# Best case scenario

WGS data

Clade of interest

🔴 MRCA (Most Resent Common Ancestor)
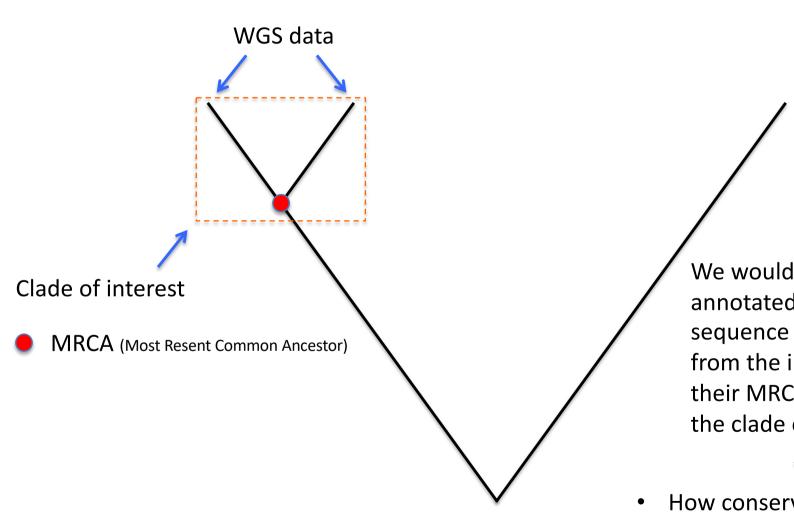
We would like to have well annotated whole genome sequence (WGS) datasets from the ingroup, with their MRCA being that of the clade of interest.

- How conserved are the CDS's?
- What's the number of introns?
- How long are the introns?