Background

* Mobile elements such as transposons and plasmids are important features of bacterial genomes.
  + They often contain resistance genes, which can compromise antimicrobial therapy
  + We seek to use *Enterococcus* as a test case to identify these transposons and plasmids.
* The goal is to create a tool to be integrated into NCBI’s Pathogen Detection pipeline

Methods

* 15,000 SRA submissions of *Enterococcus faecalis* and *Enterococcus faecium* were included
  + SKESA was used for assembly
  + AMRFinder was used to identify resistance genes
  + BLAST analysis
    - For presence of known plasmid and transposon signatures, using x cutoffs
  + gff search
    - Looking for annotations associated with mobile elements (terms such as repA, repB, repC, conjugative, and traA, traB, and traC)
  + Comparison to known plasmids
    - BLAST was done to known plasmid sequences, to ensure validity of results

Conclusion

* Combined with SKESA assemblies and AMRFinder outputs, the addition of mobile element analysis to the Pathogen Detection pipeline will be extremely useful in identifying potential transmissibility of resistance genes
  + *Enterococcus* provides a valuable test case for future roll out of this tool across all pathogens