

- Previous studies have identified host QTL associated with microbiome composition in the mouse gut
- Studies of mouse host and skin microbiome interactions are lacking

Methods

- 114 Mice from 30 Strains of the Collaborative Cross
- 16sRNA sequencing of dorsal skin swabs
- Statistical analysis done in R using Vegan and Aldex2 packages

Results

- Significantly different diversity between mouse strains
- Staphylococcus and Aerococcus abundance significantly different between high diversity and low diversity mice
- Significantly different microbiome composition between mouse strains (family level)
- Principle Component GWAS replicates a previously published QTL on Chr12, but at suggested significance level
- Principle component GWAS and Staphylococcus centred log-ratio abundance identifies a new QTL, Chr4 ~130Mbps

Conclusion

- The skin microbiome of healthy mice shows large variability between different mouse strains
- This may effect future studies investigating the skin microbiome and associations with different phenotypes, such as wound healing



Skin Microbiome Composition Varies Between Different Mouse Strains



