Methods. We sequenced our 55 representative isolates and selected other 285 genomes, from public databases, obtained across different regions (36 countries), different sources (animal, commensal, and clinical strains) and a wide range of dates of isolation (1946–2017). We characterized the genomes by presence/absence of resistance, virulence and mobile elements, and of CRISPR-Cas systems. We analyzed the phylogeny of the entire population, selected the genomes belonging to clade A to examine recombination patterns and performed Bayesian molecular clock analysis excluding recombinant regions.

Results. Two major clades were identified, as previously reported. However, a higher degree of variation in clade A was found. Indeed, we identified a subclade (sub-clade I) that diverged ~894 years ago, and clearly distinguished clinical isolates from those of animal origin (distributed among a number of smaller early-branched subclades). A further split within the clinical subclade (subclade II) that diverged around ~371 years ago was also evident. Latin American isolates were distributed within subclades I (48%) and II (42%). Isolates in “animal” branches exhibited an average recombination of 34 Kbp, where it was 5 Kbp and 21 Kbp for subclades I and II, respectively. More resistance determinants were found in subclade II (62%), followed by 1 (54%) and absence of one was the norm in the clinical subclades.

Conclusion. Inclusion of E. faecium isolates from diverse geographical regions supports a continuous evolution of these organisms causing human infections. Important evolutionary events seem to favor emergence of novel subclades capable to cause important morbidity and mortality.

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1231. Patient-Level Factors Associated with Vancomycin-Resistant Enterococci Transmission

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Background. Vancomycin-resistant Enterococcus (VRE) is transmitted from person-to-person, most commonly by healthcare workers (HCW) whose hands or attire have become contaminated while interacting with an infected or colonized patient. Our group recently found that VRE colonized patients transmitted this pathogen to HCW's gloves or their own hands 15% of the time. This study aims to describe patient-level factors associated with higher risk of transmission of VRE to HCW's gloves or gloves and thus likely to subsequent HCW's hands.

Methods. We analyzed a prospective cohort that included 43 VRE-colonized patients and 215 HCW-patient interactions in medical or surgical intensive care units at the University of Maryland Medical Center. HCW's gloves and gloves were cultured for VRE after performing patient care and before donning. Univariate and multivariable logistic regression models, using generalized estimating equations to account for patient clustering, were used to estimate the odds ratios associated with specific patient-level factors (i.e., age, race, ethnicity, comorbidity scores). Multivariable models with and without stool VRE burden were created.

Results. Isolates of VRE displayed a high genetic diversity and were clustered into two main sub-clades (clades I and II). The rate of transmission was 8.6% (95% CI 6.2%–11.3%) in the initial cohort. In the final model, the adjusted OR for transmission was 4.7 (95% CI 2.1–10.6) if the patient had at least 2 episodes of VRE colonization within 15 days prior to transmission.

Conclusion. Patient-level factors associated with higher risk of VRE transmission to HCW's gloves or gloves included a history of VRE colonization within 15 days prior to transmission. These factors may facilitate transmission by either increasing VRE stool shedding or transmission to HCW's hands.

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1232. Phylogenomics ofEnterococcus faecium From South America: Revisiting Worldwide VRE Population Structure

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Objective. Understanding of the evolutionary history of VRE is crucial for better control and management of this nosocomial pathogen. This study is the first to determine the phylogenetic history of VRE isolates from South America, using whole-genome sequencing.

Methods. A total of 272 Enterococcus faecium isolates were selected from public health care facilities in seven Latin American countries. The genomes were sequenced by the Molecularecords of the complete genome of all isolates. The whole-genome sequences were then analyzed using the BioNumerics clustering software and the neighbor-joining method. The evolutionary relationships of the isolates were inferred using the Maximum likelihood method implemented in the PhyML v3.0 software. The antimicrobial resistance determinants were identified using the Resfinder software.

Results. The isolates were divided into two main sub-clades (clades I and II) which diverged approximately 894 years ago. The most common sub-clade I exhibited an average recombination of 34 Kbp, whereas clade II exhibited a 21 Kbp recombination. The most common antimicrobial resistance determinants were VanA (a ermC gene), VanB (a vanA gene), and the mecA gene.

Conclusion. This study presents the first phylogenetic analysis of VRE isolates from South America. The results indicate that the VRE population in South America has a long history of evolution and that the isolates are distributed between two main sub-clades (clades I and II) which diverged approximately 894 years ago. The results also suggest that the most common antimicrobial resistance determinants are VanA (a ermC gene), VanB (a vanA gene), and the mecA gene.

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