, respectively. Start codon and stop codon are shown in yellow and blue, respectively. Nucleotide numbers are indicated for intact *selw* represented by strain COL.

(a)

```
                                                                                  60
TD123                   MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNAKVSFANPTDLEN
TD158                   MGELEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNAKVSFANPTDLEN
TD21                    ----------------MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD191                   ----------------MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD115                   ----------------MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD160                   ----------------MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD3                     MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD7                     MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD110                   MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD112                   MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD188                   MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
COL                     MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD8                     MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD101                   ----------------MLEEILTNSVSAIEYSDLHHKSKLNSKRLYNAKVSFANPTDLEN
                                        :** *:***.*************::**** ***:** ***:***


                                                                                 120
TD123                   KKTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGE
TD158                   KKTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGE
TD21                    KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD191                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD115                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD160                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD3                     KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
TD7                     KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
TD110                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
TD112                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD188                   KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
COL                     KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD8                     KNTKDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
TD101                   KNTNDRLLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDIYAGNYGYGCHGGA
                        *:*:****************   **************::****:***:**.*.* ****


                                                                                 180
TD123                   TNKTQCSYGGVTLSDNNKYDNDKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQLR
TD158                   TNKTQCSYGGVTLSDNNKYDNDKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQLR
TD21                    TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD191                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD115                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD160                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD3                     TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD7                     TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD110                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD112                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVQLR
TD188                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVQLR
COL                     TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVQLR
TD8                     TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQLR
TD101                   TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVQLR
                        ********************: *************:*******************:****
```

```
                                                                         240
TD123           NYLNEKYKLYEQGGDIVKGYVKYHND-EKNVEYDFYNLNGEYGHEVLKMYADNKTINSDK
TD158           NYLNEKYKLYEQGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHEVLKMYADNKTINSDK
TD21            NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEILKMYADNKTINSDK
TD191           NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEILKMYADNKTINSDK
TD115           NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADNKTINSDK
TD160           NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADNKTINSDK
TD3             NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADNKTINSDK
TD7             NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADNKTINSDK
TD110           NYLNEKYKLYEQGGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADNKTINSDK
TD112           NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK
TD188           NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK
COL             NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK
TD8             NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK
TD101           NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK
                ***********************:** *:*:**:********* *:**************

                       250
TD123           LHLDIYLFKS
TD158           LHLDIYLFKS
TD21            LHLDIYLFKS
TD191           LHLDIYLFKS
TD115           LHLDIYLFKS
TD160           LHLDIYLFKS
TD3             LHLDIYLFKS
TD7             LHLDIYLFKS
TD110           LHLDIYLFKS
TD112           LHLDIYLFKS
TD188           LHLDIYLFKS
COL             LHLDIYLFKS
TD8             LHLDIYLFKS
TD101           LHLDIYLFKS
                **********
```

(b)

```
                                                                          60
TD44            MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD97            MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
TD15            MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
N315            MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
COL             MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQLEN
                ************************************************************

                                                                         120
TD44            KNTNDRLLKHDLLFHDMFVNVASKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
TD97            KNTNDRLLKHDLLFHDMFVNVASKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
TD15            KNTNDRLLKHDLLFHDMFVNVASKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
N315            KNTNDRLLKHDLLFHDMFVNVASKKDFKVEFENEALSKKFINKNIDIYAGSYSYECHGGA
COL             KNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGA
                ********************   ********************:***:**.*.* *****

                               138                                       180
TD44            TNKTQCSYGGVTLSDNNK------------------------------------------
TD97            TNKTQCSYGGVTLSDNNK------------------------------------------
TD15            TNKTQCSYGGVTLSDNNK------------------------------------------
N315            TNKTQCSYGGVTLSDNNK------------------------------------------
COL             TNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVQLR
                ******************

                                                                         240
TD44            ------------------------------------------------------------
TD97            ------------------------------------------------------------
TD15            ------------------------------------------------------------
N315            ------------------------------------------------------------
COL             NYLNEKYKLYEQGGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSDK

                       250
TD44            ----------
TD97            ----------
TD15            ----------
N315            ----------
COL             LHLDIYLFKS
```

Figure S2. Alignment of amino acid sequences of intact SElW (**a**), truncated SElW with an intact SElW of strain COL (**b**). Amino acid numbers are indicated for intact SElW.

```
TD188           MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD112           MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
COL             MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD8             MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD7             MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD3             MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD110           MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKFDSKRLSNAKMSFIN--PT
TD123           MGEFEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKLDSKRLYNAKVSFAN--PT
TD158           MGELEVKYLTGFILILLLEGIFTNSASAIEYS--DLHHKSKLDSKRLYNAKVSFAN--PT
SEA             MKKTAFTLLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKA
                * :  .. *  : * *  . :...* .: * .  **::**:::.. * * *  :     :
                                                                          60

TD188           QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
TD112           QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
COL             QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
TD8             QLENKNTKDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
TD7             QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYEC
TD3             QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYEC
TD110           QLENKNTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKNIDIYAGSYSYEC
TD123           DLENKKTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
TD158           DLENKKTNDRLLKHDLLFHDMFVNDDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGC
SEA             KTENKESHDQFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQC
                . ***:::*::*:* :**:.:*.:..* :*: *:*:.: : .*: .*.:*::.. *.* *
                                                                         120

TD188           HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELE
TD112           HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELE
COL             HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELE
TD8             HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELD
TD7             HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELD
TD3             HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELD
TD110           HGGATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELD
TD123           HGGETNKTQCSYGGVTLSDNNKYDNDKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELD
TD158           HGGETNKTQCSYGGVTLSDNNKYDNDKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELD
SEA             AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELD
                 ** .*** * ****** ***:  : *::* ***:**:*  : * :***:** **:***:
                                                                         180

TD188           VQLRNYLNEKYKLYEQ---GGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADN
TD112           VQLRNYLNEKYKLYEQ---GGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADN
COL             VQLRNYLNEKYKLYEQ---GGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADN
TD8             VQLRNYLNEKYKLYEQ---GGDIVKGYVKYYNDDEQNVEYDFYNLNGEYGREVLKMYADN
TD7             VQLRNYLNEKYKLYEQ---GGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADN
TD3             VQLRNYLNEKYKLYEQ---GGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADN
TD110           VQLRNYLNEKYKLYEQ---GGDIVKGYVKYHNDDEQNIEYNFYNLNGEYGYEVLKMYADN
TD123           VQLRNYLNEKYKLYEQ---GGDIVKGYVKYHND-EKNVEYDFYNLNGEYGHEVLKMYADN
TD158           VQLRNYLNEKYKLYEQ---GGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHEVLKMYADN
SEA             LQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDN
                :* *.**:***:**:.   .*.: :* : ::.. * .::*:::. :*:*.  :*::* **
                                                                         240

TD188           KTINSDKLHLDIYLFKS
TD112           KTINSDKLHLDIYLFKS
COL             KTINSDKLHLDIYLFKS
TD8             KTINSDKLHLDIYLFKS
TD7             KTINSDKLHLDIYLFKS
TD3             KTINSDKLHLDIYLFKS
TD110           KTINSDKLHLDIYLFKS
TD123           KTINSDKLHLDIYLFKS
TD158           KTINSDKLHLDIYLFKS
SEA             KTINSENMHIDIYLYTS
                *****:::*:****:.*

                              257
```

Figure S3. Alignment of amino acid sequences of intact SElW and SEA. Amino acid numbers are indicated for SEA.

Table S1 Detection of PVL, TSST-1, and enterotoxin (-like) genes in nasal isolates

Toxin genes	*coa* -genotype (no. of isolates)													Total n=110 (%)
	Ia (7)	IIa (3)	IIIa (15)	IVb (11)	Va (10)	Vb (9)	VIa (22)	VIc (1)	VIIa (18)	VIIb (24)	VIIIa (1)	Xa (18)	XIb (5)	
lukS-PV-lukF-PV (PVL)	0	0	2	0	0	0	11	0	1	0	0	0	1	15 (13.6)
tst-1 (TSST-1)	0	2	1	0	0	0	0	0	0	1	0	0	0	4 (3.6)
Enterotoxin (-like) genes														
sea	0	0	0	7	0	0	12	0	1	2	0	0	0	22 (20)
seb	0	1	3	0	1	0	1	0	0	8	0	1	0	15 (13.6)
sec	0	1	0	0	1	2	10	0	0	3	0	6	0	23 (20.9)
seg	3	1	0	0	3	0	3	0	0	7	1	1	0	19 (17.3)
seh	0	0	0	0	0	0	0	0	2	1	0	2	0	5 (4.5)
sei	3	2	0	0	6	0	7	0	1	9	1	3	0	32 (29.1)
selj	0	0	0	0	0	0	0	0	0	0	0	4	0	4 (3.6)
sek	0	0	1	1	0	0	0	0	2	9	0	0	0	13 (11.8)
sel	1	0	1	0	0	3	7	0	1	5	1	6	0	25 (22.7)
sem	3	2	0	0	7	0	4	0	0	8	1	3	0	28 (25.5)
sen	4	1	0	0	6	0	1	0	0	8	0	1	0	21 (19.1)
seo	3	2	0	0	6	0	3	0	0	7	1	1	0	23 (20.9)
sep	0	0	5	0	0	0	0	0	0	3	0	0	0	8 (7.3)
seq	0	0	1	1	0	0	0	0	1	6	0	0	0	9 (8.2)
ser	0	0	0	0	0	0	0	0	0	0	0	3	0	3 (2.7)
ses	0	0	0	0	0	0	0	0	0	0	0	3	0	3 (2.7)
set	0	0	0	0	0	0	0	0	0	0	0	3	0	3 (2.7)
selu	3	1	0	0	3	0	3	0	0	4	1	1	0	16 (14.5)
selw	4	3	10	8	7	7	17	1	13	20	1	14	2	107 (97.3)
selx	4	3	10	8	8	7	17	1	13	19	1	14	1	106 (96.4)
sely	1	0	0	1	0	0	1	0	9	11	0	6	4	33 (30)
Enterotoxin genes clusters														
g, i, m, n, o, u	4	1	1	0	2	0	1	0	0	3	0	1	0	13 (11.8)
g, i, m, n, o	0	0	0	0	0	0	0	0	0	2	0	0	0	2 (1.8)
j, r, s, t	0	0	0	0	0	0	0	0	0	0	0	3	0	3 (2.7)
k, q	0	0	1	1	0	0	0	0	1	6	0	0	0	9 (8.1)

Table S2 Detection of PVL, TSST-1, and enterotoxin (-like) genes in hand isolates

Toxin genes	*coa* -genotype (no. of isolates)													Total n=34 (%)
	Ia (7)	IIa (3)	IIIa (15)	IVb (11)	Va (10)	Vb (9)	VIa (22)	VIc (1)	VIIa (18)	VIIb (24)	VIIIa (1)	Xa (18)	XIb (5)	
lukS-PV-lukF-PV (PVL)	0	0	0	0	1	0	1	0	1	0	0	0	0	3 (11.3)
tst-1 (TSST-1)	0	0	1	0	0	0	0	0	0	0	0	0	0	1 (2.9)
Enterotoxin(-like) genes														
sea	0	0	0	2	1	0	4	0	1	1	0	0	0	9 (26.5)
seb	0	0	2	0	1	0	0	0	0	2	0	0	0	5 (14.7)
sec	0	0	0	0	0	0	3	0	1	1	0	3	0	8 (23.5)
seg	3	0	0	0	2	0	0	0	0	2	0	0	0	7 (20.6)
sei	3	0	0	0	2	0	1	0	0	2	0	1	0	9 (26.5)
selj	0	0	0	0	0	0	0	0	0	0	0	1	0	1 (2.9)
sek	0	0	2	0	1	0	0	0	2	2	0	0	0	7 (20.6)
sel	0	0	0	0	0	1	3	0	1	1	0	3	0	9 (26.5)
sem	3	0	1	0	2	0	0	0	0	2	0	1	0	9 (26.5)
sen	2	0	0	0	2	0	0	0	0	2	0	1	0	7 (20.6)
seo	3	0	0	0	2	0	0	0	0	2	0	0	0	7 (20.6)
sep	0	0	2	0	1	0	0	0	0	2	0	0	0	5 (14.7)
seq	0	0	2	0	1	0	0	0	2	2	0	0	0	7 (20.6)
ser	0	0	0	0	0	0	0	0	0	0	0	1	0	1 (2.9)
ses	0	0	0	0	0	0	0	0	0	0	0	1	0	1 (2.9)
set	0	0	0	0	0	0	0	0	0	0	0	1	0	1 (2.9)
selu	3	0	0	0	2	0	0	0	0	2	0	0	0	7 (20.6)
selw	3	0	5	3	3	2	5	0	5	4	0	4	0	34 (100)
selx	3	0	5	3	2	2	5	0	5	4	0	4	0	33 (97.9)
sely	1	0	1	0	0	0	0	0	2	0	0	3	0	7 (20.6)
Enterotoxin genes clusters														
g, i, m, n, o, u	2	0	0	0	2	0	0	0	0	2	0	0	0	6 (17.6)
g, i, m, n, o	0	0	0	0	0	0	0	0	0	1	0	0	0	1 (2.9)
j, r, s, t	0	0	0	0	0	0	0	0	0	0	0	1	0	1 (2.9)
k, q	0	0	2	0	1	0	0	0	2	2	0	0	0	7 (20.6)

Table S3 Identical *coa* types and toxin gene profile in same individual

No.	Age/ Sex	Isolate ID	Hand swab (H) / Nasal swab (N)	*coa* type	enterotoxin(-like) genes, PVL genes
1	22/M	TD10	H	Xa	*sec, sei, sel, selx, sely, selw*
		TD9	N		
2	27/M	TD16	H	IVb	*sea, selx*
		TD15	N		
3	22/M	TD20	H	VIa	*sea, sei, sel, selx, selw*
		TD19	N		
4	25/F	TD22	H	Xa	*sei, ses, set, ser, selx, selw*
		TD21	N		
5	26/M	TD35	H	IVb	*sea, selx, sew*
		TD34	N		
6	25/M	TD42	H	VIIa	*selx, selw*
		TD41	N		
7	22/M	TD46	H	IIIa	*seb, sep, selx*
		TD45	N		
8	40/M	TD155	H	Vb	*selx, selw*
		TD107	N		
9	22/F	TD156	H	VIIb	*sea, seg, sei, sem, sen, seo, seu, selx*
		TD104	N		
10	28/M	TD157	H	VIa	*sea, sel, selx, selw, pvl* (*lukS-PV-lukF-PV*)
		TD110	N		
11	22/M	TD156	H	Ia	*seg, sei, sem, sen, seo, seu, selx, selw*
		TD104	N		
12	25/M	TD165	H	Vb	*sel, selx, selw*
		TD164	N		
13	25/F	TD100	H	VIa	*selx, selw*
		TD99	N		
14	28/M	TD166	H	VIIa	*selx, selw*
		TD132	N		
15	29/M	TD104	H	VIIb	*seb, sek, sep, seq, selx, sely, selw*
		TD103	N		
16	32/F	TD177	H	VIa	*sea, selx, selw*
		TD106	N		
17	40/M	TD102	H	Xa	*sec, sel, selx, sely*
		TD141	N		

Table S4 Different *coa* types and/or toxin gene profile in same individual

No.	Age/Sex	Strain ID	Hand swab (H) / Nasal swab (N)	*coa* type	enterotoxin (-like) genes, TSST-1 gene
1	24/F	TD18	H	IIIa	*selx, selw*
		TD17	N	VIIb	*sec, seg, sei, sel, sem, sen, seo, selx*
2	42/M	TD30	H	VIIb	*sec, seg, sei, sel, sem, sen, seo, seu, selx*
		TD29	N	VIIb	*sec, seg, sei, sel, sem, sen, seo, selx*
3	45/F	TD158	H	Va	*sea, seg, sei, sem, sen, seo, seu, selx, selw*
		TD111	N	Va	*seg, sei, sem, sen, seo, seu, selx*
4	23/F	TD159	H	IIIa	*sek, sel, seq, selx, tst-1*
		TD112	N	IIIa	*sek, sem, seq, selx, tst-1*
5	24/F	TD160	H	VIIa	*sek, seq, selx, selw*
		TD115	N	VIIa	*seh, sek, selx, selw*
6	27/M	TD97	H	Ia	*seg, sei, sem, sen, seo, seu, selx, sely, selw*
		TD118	N	Xa	*seg, sei, sem, sen, seo, seu, selx, selw*
7	25/M	TD98	H	VIIa	*sea, sec, sek, sel, seq, selx, selw*
		TD118	N	VIIa	*sea, seh, sei, sek, sel, seq, selx, selw*
8	23/M	TD161	H	VIa	*sea, sel, selx, selw*
		TD121	N	VIIb	*sea, sei, sel, selx, selw*
9	21/F	TD163	H	VIIb	*seb, sek, sep, seq, selx, sely, selw*
		TD127	N	VIIb	*seb, sek, sep, selx, sely, selw*
10	28/F	TD128a	H	VIa	*seb, seg, sei, sem, seo, seu*
		TD128b	N	VIIa	*selx, selw*
11	26/F	TD134	H	Ia	*seg, sei, sem, seo, seu, selx, selw*
		TD133	N	Ia	*seg, sei, sem, sen, seo, seu, selx, selw*
12	29/M	TD167	H	IVb	*selx, selw*
		TD136	N	Xa	*sej, ses, set, ser, selx, selw*
13	29/F	TD139	H	IIIa	*sek, sep, seq, selx, sely, selw*
		TD138	N	VIIb	*sek, selx, sely, selw*
14	25/F	TD173	H	Va	*seb, sek, sep, seq*
		TD144	N	Va	*sei, sem, seo, seu, selx, selw*
15	27/F	TD174	H	Va	*seg, sei, sem, sen, seo, seu, selx*
		TD145	N	VIIb	*seg, sei, sem, sen, seo, seu, selx*
16	22/M	TD105	H	Xa	*sec, sel, sem, sen, selx, sely*
		TD146	N	Xa	*sec, sel, sem, selx, sely*
17	27/M	TD176	H	IIIa	*seb*
		TD147	N	IIIa	*seb, sep, selx*

Table S5 Identities (Percentage) of *selw* nucleotide sequences (upper right) and deduced amino acid sequences (lower left) among the selected strains

	Identity with strain																					SEA
	Group1					Group2			Group3					Group4				Group5			Group6	
Strain	TD101	TD123	TD158	H-EMRSA-15	RF-122	TD112	TD188	COL	TD160	TD115	TD191	TD21	MW2	TD44	TD97	TD15	N315	TD7	TD3	TD110	TD8	
TD101		91.0	91.5	90.2	87.4	96.2	96.0	92.7	91.5	91.5	91.1	91.1	91.5	87.7	87.7	87.7	87.7	89.7	89.7	89.7	91.5	58.2
TD123	96.0		99.2	95.2	93.3	94.4	94.4	94.4	92.3	92.3	91.1	91.1	91.5	89.3	89.3	89.3	88.5	92.1	92.1	92.1	94.0	57.5
TD158	96.3	99.5		95.2	92.4	94.4	94.4	94.4	92.7	92.7	92.3	92.3	91.1	88.6	88.6	88.6	87.8	92.1	92.1	92.1	94.0	57.4
H-MRSA-15	95.8	97.3	97.6		90.8	92.9	92.9	93.6	91.5	91.5	91.0	91.0	90.7	87.1	87.1	87.1	88.4	90.5	90.5	90.5	92.5	57.8
RF122	96.3	97.1	97.2	97.1		89.1	89.1	87.6	84.5	84.5	84.5	84.5	82.9	87.4	87.4	87.4	87.4	89.9	89.9	89.9	88.2	58.5
TD112	96.2	96.2	96.2	96.2	95.8		100	100	96.2	96.2	95.7	95.7	95.3	94.3	94.3	94.3	93.5	95.6	95.6	95.6	98.8	58
TD188	96.0	96.3	96.3	96.3	95.9	99.9		100	96.2	96.2	95.7	95.7	95.3	94.3	94.3	94.3	93.5	95.6	95.6	95.6	98.8	57.8
COL	96.3	96.1	96.3	96.3	95.8	100	99.9		96.2	96.2	95.7	95.7	95.3	94.3	94.3	94.3	93.5	95.6	95.6	95.6	98.8	56.1
TD160	95.6	95.6	95.9	95.9	95.6	97.3	97.5	97.5		100	99.6	99.6	100	91.0	91.0	91.0	91.0	96.6	96.6	96.6	96.6	58
TD115	95.6	95.6	95.9	95.9	95.6	97.3	97.5	97.5	100		99.6	99.6	100	91.0	91.0	91.0	91.0	96.6	96.6	96.6	96.6	58
TD191	95.5	95.5	95.8	95.8	95.5	97.2	97.3	97.3	99.9	99.9		100	99.6	91.0	91.0	91.0	91.0	96.2	96.2	96.2	96.2	58
TD21	95.5	95.5	95.8	95.8	95.5	97.2	97.3	97.3	99.9	99.9	100		99.6	91.0	91.0	91.0	91.0	96.2	96.2	96.2	96.2	58
MW2	95.5	95.8	95.8	95.8	95.6	97.5	97.6	97.5	99.9	99.9	99.7	99.7		89.5	89.5	89.5	89.5	95.8	95.8	95.8	95.8	56
TD44	95.0	94.7	95.2	95.2	95.4	97.2	97.4	97.2	96.4	96.4	96.3	96.3	96.6		100	100	99.3	97.9	97.9	97.9	93.6	57.9
TD97	95.0	94.7	95.2	95.2	95.4	97.2	97.4	97.2	96.4	96.4	96.3	96.3	96.6	100		100	99.3	97.9	97.9	97.9	93.6	57.9
TD15	95.0	94.7	95.0	95.2	95.2	97.2	97.4	97.2	96.4	96.4	96.3	96.3	96.6	100	100		99.3	97.9	97.9	97.9	93.6	57.9
N315	95.1	94.7	95.4	95.4	95.4	97.2	97.3	97.2	96.6	96.6	96.4	96.4	96.6	100	100	100		97.1	97.1	97.1	92.8	57.9
TD7	94.6	95.1	95.1	95.1	95.8	97.4	97.5	97.3	98.1	98.1	98.0	98.0	98.3	98.3	98.3	98.3	98.3		100	100	96.0	57.6
TD3	94.6	95.1	95.1	95.1	95.8	97.4	97.5	97.3	98.1	98.1	98.0	98.0	98.3	98.3	98.3	98.3	98.3	100		100	96.0	57.6
TD110	94.6	95.1	95.1	95.1	95.8	97.4	97.5	97.3	98.1	98.1	98.0	98.0	98.3	98.3	98.3	98.3	98.3	100	100		96.0	57.6
TD8	95.5	96.0	95.8	95.8	95.6	99.1	99.2	99.1	98.0	98.0	97.9	97.9	98.1	96.8	96.8	96.8	96.8	98.0	98.0	98.0		57.4
SEA (similarity)	76.2	73.2	73.2	67.5	70.8	74	74	77.7	77.2	76.4	77.2	76.4	76.4	78.2	78.2	71.2	71.2	74.4	78.2	78.2	73.6	
SEA (identity))	41.4	40.6	40.9	40.9	31.7	39.4	39.4	41.7	42.6	40.3	42.6	40.3	40.3	39.1	39.1	34.5	34.5	39.4	39.1	39.1	39.8	

Table S6 Primers used for PCR amplification of *S. argenteus* genes

Target gene	Primer	sequence (5'-3')	Product size
thermonuclease	Sta-arg-nucF1	CTATTAAATAATTGTAAAAGTGTAG	
	Sta-arg-nucR1	CTGATTCGATAATAAAACATAACGTG	840bp (+Sta-arg-nucF1)
orfX-cas1	orfX-AB	ATGAAAATCACCATTTTAGCTGTAGG	
	Sta-argR3	ATTCTCCGCCACAATAGCTGC	ca. 600bp (+orfX-AB)
	Sta-argR1	AAGCCTTTGCGCTTTGTGCGACTGA	ca. 1kb (+orfX-AB)
	Sta-argF1	CATAAATCCAAAAACAGGCTCTACATC	
	Sta-argR2	CCAAATTCTATCTCTAGTTCTCCCAG	ca. 4kb (+Sta-argF1)
	Sta-argR4	GATGGTAAAGGCGGCGTCATTTGG	ca. 1.7kb (+Sta-argF1)
	Sta-argF2	CTTAATAATCCTTTACCAGAGCGACC	ca. 2.5kb (+Sta-argR2)
	Sta-argF5	TGAGAGTTCTAAATCTCCAC	
	Sta-argR5	CCGAGTTCTAATAATCGAGTACGA	ca. 2.6kb (+Sta-argF5)