



## Novelty: Longitudinal Heritability of Colonization

To what extent do behaviors and genetics influence the composition of the skin microbiome?

- High temporal resolution (yearlong) measurement of *S. aureus* colonization of 3 body sites (nares, axilla, groin) across 692 individuals in 150 households
- Development of statistical definitions of longitudinal colonization
- Estimation of *S. aureus* SSTI and staphylococcal infection heritability and preventabilities across multiple study populations

Heritability and Preventability:  
Variance Components

Phenotypic variation of a trait such as height, hair color, or infection susceptibility can be broken down into variation attributable to additive genetic effects, dominance effects, and environmental effects, as well as their interactions:

$$V_p = V_{Ag} + V_E + V_{Ag} * V_E + r$$

Phenotypic Variance of a Population      Additive Genetic Variance      Environmental Variance      'GxE' Interactions

**Preventability ( $e^2$ ):** Portion of phenotypic variation attributable to a specific, shared environment across a subset of a population, such as a shared household, county, or neighborhood.

**G Heritability ( $h^2$ )** Portion of phenotypic variation describing additive genetic effects

**H Household Preventability** individuals sharing the same household environment

**C Couple Preventability:** cohabitating couples sharing the same environment

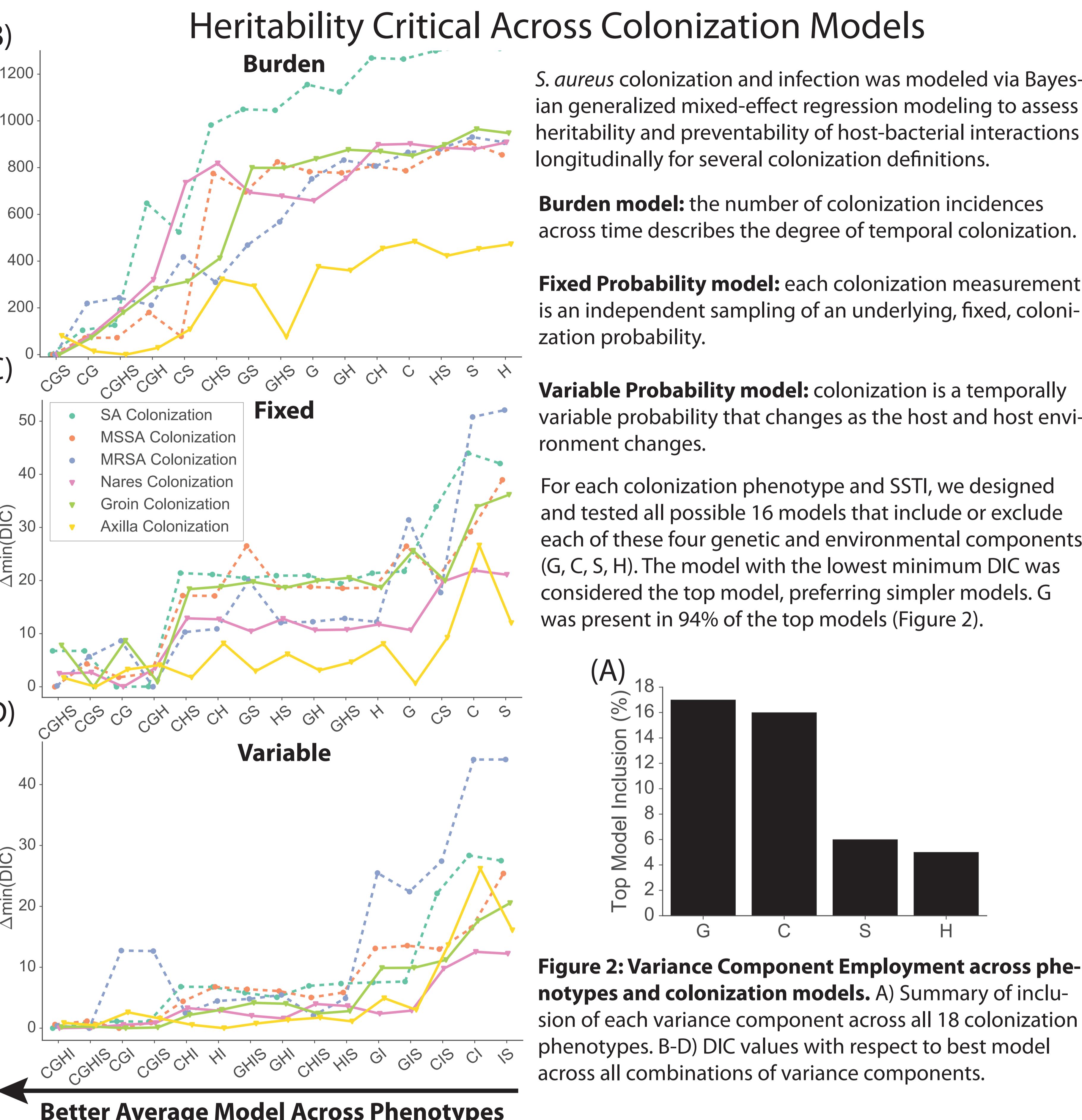
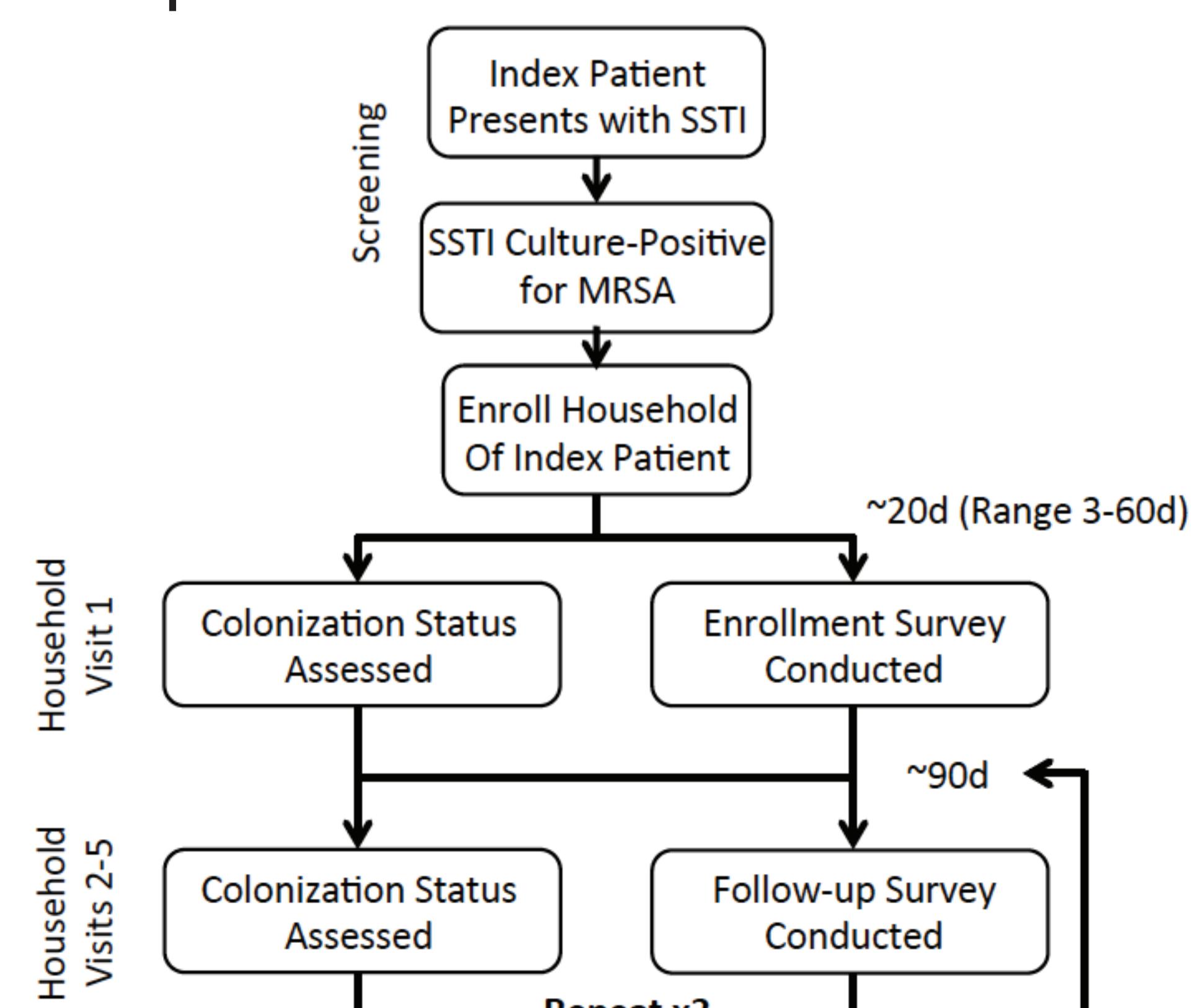
**S Sibling Preventability:** individuals sharing the same upbringing

**I Individual Preventability** the environment shared by the same person longitudinally

Study Population:  
MRSA SSTI Exposed Families in St. Louis

Figure 1: Colonization Assessment Work-flow.

Households were recruited from St. Louis Children's Hospital, Cardinal Glennon Children's Hospital, or a community pediatric practice in metropolitan St. Louis. 150 households with 692 individuals were enrolled from 2012-2015.

*S. aureus* SSTI Heritable Across Multiple Populations

Heritability of *S. aureus* SSTI's was estimated by modeling follow-up reports of SSTI's (total 257) across households. Staphylococcal infection was also measured from 156,133 family medical records over a 6 year period from the Truven MarketScan Database and modelled to provide a second estimate of heritability. SSTI was found to be highly heritable as judged by the top model identified in the model selection procedure (Figure 5).



Figure 4: Heritability Estimates Consistent Across St. Louis Households and Truven. Estimates were derived using MCMCglmm 'threshold' family models undergoing model selection.

## Colonization Exhibits High Degree of Memory

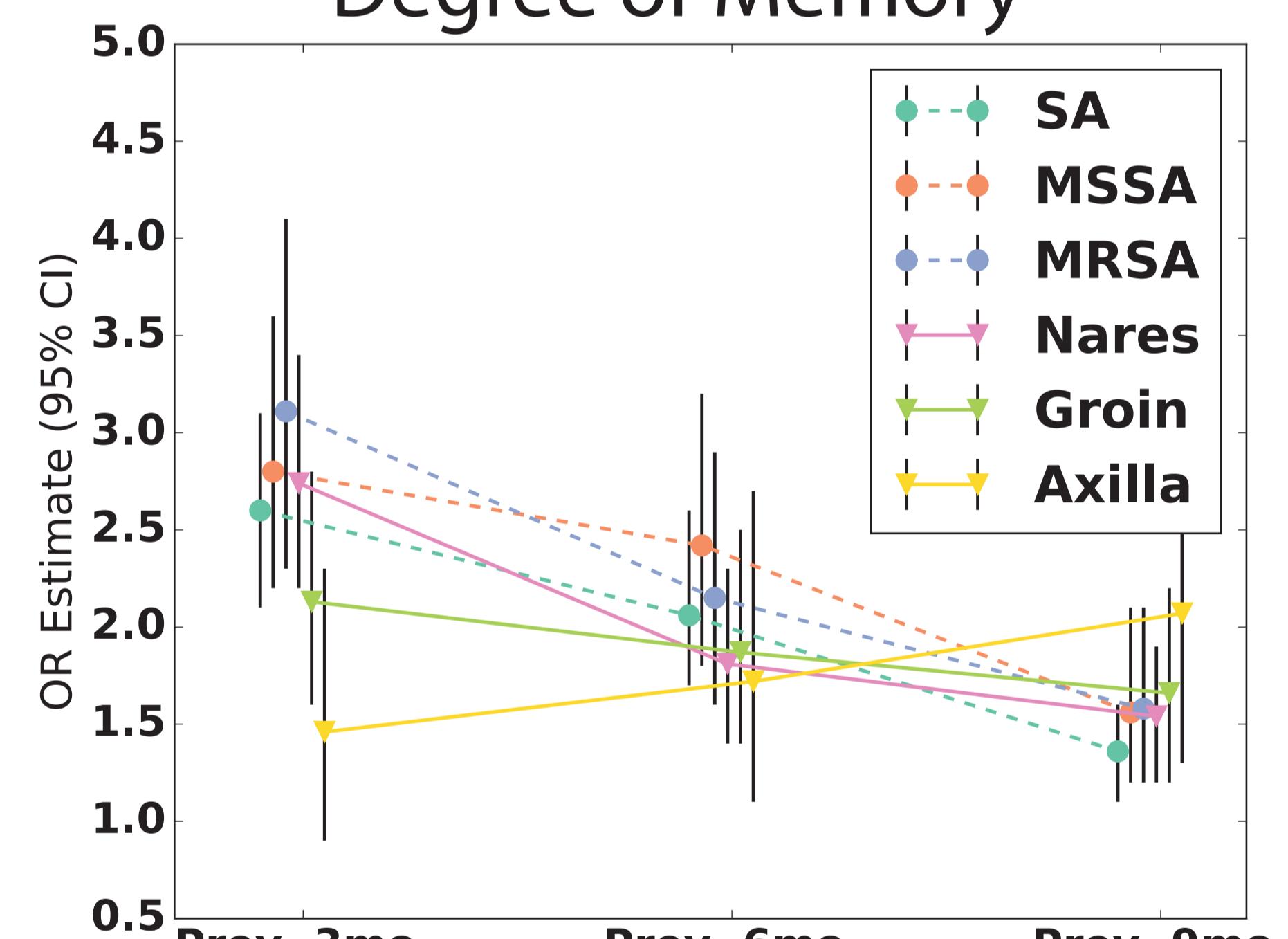
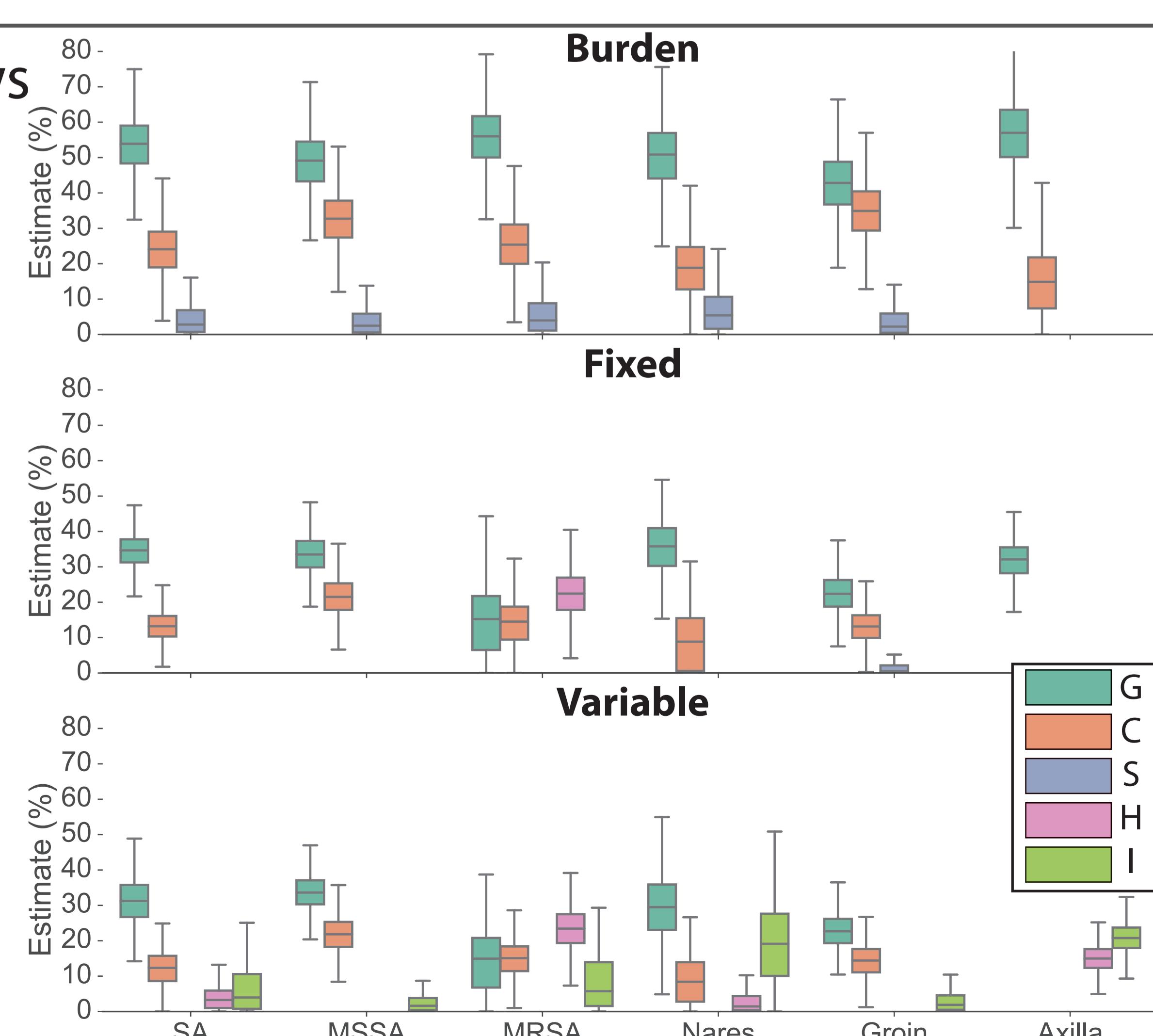


Figure 5: Colonization Memory Stabilizes by 6mo. Autoregressive colonization models were assembled across phenotypes including 3, 6, and 9mo. look back. Reported above are odds ratio (OR) estimates from a variable probability model ('ordinal' family) fit by MCMCglmm.

## MRSA Colonization Shows Significant Household Preventability

Compared to MSSA colonization, MRSA colonization shows a significant household effect in both fixed and variable probability models. This indicates that household hygiene and behaviors can be influenced to significantly reduce MRSA colonization.

Figure 3: Variance Component Estimates across phenotypes and colonization models. Top models were selected by DIC and simplicity. Abbreviations: *S. aureus* (SA).



## Major Conclusions

- The skin microbiome is critically shaped by additive genetic effects that stabilize the composition of this microbiome in everyday life.
- *S. aureus* SSTI is high and consistent (42%, 95% CI 12-67% and 47%, 42-52%) across two diverse study populations.
- Colonization by pathobionts like *S. aureus* is a resistance phenotype. Controlled exposure to *S. aureus* across the study population was necessary to properly measure colonization heritability.