Title
The CDC SHIELD Orange County Project - Baseline Multi Drug-Resistant Organism (MDRO) Prevalence in a Southern California Region

Permalink
https://escholarship.org/uc/item/8cx6317x

Journal
Open Forum Infectious Diseases, 4(suppl_1)

ISSN
2328-8957

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Publication Date
2017-10-01

DOI
10.1093/ofid/ofx162.109

Peer reviewed
Background. MDROs can spread between hospitals, nursing homes (NH), and long-term acute care facilities (LTACs) via shared patients. SHIELD OC is a regional decolonization collaborative involving 38 of 104 countywide adult facilities identified by their high degree of direct and indirect patient sharing with one another. We report baseline MDRO prevalence in these facilities.

Methods. Adult patients in 38 facilities (17 hospitals, 18 NHs, 3 LTACs) underwent point-prevalence screening between September 2016–April 2017 for MRSA, VRE, ESBL, and CRE using nares, skin (axilla/groin), and peri-rectal swabs. In NHs and LTACs, residents were randomly selected until 50 sets of swabs were obtained. Seaboard hospitals involved all patients in contact precautions. An additional set of swabs were also performed for all LTAC admissions from November 2016–February 2017.

Results. The overall prevalence of any MDRO among patients was 64% (44%–88%) in NHs, 80% (range 72%–86%) in LTACs, and 64% (54–84%) in hospitals (contact precaution patients) (Table 1). Only 25%, 64%, and 81% of patients were already known to harbor an MDRO in NHs, LTACs, and hospitals, respectively. Known MDRO patients also harbored another MDRO 49%, 63%, and 34% of the time for NHs, LTACs, and hospitals. The overall MRSA point prevalence was 38% higher than the usual admission prevalence (65% higher for MRSA, 34% higher for VRE, 95% higher for ESBL, and 50% higher for CRE).

Conclusion. MDRO carriage in highly inter-connected NHs and LTACs was widespread. carriage in hospitalized patients (13%–46%) in LTACs, MRSA, VRE, and ESBL carriage far outnumbered CRE carriage. A history of MDRO was insensitive for identifying MDRO carriers, and many patients carried multiple MDROs. The extensive MDRO burden and transmission in long-term care settings suggests that regional MDRO prevention efforts must include MDRO control in long term care facilities.
1762. Complicated Staphylococcus aureus Bacteremia (SAB) Is Associated with Genetic Variation in GLS2
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Background. SAB is a serious, common infection. We used whole exome sequencing (WES) to examine the cumulative effect of coding variants in each gene on risk of complicated SAB in a discovery set of patients, and then evaluated the nominally significant genes in a replication set using custom-capture sequencing.

Methods. The discovery set comprised 84 complicated SAB cases (endocarditis or bone/joint infection) frequency-matched by age (in decades), sex, and bacterial clonal complex (CC5/30, CC8) to 84 uncomplicated SAB controls. All were white inpatients at Duke University. WES utilized Agilent SureSelect 72Mb capture kits, followed by sequencing on an Illumina HiSeq2000, alignment and base calling with a standard bioinformatics pipeline, and association testing with PRSIF R. The SKAT-O and ESPACTS packages were used for gene-based association tests and logistic regression models with Firth bias correction, respectively. Both were controlled for age, sex, and clonal complex as covariates. The replication set of 122 complicated SAB cases and 118 uncomplicated SAB controls was frequency matched by age, sex, and clonal complex. All were white Europeans collected by the Statens Serum Institute. An Agilent SureSelect 2Mb capture array captured genic sequence for 342 genes nominally associated with complicated SAB in discovery (SKAT-O P < 0.035). Sequencing and data analysis proceeded as for WES. A Bonferroni-corrected gene-based test P-value of 1.5 × 10^-4 determined significance in the replication set.

Results. One gene, GLS2, was significantly associated with complicated SAB in the replication set (P = 1.2 × 10^-4). The strongest single-variant association in all 342 genes was rs2657878 in GLS2 (p = 5 × 10^-10). This variant is strongly correlated with a missense variant (rs2657879, p = 4.4 × 10^-10), in which the minor allele (associated here with complicated SAB) has previously been shown to reduce circulating glutamine levels.

Conclusion. Comprehensive examination of the coding sequence for association with complicated SAB in a gene-based candidate gene screen, GLS2 is an interesting candidate for complicated SAB due to its role in regulating glutamine production, a key factor in activation of T-cell production.

Disclosures. V. Fowlner Jr, Pfizer, Novartis, Galderma, Novadigm, Durata, Debiopharm, Gentech, Alexion, and Achaogen, Medicines Co., Cempra, Takeda, Trius, MedImmune, Bayer, TheraVance, Cubist, Basilea, Affinergy, Janssen, xBiotech, Contrafect: Consultant, Consulting fee; NIH, Basilea, MedImmune, Cerexa/Forest, Actavis/Allergan, Pfizer, Advanced Liquid Logics, TheraVance, Novartis, Cubist/ Merck, and Sanofi: Research grants; Schering-Plough: Consulting fee; Trius: Research grant; Green Cross, Cubist, Cubist, Durata, TheraVance; Debiopharm: Consultant, Consulting fee; UpToDate: author on several chapters, Royalties

1763. Role of M Cells in Human Mucosal Immunity to Mycobacterium tuberculosi
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Background. Mycobacterium tuberculosis (Mt), the causative agent of tuberculosis (TB), is a bacterial pathogen that infects roughly one-third of the world’s population and causes 1-2 million deaths per year. The current paradigm is that Mycobacterium (Mt) by pathogen-elicited M cells could potentially serve as the basis for novel therapeutic targets against primary or reactivated tuberculosis (TB), is a bacterial pathogen that infects roughly one-third of the world’s population and causes 1-2 million deaths per year. The current paradigm is that Mt transcytosis by primary human tissue within 60-120 minutes. Using flow cytometry we find that Mt is first ingested by M cells and then after transcytosis, by tissue resident antigen-presenting cells. Explanted adenoids from 10 independent donors display a wide range of Mt uptake.

Conclusion. We conclude that Mt ESAT6 is necessary for Mt uptake by M cells and that binding and transcytosis require a host receptor. Because explanted adenoids display a wide range of Mt uptake, M cells mediated transcytosis may confer differential susceptibility to scrofula and disseminated disease. These findings are significant as M cells could potentially serve as the basis for novel therapeutic targets against Mt infection.

Disclosures. All authors: No reported disclosures.

1764. Investigating Immune Correlates of Protection to Tuberculosis Using an Ultra-Low Dose Infection in a Mouse Model
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