Advanced Animal Breeding			2013/2014

Codi: 42928
Crèdits: 6

Titulació	Tipus	Curs	Semestre
4313802 Genètica avançada/Advanced Genetics	OT	0	1

Professor de contacte

Nom: Josep Maria Folch Albareda

Correu electrònic: JosepMaria.Folch@uab.cat

Utilització d´idiomes

Llengua vehicular majoritària: anglès (eng)

Prerequisits

A basic understanding of molecular genetics, population genetics, quantitative genetics and statistics is required.

Objectius

The main goal of the course is to acquire the theoretical and practical knowledge about quantitative genetics and genomics applied to animal breeding. The specific objectives are:

• Learn the statistical methodology to understand the genetic evaluation of animals and plants both using the IBD and molecular coancestry approaches.

• Develop strategies to optimize genomic selection.

• Introduce the student to the Bayesian methodology.

• Learn new methods for the analysis of the genetic diversity of populations.

• Learn the methods used in the genome analysis of domestic animals.

• Introduce the student to the methods used to identify and analyze genes that contribute to the variability of complex traits in animals.

• Acquire bioinformatics skills for the genome analysis of domestic animals.

• Infer the processes that contributed to the formation of domestic animal populations from molecular data.

Competències

Genètica avançada/Advanced Genetics
- Demonstrate a mastery of genetic analysis as a transversal tool applicable to any field of genetics.
- Demonstrate responsibility in management of information and knowledge.
- Design and apply scientific methodology in resolving problems.
- Identify and propose scientific solution for problems related to genetic research at both molecular and organism levels and demonstrate an understanding of the complexity of living beings.
- Possess and understand knowledge that provides a basis or opportunity for originality in the development and/or application of ideas, often in a research context
- Student should possess an ability to learn that enables them to continue studying in a manner which is largely self-supervised or independent

- Students should know how to apply the knowledge they acquire and be capable of solving problems in new or little-known areas within broader contexts (or multidisciplinary contexts) related to their area of study
- Use and manage bibliographical information and other resources related to genetics and related fields.
- Use scientific terminology to argue the results of the research and show how to communicate in spoken and written English in an international setting.

Resultats d´aprenentatge

1. Apply bibliographical information on genetic improvement to the design of systems of improvement.
2. Apply methodology and knowledge acquired in the solution of practical problems of genetic improvement.
3. Demonstrate advanced knowledge of quantitative genetics and its application in genetic improvement.
4. Demonstrate responsibility in the management of information and knowledge and in the direction of groups and/or projects in multidisciplinary teams.
5. Demonstrate up-to-date knowledge of biocomputing methodology in the interest of genetic improvements.
6. Demonstrate up-to-date knowledge of the methodologies of molecular analysis of genetic variability and animal genomics.
7. Preparation and presentation of seminars
8. Student should possess an ability to learn that enables them to continue studying in a manner which is largely self-supervised or independent
9. Use scientific terminology to argue the results of the research and show how to communicate in spoken and written English in an international setting.
10. Write a report that considers the use of the methodology used in the module to resolve a specific problem
11. Write critical summaries about the taught seminars

Continguts

1. Quantitative Genetics

1.1. Fixed linear models.

1.2. Mixed linear models. Additive (IBD) relationship matrix. Additive (and dominance) models.

1.3. Variance component estimation (ML and ReML).

1.4. Genomic selection approaches: Genomic relationship matrix. Estimation of QTL effects. Mixed model equations including the genomic relationship.

1.5. A Bayesian approach to the mixed model equations.

2. Molecular genetics and genomics

2.1. New methods for the analysis of genetic variability applied to domestic animals. High-thoughput screening approaches. NGS sequencing platforms. SNP discovery. Genotyping platforms. Methods of genotyping. CNVs detection and analysis. Epigenetics protocols and applications. Metagenomics and the analysis of microbiomes.

2.2. Genomic analysis of domestic animals. Databases and tools for animal genomes data mining. Strategies for the identification of QTLs of interest in animal breeding. From the QTL to the gene and causal polymorphism. New genomic tools: eQTLs, RNA-Seq, selective sweeps with whole-genome sequences, systems biology. Discussion of case studies. Epigenetics and its role in shaping phenotypes in animals: Biological mechanisms, detection approaches, and analysis to identify functional genetic variation.

2.3. Genetic diversity of domesticated animals. Application of molecular tools to elucidate the domestication of livestock and dogs. Genetic consequences of the formation of breeds. Impact of artificial selection and modern

breeding on the genetic diversity of animal domesticates.

Metodologia

The activities of the course will include:

-Theoretical dissertations. In theses lectures the student will learn the fundamental concepts of the course. The theoretical dissertations will be complemented with applied examples and problems to be solved in class. In addition, the Quantitative Genetics part will be complemented with some computer programs. Students will be required to use their own laptops with the R program installed.

-Self-study - presentation of scientific articles. In the Molecular Genetics and Genomics section of the course, a recent scientific article will be assigned to the student for its critical reading and presentation in class.

-Self-study - work in group. Quizzes and exercises will be assigned to the students to be solved in groups. This work will require the use of bibliographic searches and bioinformatics resources.

-Tutorial class: tutorial sessions will be programmed for the resolution of questions and to guide students in the presentation of scientific articles and the resolution of exercises.

Activitats formatives

Títol	Hores	ECTS	Resultats d´aprenentatge
Tipus: Dirigides			
Presentation of scientific articles	5	0,2	1, 4, 7, 9
Theoretical dissertations	18	0,72	2, 3, 5, 6, 8
Tipus: Supervisades			
Self-study presentation of scientific articles	25	1	1, 7, 9
Self-study work in group	15	0,6	1, 2, 9, 10, 11
Tipus: Autònomes			
Self-study	80	3,2	1, 3, 5, 6, 8

Avaluació

For the first part, Quantitative genetics, students will be marked through a written exam (50%) and 3 assignments (50%).

For the second part, Molecular genetics and genomics, the assessment will be through a written exam (50%), the presentation of a scientific article (30%) and one assignment (20%).

Activitats d´avaluació

Títol	Pes	Hores	ECTS	Resultats d´aprenentatge
Molecular genetics and genomics assignment	0.1	0	0	2, 5, 6, 9, 10, 11
Molecular genetics and genomics exam	0.25	1	0,04	5, 6, 8

Presentation of a scientific article	0.15	5	0,2	1, 4, 9
Quantitative genetics assignments	0.25	0	0	2, 3, 5, 9, 10, 11
Quantitative genetics exam	0.25	1	0,04	3, 5, 8

Bibliografia

Books

Brown, T. A. (2002). Genomes. 2nd ed. Oxford, UK: BIOS Scientific Publishers, Ltd; 2

Galas DJ i Mc Cormack SJ. (Ed.) (2002). Genomic technologies. Present and Future. Caister Academic Press, Norfolk, UK

Lynch M., Walsh B. 1998. Genetics and analysis of quantitative traits. Sinnauer, Sunderland.

Mount DW. (2001) Bioinfomatics. Cold Spring Harbor Laboratory Press

Searle S.R. 1982. Matrix algebra useful for statistics. Wiley, NewYork.

Searle S.R., Casella G., McCulloch C.E. 1992. Variance components. Wiley, NewYork.

Strachan, Tom and Read, Andrew P. (1999). Human Molecular Genetics 2. 2nd ed. Oxford, UK: BIOS Scientific Publishers Ltd

Articles

Abasht B, Dekkers JC, Lamont SJ. (2006). Review of quantitative trait loci identified in the chicken. Poult Sci. Dec;85(12):2079-96.

Andersson L. (2001). Genetic dissection of phenotypic diversity in farm animals. Nat Rev Genet., 2: 130-138.

Andersson L, Georges M. Domestic-animal genomics: deciphering the genetics of complex traits. Nat Rev Genet. 2004 Mar;5(3):202-12.

Dekkers JC y Hospital F. (2002). The use of molecular genetics in the improvement of agricultural populations. Nat Rev Genet., 3: 22-32.

Fadiel A, Anidi I, Eichenbaum KD. (2005). Farm animal genomics and informatics: an update. Nucleic Acids Res. Nov 7;33(19):6308-18.

Georges M. (2007). Mapping, fine mapping, and molecular dissection of quantitative trait Loci in domestic animals. Annu Rev Genomics Hum Genet.; 8:131-62.

Goddard M.E. y Hayes B.J. (2009). Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nature Reviews Genetics, 10:381-391.

Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, Pilling D, Negrini R, Finlay EK, Jianlin H, GroeneveldE, Weigend S; GLOBALDIV Consortium. 2010. Genetic diversity in farm animals--a review. Anim Genet. 41 Suppl 1:6-31

Henderson C.R. 1973. Sire evaluation and genetic trends. Proc. of the Animal Breedinga and Genetic Symposium in Honor of Dr. J.L. Lush. ASAS y ADSA, Urbana-Champaign, IL, 10-41.

Henderson C.R. 1975. Comparison of alternative sire evaluation methods. J. Anim. Sci. 41, 760-770.

Henderson C.R. 1976. A simple method for computing the inverse of a numerator relationship matrix in prediction of breeding values. Biometrics 32, 69-83.

Henderson C.R., Kempthorne O., Searle S.R., von Krosigk C.M. 1959. The estimation of genetic and environmental trends from records subject to culling. Biometrics, 15, 192-218.

Hofer A. 1998. Variance component estimation in animal breeding: a review. J. Anim. Breed. Genet. 115, 247-265.

International Chicken Genome Sequencing Consortium. 2004. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature 432:695-716

Kennedy B.W., Sorensen D.A. 1989. Properties of mixed-model methods for prediction of genetic merit. En B.S. Weir, E.J. Eisen, M.M. Goodman, G. Namkoong (eds.) Proc. of the Second International Conference on Quantitative Genetics, pp 91-103. Sinauer, Sunderland.

Lenstra JA, Groeneveld LF, Eding H, Kantanen J, Williams JL, Taberlet P, Nicolazzi EL, Sölkner J, Simianer H, Ciani E, Garcia JF, Bruford MW, Ajmone-Marsan P, Weigend S. 2012. Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. Anim Genet. 43: 483-502.

Lindblad-Toh et al., (2005). Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature. 2005 Dec 8;438(7069):803-19.

Meuwissen T., Goddard M. 2010. Accurate prediction of genetic values for complex traits. Genetics, 185, 623-631.

Meuwissen T., Hayes B., Goddard M. 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics, 157, 1819-1829.

Meuwissen T., Hayes B., Goddard M. 2013. Accelerating improvement of livestock with genomic selection. Annu. Rev. Anim. Biosci., 1, 221-237.

Rockman MV, Kruglyak L. Genetics of global gene expression. Nat Rev Genet. 2006 Nov;7(11):862-72.

Rothschild MF, Hu ZL, Jiang Z. (2007). Advances in QTL mapping in pigs. Int J Biol Sci. Feb 10;3(3):192-7.

Toro M.A., García-Cortés L.A., Legarra A. 2011. A note on the rationale for estimating genealogical coancestry from molecular markers. Genet. Sel. Evol., 43, 27.

Wiener P, Wilkinson S. 2011. Deciphering the genetic basis of animal domestication. Proc Biol Sci. 278: 3161-70.

Internet resources

Books-NCBI: http://www.ncbi.nlm.nih.gov/books

U.S Pig Genome Mapping Site: www.animalgenome.org/pigs/

OMIA - Online Mendelian Inheritance in Animals: http://omia.angis.org.au/home/

The Bovine Genome Database: http://genomes.arc.georgetown.edu/drupal/bovine/