**Review article = read x number of papers, methodical way of collecting information “ I reviewed 20 articles, this is where I got it from” set goals and objectives of the review. Need to use tables and figures… probably a summary table with sources in that. Think of it as a meta-analysis. Harvest info🡪 summary or analysis or look at trends-🡪 show some gaps 🡪 create table and figures**

**Literature Review= read paper, make some notes (like annotated bibliography)🡪 less organized and less focused. Just introduction to what is already in the literature**

**Think about scale and scope of review. Do not go too big. Don’t set the scope too large… narrow it to 20-25 papers. Get specific about objectives. Make table be harmonious with the objectives.**

**Looking for pattern and trends between all of the works… identify**

**Let my own situation dictate formatting**

**What is the scope? How wide a net am I casting? Don’t cast too wide.**

**Review paper should self-organize**

**Intro**

**Methods section that goes over how we selected articles.**

**Talk about what you systematically pull out**

**Make sense of that 🡪 pulled info, set an objective, how to organize and highlight patterns or gaps**

**IMRaD format**

**At least 12 articles cited in paper, 10 pages of writing**

**For a review article, generally about twice that… 20-25 papers for this class and thesis. Start with the idea of a couple dozen and go with that.**

**Ex: I want to review papers that reveals alleles under selection… less taxonomic**

**We all live downstream: applications from whole genome sequencing within adaptive loci**

**See how people are preserving specimens for high quality DNA extraction🡪 reach out to PacBio**

**Try gill, leg, and abdomen tissue for extraction**

**The rest can be in liquid nitrogen and store in -80 C**

**I think I will delete:**

**Forward Genetics (“Top-Down Approach”) 🡪 keep discussion brief**

Forward genetics is a popular strategy for finding the genetic basis of an already known phenotype. For example, the Tasmanian devil is a conservation case that many people use to study the methodology of conservation genomics. The Tasmanian devil was severely endangered due to a transmissible facial cancer, DFDT. Some individuals displayed a resistance to DFDT and even showed evidence of tumor regression. Using genome-wide association studies, they were able to locate the loci responsible for that resistant phenotype and use that information for implementing conservation strategies and potential treatment. Genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping and two tools often used in forward genetics approaches. GWAS is used mainly for extreme phenotypic variation and large effect loci.

GWAS = uses linkage disequilibrium. The strength and accuracy of the association study depends on phenotypic variance of the given population. This is determined by effect size and frequency in a sample. Therefore, GWAS is more efficient when studying large-effect loci. The need for detecting large-effect loci can be reduced by using very large sample size. This is typically not an option when working with conservation biology, as most populations are smaller or more likely on a downward trend.

Ex: mimicry supergene in swallowtail butterfly (*Papilio polytes)* 🡪used association mapping to find that a single gene *doublesex* is at the functional level of this adaptive phenotype.

QTL mapping= Not as used not and not suitable for fisheries = is another method in forward genetics that relates the adaptive trait to its genomic basis. Many times, RAD-seq is used. Restriction is “not obtaining enough recombinant offspring…due to the nature of many organisms”. Not very suitable for small sample sizes = ‘Beavis effect’. Cannot detect small and medium effect size.

Add examples of using the genome in forward genetics, and cases of conservation.

**General Adaptive Loci Info or nonspecific techniques:**

**Landscape Genomics**

**Genome Scan**

**Conservation**

Improving Bee Health