Course Syllabus

Fish/Biol 340: Introduction to Genetics and Molecular Ecology

An overview of the fundamentals of molecular genetics and the application of genetic techniques to problems in ecology, evolution and natural resource management

Autumn Quarter 2016, 5 Credits

Lectures: Tue, Th 10:30 - 11:50, FSH 107
Labs: Section A: Th, 1:30 - 4:20 Section B: F, 9:30 - 12:20 Section C: F, 1:30-4:20
Molecular Labs: FTR 113; Computer Labs: FSH 136

Course Description

Rationale

In the past few decades, molecular genetics has become one of the fastest growing fields in the life sciences. The application of molecular methods has spread to virtually all fields of modern biology, including ecology, conservation, breeding and natural resource management, leading to the establishment of a new discipline, Molecular Ecology. With the expansion of the application of molecular tools, it has become crucial that all biologists have a basic understanding of genetics and molecular biology, and the application of molecular tools to the detection of kin, the identification of populations, the reconstruction of phylogenetic relationships, and more recently,

to the understanding of local adaptation and evolution. Rather than providing an overview of classical genetics, the aim of the course is to provide an understanding of the genetic principles underpinning these applications, thus allowing an assessment of the potential and limitations of molecular approaches to specific questions in ecology, evolution and resource management.

The course will be important to students for the following main reasons:

- **Basic understanding**: The current ubiquity of molecular genetic studies in virtually all fields of biology requires some basic understanding of the genetic principles underpinning molecular methods. Continuing developments in molecular technology, statistical analyses and computer power will further widen potential applications. Thus, even if students do not envisage using genetics in their own research, some genetic knowledge will be necessary in almost any career track.
- **Practical application**: If molecular genetic methods are to be applied effectively in ecology, evolution and general biology, they have to be carefully chosen according to the ecological and biological circumstances, assumptions of the methods and the specific aims of the study. Furthermore, an understanding of the evolutionary dynamics of molecular markers in the context of the biological question of the research is a crucial prerequisite for the interpretation of genetic data. It is thus necessary that students have a good overview of available methods, their appropriate application and potential shortcomings.
- **Communication**: Many of the current problems in the application of genetic data are founded in conceptual misunderstandings between scientists applying genetic methods and the end users of their research (fisheries managers, breeders, forest managers, conservationists). It is therefore important that students are aware of these misunderstandings and are able to understand and explain genetic research.

Aim and Objectives

To provide students with a fundamental understanding of genetic principles underlying the application of molecular genetic techniques.

Students will be able:

- To understand basic principles of molecular genetics
- To apply such principles to ecological, environmental and conservation research
- To interpret genetic data in an applied context
- To communicate and disseminate the results of their research

Basic Approach

We will achieve the above aim and objectives by the following means

- **Lectures:** lectures will be the basic means of teaching in this class. These lectures will be much more useful if you interrupt me and ask questions if anything at all is unclear. Despite the large class size, I am aiming for a dialogue rather than a monologue. We will

use clickers to allow everybody to participate - please purchase and register Turning Point clickers early in the quarter. Most clicker questions will be graded, especially those at the beginning of class, when we will consider some questions from the previous lectures, and we will also work through some exam questions from previous years.

- **Textbook:** there is no required textbook for this class, but some are highly recommended (see Readings page). On the last slide of each lecture, I will provide a study guide with reference to specific sections in the textbook. These sections will be material that may be on the exam.
- **Primary literature:** There are links to primary literature in the field on the Readings page. All these papers are fairly brief and easy. Don't worry too much about details of the methods, but consider the problem, the approach the authors took, their general results and their interpretation of the results. You should read these papers - although they won't be on the exam per se, they may be used as examples in exam questions aiming at lecture material. Furthermore, they will help you deciding on style and detail needed for your project report.
- **Laboratories:** computer labs and molecular labs will be used to improve and deepen your understanding of concepts and procedures from lecture and textbook. (see also the lab section on the Modules page). In the computer laboratories we will use simulation programs to learn about genetic processes and analysis programs to analyze sample data sets. The molecular laboratories demonstrate some commonly used methods, and will be used for a lab project on the species identification of Alaskan mayflies.
- **Project Report**: In the molecular laboratories, we will conduct a study on the species identification of aquatic insect larvae in Alaskan streams. Previous research has shown that timing of insect emergence is tightly linked to the return timing of salmon, with earlier emerging insects in streams with early returning salmon. The question is whether this represents local adaptation in a single insect species, or whether different streams harbor different insect species. This is original research, and we don't know yet the answer - we may even detect new insect species. Students will submit a 2500 word (about 8-10 double spaced pages) project report on this project, which aims at integrating lecture material, laboratory experiments and literature and also will help to improve communication skills. The project report will be structured like a scientific paper (Introduction, Methods, Results, Discussion), and we will write sections for this report as the quarter progresses. These draft sections will be reviewed by class mates, using an online peer review system (SWORD, now Peerceptiv). We will start early with this process (the Introduction will be due in week 2), so you can submit your final report well before the final exam. See the Lab Project page for more details and specific instructions.

See the 'Pages' (Front Page) link for more information about the course, lecture notes and lab handouts. If there are general questions, please ask via 'Piazza' (link on the left). For personal questions only, send an e-mail (lhauser@uw.edu).

Strategies for success

The most important thing in this class is to be an active participant, and be prepared for lectures and laboratories. Make sure you stay up to date with the lecture material, and ask if anything is unclear. DO NOT leave revisions until the day before the exam. Also, make sure to read lab

handouts before lab, and submit your lab reports in time. Be aware that the project report (together with the drafts) counts for 35% of the class grade - you won't pass this class without submitting a final project report. Make sure to submit your drafts and reviews on time, and most importantly, keep on revising your drafts throughout the quarter.

Time table

W	D		L	Lecture Topic	Lab
1	Th	9/29	1	Introduction, Project	DNA extraction
2	Tu	10/4	2	DNA, replication	
	Th	10/6	3	PCR & sequencing	PCR, qPCR
3	Tu	10/11	4	Sequencing	
	Th	10/13	5	Sequencing, Report, Mendel	Electrophoresis
4	Tu	10/18	6	Mendel, Relatedness	
	Th	10/20	7	Hardy-Weinberg equilibrium	Relatedness
5	Tu	10/25	8	Fixation indices	
	Th	10/27	9	Trees	Project data analysis
6	Tu	11/1		**Mid term exam**	
	Th	11/3	10	Report, FST	Hardy-Weinberg
7	Tu	11/8	11	drift, Ne	
	Th	11/10	12	selection	**No lab - Veterans day**
8	Tu	11/15	13	migration	
	Th	11/17	14	phylogeography	Population genetic simulations
9	Tu	11/22	15	phylogeny	
	Th	11/24		**Thanksgiving**	
10	Tu	11/29	16	Gene Expression, GMO	
	Th	12/1		Functional genetics	Paper discussion
11	Tu	12/6	17	Genomics	
	Th	12/8	18	Genomics	Review
12	Mon	12/12		**Final exam**	

Lab Project:

Species identification of insect larvae in Alaskan streams with and without salmon

Aim

Most of the molecular labs (and one computer lab) in this class are part of a single project, the species identification of insect larvae in Alaska. This project has several aims

- To demonstrate the application of molecular markers to a very practical problem in management and
- To integrate laboratory procedures, lecture materials and literature into a single project
- To provide you with an opportunity to exercise your scientific communication skills by writing a project report.

Background

Alaskan sockeye salmon not only support one of the largest salmon fisheries in the world, but also affect the freshwater ecosystems they use for spawning. In particular, the annual return and subsequent death of millions of spawners supports entire food webs and brings marine derived nutrients into otherwise relatively oligotrophic (nutrient-poor) freshwater systems. Because of their sheer abundance, they also disturb freshwater habitat by digging nests. Aquatic insects, for example, are virtually absent

Fig 1: Sockeye salmon in Alaska. Photo: Jonny Armstrong

during the salmon spawning season in many creeks. Moore & Schindler (2008) showed that insects in streams with salmon emerged just before the return of salmon, while they were present in salmon-free creeks throughout the summer. In experiments, they showed that insects from salmon bearing creeks emerged early even in the absence of salmon. Because of the difficulties in identifying aquatic insect larvae to species, however, they could not determine whether there were different insect species in salmon and non-salmon streams, or if populations of the same species adapted to the presence of salmon by adjusting their emergence time. The question is of considerable evolutionary importance because adjustment of emergence timing to salmon return timing in a single insect species would represent extreme local adaptation and possibly incipient speciation.

There are early stages (nymphs) of many insect species in these streams, most notably, mayflies (Ephemeroptera), caddisflies (Trichoptera) and stoneflies (Plecoptera). We will concentrate in the mayfly genus *Cinygmula,* which

Fig 2: Mayfly nymph of the genus *Cinygmula.* Photo: Bob Henricks.

occurs in both salmon-bearing and salmon-free streams, but which cannot easily be identified to species.

Our approach is similar to the DNA barcode of life approach, which aims to identify all species by DNA sequences (see also Smith *et al.* 2008.pdf). We will extract DNA from insects, amplify and sequence the cytochrome oxidase I gene of the mitochondrial DNA and use phylogenetic methods to identify species. In addition, we will use databases to compare our insects to previously studied taxa. At this stage, we do not know the outcome of this research project, and we may even discover a new species!