Results. Here, we report the first 7 SPS3-specific humAbs isolated: 5 used encoded light chains and two encoded kappa light chains. Six of these humAbs used variable heavy (VH) and light (VL) gene elements. Kappa humAbs used VH3-30 or VH3-7, whereas lambda humAbs used VH3-9, VH3-72 or VH3-23. Sequence analysis revealed somatic mutations in complementary determining as well as framework regions. Initial studies show that several humAbs aggregated in vitro in relation to vaginal fluids. This ongoing to identify specific determinants of SPS3 binding and biological efficacy against ST3 in vitro and in vivo.

Conclusion. The results of this study provide further understanding of the biology of SPS3 antibodies and may facilitate design of adjunctive immunotherapy to treat and prevent ST3 disease.

Disclosures. All authors: No reported disclosures.

648. Urinary Tract-Associated Escherichia coli Bacteria Strains Are Genetically More Virulent than Those Originating From Non-urinary and Neutropenic Infective Foci

Background. E. coli is the leading cause of bacteremia in the United States and globally. Although pneumococcal conjugate vaccines are highly effective against invasive pneumococcal disease, they are less effective against pneumo-

Methods. We sorted individual SPS3-specific memory B cells from PBMCs isolated on days 0 and 7 post-vaccination from pneumococcal polysaccharide (PPS)-based vaccine (Pneumovax or Prevnar13) recipients using fluorescently labeled PPS3. Immunoglobulin heavy (IgH) and light (IgL) chains were sequenced, cloned into Igh and/or IgL vectors, and expressed in HEK-293 cells. PPS3 specificity was confirmed using ELISA.

Results. Here, we report the first 7 SPS3-specific humAbs isolated: 5 used encoded light chains and two encoded kappa light chains. Six of these humAbs used variable heavy (VH) and light (VL) gene elements. Kappa humAbs used VH3-30 or VH3-7, whereas lambda humAbs used VH3-9, VH3-72 or VH3-23. Sequence analysis revealed somatic mutations in complementary determining as well as framework regions. Initial studies show that several humAbs aggregated in vitro in relation to vaginal fluids. This ongoing to identify specific determinants of SPS3 binding and biological efficacy against ST3 in vitro and in vivo.

Conclusion. The results of this study provide further understanding of the biology of SPS3 antibodies and may facilitate design of adjunctive immunotherapy to treat and prevent ST3 disease.

Disclosures. All authors: No reported disclosures.

649. The Clinical Significance of Sequence Type 17 of Vancomycin-Resistant Enterococcus faecium

Background. vancomycin-resistant Enterococcus faecium (VREF) is known to be associated with nosocomial isolates. However, there is no evidence of the effect of ST17 VREF on the patient’s clinical outcome. We conducted a retrospective cohort study to identify ST17 VREF would contribute to developing subsequent bacteremia among VREF-colonized patients.

Methods. VREF-colonized patients and its non-invasive rectal VREF isolates were collected between March 2014 and February 2015. Subsequent bacteremia event within 1 year after colonization was reviewed from electronic medical records. STs were identified by multi-focus sequence typing. Cohort was defined as VREF with ST17 or non-ST17. Multivariable Cox regression model was used to adjust effect of ST17 for developing subsequent bacteremia. If available, pulsed field gel electrophoresis (PFGE) was conducted to compare similarity between rectal and blood VREF isolates.

Results. Fifty-two patients with ST17 and 169 patients with non-ST17 VREF carriage were included in each cohort. There were six cases and 10 cases of subsequent bacteremia in cohorts ST17 and non-ST17, and 1-year VREF bacteremia free rates were 85.9% and 90.2%, respectively. There was no significant difference of subsequent bac-

Conclusion. In our study, ST17 VREF was risk factors of subsequent bacteremia and the strain that showed strong concordance between rectal and blood isolates. Further study is needed to improve clinical outcome of patients carrying VREF using genotype data of rectal VREF isolates.

Figure 1: Recital isolates

Figure 2: Blood isolates

Disclosures. All authors: No reported disclosures.

650. Genomic Analysis of Shiga Toxin-producing Escherichia coli From Symptomatic Patients and Asymptomatic Carriers

Background. Shiga toxin-producing Escherichia coli (STEC) is the leading cause of bacteremia with mul-

Methods. We sorted individual SPS3-specific memory B cells from PBMCs isolated on days 0 and 7 post-vaccination from pneumococcal polysaccharide (PPS)-based vaccine (Pneumovax or Prevnar13) recipients using fluorescently labeled PPS3. Immunoglobulin heavy (IgH) and light (IgL) chains were sequenced, cloned into Igh and/or IgL vectors, and expressed in HEK-293 cells. PPS3 specificity was confirmed using ELISA.

Results. Here, we report the first 7 SPS3-specific humAbs isolated: 5 used encoded light chains and two encoded kappa light chains. Six of these humAbs used variable heavy (VH) and light (VL) gene elements. Kappa humAbs used VH3-30 or VH3-7, whereas lambda humAbs used VH3-9, VH3-72 or VH3-23. Sequence analysis revealed somatic mutations in complementary determining as well as framework regions. Initial studies show that several humAbs aggregated in vitro in relation to vaginal fluids. This ongoing to identify specific determinants of SPS3 binding and biological efficacy against ST3 in vitro and in vivo.

Conclusion. The results of this study provide further understanding of the biology of SPS3 antibodies and may facilitate design of adjunctive immunotherapy to treat and prevent ST3 disease.

Disclosures. All authors: No reported disclosures.

651. Pathogenesis and Immune Response

Background. Sequence type (ST) 17 of nonoxacycin-resistant Enterococcus faecium (VREF) is known to be associated with nosocomial isolates. However, there is no evidence of the effect of ST17 VREF on the patient’s clinical outcome. We conducted a retrospective cohort study to identify ST17 VREF would contribute to developing subsequent bacteremia among VREF-colonized patients.

Methods. VREF-colonized patients and its non-invasive rectal VREF isolates were collected between March 2014 and February 2015. Subsequent bacteremia event within 1 year after colonization was reviewed from electronic medical records. STs were identified by multi-focus sequence typing. Cohort was defined as VREF with ST17 or non-ST17. Multivariable Cox regression model was used to adjust effect of ST17 for developing subsequent bacteremia. If available, pulsed field gel electrophoresis (PFGE) was conducted to compare similarity between rectal and blood VREF isolates.

Results. Fifty-two patients with ST17 and 169 patients with non-ST17 VREF carriage were included in each cohort. There were six cases and 10 cases of subsequent bacteremia in cohorts ST17 and non-ST17, and 1-year VREF bacteremia free rates were 85.9% and 90.2%, respectively. There was no significant difference of subsequent bacteremia (P = 0.257) in log-rank test. However, after adjusted in multivariable models, VREF ST 17 was associated with subsequent bacteremia (adjusted relative risk, 4.02; 95% CI, 1.32–12.29, P = 0.015). Of 16 patients who had developed to subsequent VREF bacteri-

Conclusion. In our study, ST17 VREF was risk factors of subsequent bacteremia and the strain that showed strong concordance between rectal and blood isolates. Further study is needed to improve clinical outcome of patients carrying VREF using genotype data of rectal VREF isolates.

Figure 1: Recital isolates

Figure 2: Blood isolates

Disclosures. All authors: No reported disclosures.