

O068

**Oral Session**

**Basic science: pathogenesis and epidemiology of Gram-positive bacteria**

**HOW MRSA BEHAVES INSIDE THE HOUSEHOLD: THE COMMUNITY-ONSET**

**STAPHYLOCOCCUS AUREUS HOUSEHOLD COHORT (COSAHC) STUDY, AUSTRALIA**

**C. Bennett**<sup>1</sup>, G. Coombs<sup>2</sup>, G. Wood<sup>3</sup>, E. Bogatyreva<sup>1</sup>, B. Howden<sup>4</sup>, P. Johnson<sup>4</sup>

<sup>1</sup>Epidemiology, Deakin University, Burwood, Australia ; <sup>2</sup>Microbiology and Infectious Diseases, Curtin University, Perth, Australia ; <sup>3</sup>Microbiology, Dorovitch Pathology, Heidelberg, Australia ; <sup>4</sup>Microbiology and Immunology, Austin Health, Melbourne, Australia

**OBJECTIVES:**

To further our understanding of *S. aureus* epidemiology in the community, and MRSA in particular, we:

- 1) Describe the prevalence and dissemination of *S. aureus* strains in 291 households with community-onset infections; and
- 2) Monitor changes to nasal colonisation for the index patient and their household contacts for up to 2 years.

**METHODS:** 291 patients with community-onset *S. aureus* infections were identified via specimens submitted to a community-based pathology service (Oct 2008-Dec 2010). All MRSA isolates and a frequency-matched random subset of methicillin sensitive *S. aureus* (MSSA) were followed up. Patients and household (HH) contacts provided nose and axilla swabs (a subset of 92 also provided throat and groin) and detailed demographic information, medical history, exposure history including occupation, sporting activities, pets, and interactions among HH members. All isolates were characterised using PFGE, MLST, *spa*, and *pvl*.

**RESULTS:** 729 people from 291 households participated (156 with initial MSSA infections, 135 with MRSA). *S. aureus* carriage was common (64% of index cases colonised in nose and/or axilla, and 46% of HH contacts). *S. aureus* nasal carriage for the total sample was 47% (10% MRSA, 37% MSSA). When carriage in the nose, throat, axilla and groin were compared for a subset of 92, 47% were colonised in the nose (17.4% nose only, 8.7% nose and groin, 13% nose and throat and 7.6% at all three sites). An additional 23% were identified who were colonised in the groin and/or throat but not the nose. However when we examined MRSA colonisation, participants colonised in the throat, axilla and/or groin were all also colonised in the nose (15). MRSA nasal colonisation was most common in households with an initial MRSA infection, with highest prevalence in index cases (29%), invariably with the same strain as the initial infection. Nasal colonisation rates diminish over the two year follow-up period for most MRSA strains, however some strains persisted in the index case and contacts (WA-MRSA1 [ST1], EMRSA15 [ST22]). Despite the high prevalence in clinical isolates, WSSP (ST30) and Queensland (ST93) clones were generally absent from nose swabs collected from these households over the two years following the infection.

**CONCLUSIONS:** We found high colonisation rates for nose and/or axilla for *S. aureus* (53%) and for MRSA (12%) but the patterns of colonisation are complex and vary by strain. Some clones persist in households for up to two years whilst others did not colonise the index case or other household members in the two year follow-up. This is particularly important as the strains not persisting tend to be the community *pvl* positive community MRSA strains and these strain differences in persistence and penetration in the household environment can be used to guide management of patients and their household contacts.