

Quantitative Genetics and Breeding

Code: 101960
ECTS Credits: 6

Degree	Type	Year	Semester
2500890 Genetics	OB	3	1

Contact

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Use of Languages

Principal working language: catalan (cat)
Some groups entirely in English: No
Some groups entirely in Catalan: No
Some groups entirely in Spanish: No

Teachers

Marcelo Amills Eras
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Prerequisites

- To know the fundamental concepts of Mendelian and Population Genetics, Biostatistics and Genomics.
- To be able to read scientific texts in English.
- To be able to use the basic informatic tools.

Objectives and Contextualisation

Quantitative genetics addresses the genetic analysis of quantitative or complex traits, such as some of the involved in the evolution of species, the ones determining most of the productive traits in plants and animals, and also the predisposition to diseases. Its most applicative side has been, and continues to be, the genetic selection, that is made to improve plant and animal production.

There is a phenomenon clearly observable, the resemblance between relatives, for which Quantitative Genetics has developed a model based upon previous concepts of Population genetics. This model assumes that complex traits are determined by a large number of genes. By applying several statistical concepts it is possible to estimate a number of genetic parameters that will inform if the trait is susceptible to be selected. All this theory is based in classic papers from Fisher, Wright, Lush and others.

In addition to selection that is done within populations, crossing among populations is a strategy widely used to improve production traits. This course covers both the theoretical and applicative aspects of both methodological approaches, and also the population structures that make the genetic improvement more efficient.

On the other hand, in the last years there has been a growing interest regarding the identification of particular genes that determine quantitative or complex traits. Currently we have different molecular genetics tools that allow us to genotype a high number of SNP (single nucleotide polymorphism) loci that are markers for

quantitative trait loci (QTL) dispersed across the genome. This strategy of identification is known as "Genome wide association studies". This course covers the explanation of this strategy and another related strategy such as genomic prediction.

The specific learning objectives are:

- To understand a model explaining the variability of complex traits and become familiar with different methodologies used to measure the degree of resemblance between relatives.
- To develop evaluation methods of candidates to selection and to understand the factors determining selection response in different selection strategies.
- To know the implications of the different mating systems.
- To become familiar with the current methods for detecting genes affecting complex traits and their application in the context of medicine and genetic improvement.
- To know examples of improvement programs in animals and plants.

Competences

- Apply knowledge of theory to practice.
- Apply scientific method to problem solving.
- Describe and interpret the principles of the transmission of genetic information across generations.
- Design and interpret studies associating genetic polymorphisms and phenotypical characters to identify genetic variants that affect the phenotype, including those associated to pathologies and those that confer susceptibility to human illnesses or those of other species of interest.
- Design experiments and interpret the results.
- Measure and interpret the genetic variation in and between populations from a clinical, conservational and evolutionary perspective, and from that of the genetic improvement of animals and plants.
- Perceive the strategic, industrial and economic importance of genetics and genomics to life sciences, health and society.
- Produce, direct, execute and assess projects where knowledge of genetics or genomics is necessary.

Learning Outcomes

1. Apply knowledge of theory to practice.
2. Apply scientific method to problem solving.
3. Apply statistical technologies and methodologies to genotype/phenotype association studies.
4. Design experiments and interpret the results.
5. Enumerate and describe the forces that modulate genetic variation in populations in isolation or in conjunction.
6. Estimate the genetic parameters of a character from crossbreeding.
7. Evaluate the economic interest in genetically improving livestock species.
8. Evaluate the importance of having a map of correspondences between genotype and phenotype variation as the basis for selecting new livestock varieties and creating personalised drugs and foods.
9. Produce and assess genetic improvement projects.

Content

1. Quantitative Genetics and its application to the analysis of complex traits and the genetic selection.
2. The infinitesimal model in quantitative or complex traits: experimental and theoretical justification. Gene effects, breeding value, dominance and interaction deviations.
3. Partition of phenotypic variance: additive, dominance, interaction and environmental.
4. Estimation of variance components in ANOVA designs. Repeatability.
5. QTL detection: Genome wide association studies.
6. Pedigree analysis: coancestry and relationship. Molecular coancestry. Resemblance and genetic covariance between relatives.
7. Heritability and genetic correlations: estimation methods.
8. Genetic evaluation: selection indexes, BLUP (Best linear unbiased prediction) and genomic prediction.

9. Selection response and factors determining it.
10. Optimization of selection response: generation interval and annual response. Selection methods.
11. Observed response to selection. Experiments of divergent selection. Selection limits.
12. Inbreeding depression. Crossing: heterosis and complementarity. Crossing types.
13. Diffusion of the genetic progress.
14. Examples of breeding programs.

Methodology

The teaching methodology used along the learning process will be based upon the student's work, and the teacher will be in charge of helping the student in acquiring and interpreting the information related to the contents of the subject.

According to this methodology, the activities that are the following:

Lectures: Lectures will address the fundamental knowledge of the subject. Lectures will be interactive and will foment the dialog with and among students. They will be based on audiovisuals (mainly ppt presentations) that will be uploaded into Campus Virtual before the lectures. This activity will be complemented with classes devoted to solving problems, tutorial sessions and practical sessions in the computer laboratory.

Problems seminars: There will be 2 groups of about 30 students each. The seminars will consist of solving problems in an active manner. This will help the reasoning in the context of Quantitative Genetics and the understanding of the fundamental concepts of the subject. There will be problems solved in the classroom and others that the student will have to solve by him/her self. It is assumed that all the problems will be worked out by the students prior to the seminar.

Self learning and study group: In addition to solving problems in the classroom, groups of 2 different students will have to solve 6 exercises representing the most important items of the course.

Computer practices: Formally they are included in the course "Laboratori Integrat V", but they are a great support to better understand what has been taught in the lectures.

Tutorials: Concerted sessions to solve doubts discuss specific contents of the course.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Lectures	30	1.2	2, 1, 3, 7, 8, 4, 9, 5, 6
Problems lab	15	0.6	2, 4, 9, 5, 6
Type: Supervised			
Tutorials	5	0.2	2, 1, 3, 7, 8, 4, 9, 5, 6
Type: Autonomous			
Individual study and self learning	55	2.2	
Problem solving	42	1.68	2, 1, 4, 5, 6

Assessment

There will be a continuous assessment on a personal basis in the context of the programmed learning activities.

Two mid-term exams of 40 questions with 4 alternative answers will be made. The exams will contain questions on theory (32) and problems (8) and will last 90 minutes. The scores obtained in the 2 mid-term exams will represent 80% of the final mark (40% each).

In addition to that, aiming at verifying if the students make progresses on the understanding of the subject problems, the obligatory resolution of 6 exercises will be requested. These exercises will be made in groups of 2 different students and after assessment will represent 20% of the final mark.

The minimum mark to pass the course is 5 (on a maximum of 10). This final mark will be calculated weighing the scores of the two mid-term exams and the exercises. To compute this weighted average, each score must be at least 4. In the test exams, the students will have to attain a score of at least 4 in each of the questions of theory and problems.

In the case the student does not pass the subject with this continuous assessment, the students will be able to make a retake examination of one or two of the mid-term exams. To be eligible for the retake process, the student should have been previously evaluated in a set of activities equaling at least two thirds of the final score of the course or module. Thus, the student will be graded as "No Avaluable" if the weighthin of all conducted evaluation activities is less than 67% of the final score. This retake examination, similar to that described for the mid-term exams, will contain 40 questions if the two mid-term exams are recovered or 25 questions if only one mid-term exam needs to be recovered. For students that want to improve their marks, thesame applies. In this case, the score that will be taken into account for the final mark will be the one obtained in the last exam.

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Mid-term exam 1	40%	1.5	0.06	2, 1, 3, 7, 8, 4, 9, 5
Mid-term exam 2	40%	1.5	0.06	2, 1, 4, 5, 6
Problem solving in groups	20%	0	0	2, 1, 3, 7, 8, 4, 9, 5, 6
Recovery exam (theory and problems)	0	0	0	2, 1, 3, 8, 5, 6

Bibliography

General

Caballero A. 2017. *Genética Cuantitativa*. Síntesis, Madrid.

Falconer D.S., Mackay T.F.C. 2001. *Introducción a la Genética Cuantitativa*. Acribia, Zaragoza.

Lynch M., Walsh B. 1997. *Genetics and analysis of quantitative traits*. Sinauer, Sunderland.

Animals

Minvielle F. 1990. *Principes d'amélioration génétique des animaux domestiques*. INRA, Paris.

Nicholas F.W. 2003. *An introduction to Veterinary Genetics*. Blackwell Publishing, Oxford.

Piedrafita J. 1998. *Notas sobre teoría de mejora genética*. Col·lecció Materials, 49. Servei de Publicacions UAB, Bellaterra.

Plants

Acquaah G. 2012. *Principles of Plant Genetics and Breeding*, 2nd Ed. Wiley, Wiley-Blackwell.

Allard R.W. 1999. *Principles of plant breeding*. Wiley, New York.

Cubero J.I. 2013. *Introducción a la Mejora Genética Vegetal*. 3a ed. Mundi-Prensa, Madrid.

Kang M.S. 2002. *Quantitative genetics, genomics and plant breeding*. CABI, Wallingford.

Rodríguez Borruezo A. 2009. *A primer of Genetics and Plant Breeding*. UPV, Servicio de Publicación, Valencia.

Web sites

Genup: <http://www-personal.une.edu.au/~bkinghor/genup.htm>

PQGen: <https://sites.google.com/a/unizar.es/pqgen/>

PLINK: <http://pngu.mgh.harvard.edu/~purcell/plink/>

R: <http://cran.r-project.org/>