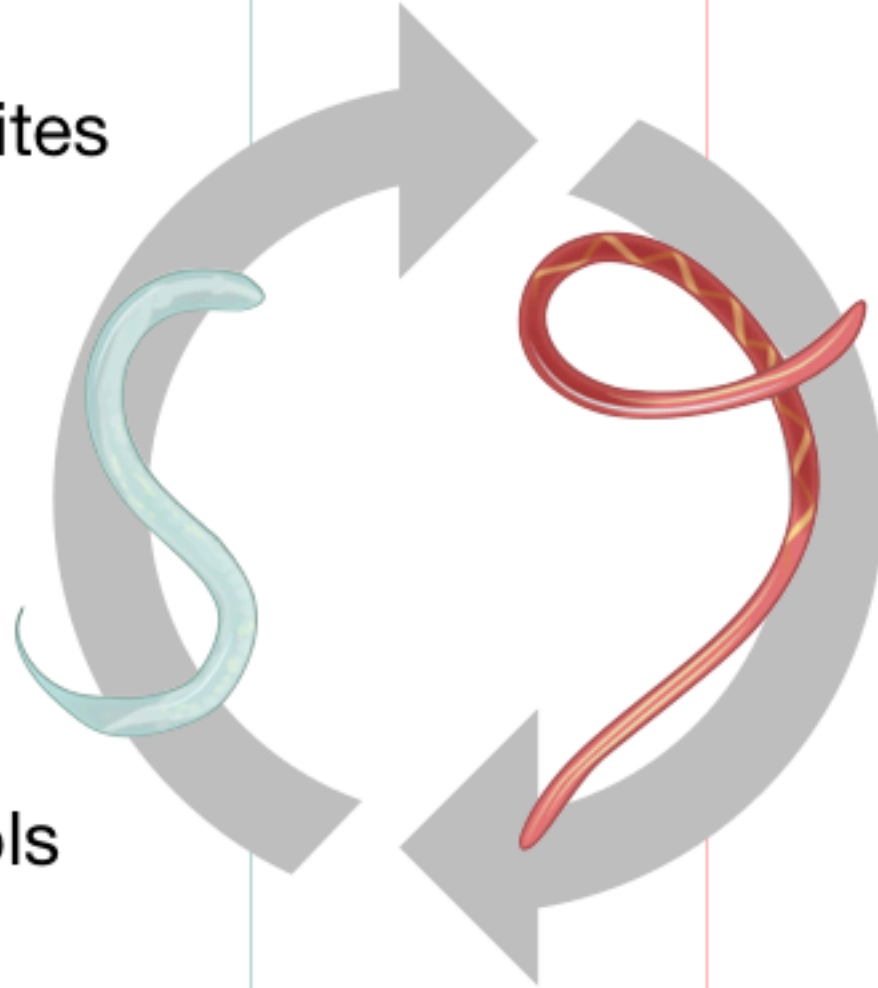**Caenorhabditis elegans**

1. Selfing hermaphrodites

2. Controlled genetic backgrounds

3. Mapped genome-wide variation

4. Genome-editing tools

5. High-throughput phenotyping

Haemonchus contortus

1. Parasitic mechanisms

2. Host-pathogen interactions

3. Large outbreeding populations

4. High genetic diversity

5. Anthelmintic selection and genomic crosses