Sveučilište u Zagrebu Agronomski fakultet
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Molecular Diversity and Evolution (281933)

Nositelj kolegija

prof. dr. sc. Zlatko Šatović

Opis kolegija

This course is designed to offer students a fundamental understanding of the use of molecular markers in biodiversity studies. The course emphasizes a hands-on approach to molecular diversity studies by combining lecture presentations with computer exercises and discussion of original scientific literature. The lectures will cover the following topics: molecular marker systems, statistical methods in biodiversity studies, multivariate statistical techniques, basic concepts of population genetics, genetic structure, spatial and landscape genetics. Computer-based labs will give students the opportunity to get acquainted with commonly used molecular genetic software. Students will use real data from research projects carried out by the instructors of the course.

ECTS: **6.00**

E-učenje: **R1**

Sati nastave: 60
Predavanja: 40
Vježbe u praktikumu: 16
Seminar: 4

Izvođač predavanja

- prof. dr. sc. Zlatko Šatović
- prof. dr. sc. Ivan Pejić
- prof. dr. sc. Martina Grdiša

Izvođač vježbi

- prof. dr. sc. Martina Grdiša

Izvođač seminara

- prof. dr. sc. Martina Grdiša

Ocjenjivanje

Dovoljan (2): 60-69 %
Dobar (3): 70-79 %
Vrlo dobar (4): 80-89 %
Izvrstan (5): >90%

Vrsta kolegija

- Graduate studies / MS Courses taught in English (Izborni kolegij, 2. semestar, 1. godina)

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Opće kompetencije

The students acquire basic knowledge concerning the use of molecular markers in biodiversity studies.

Oblici nastave

- Lectures
  Lectures will provide a theoretical background and introduce basic concepts of molecular genetics, biometrics and population genetics.
- Practicum
  Practicum allows students the opportunity to gain practical experience in molecular data analysis by getting acquainted with commonly used molecular genetics software.
- Seminars
  Seminars are dedicated to practical examples from the original scientific literature and the discussion on suitability of the methods applied in the research.

Tjedni plan nastave

1. Introduction. Conducting a scientific investigation. L - Introduction to molecular diversity analysis; review of classical and molecular genetics. An example of scientific investigation: Genetic diversity and relationships of wild and cultivated olives.
2. Genetic markers: Randomly amplified molecular markers. Genetic markers: Sequence-based molecular markers. L - Morphological and molecular markers; isozymes; DNA-based molecular markers; Random Amplified Polymorphic DNA (RAPDs); Amplified Fragment Length Polymorphisms (AFLPs). Restriction Fragment Length Polymorphisms (RFLPs); microsatellite markers (Single-Sequence Repeats; SSRs); Single Nucleotide Polymorphisms (SNPs).
3. Practicum: DNA extraction and PCR. Practicum: AFLP. P - DNA extraction and Polymerase Chain Reaction (PCR). Genetic diversity analysis using AFLPs.
4. Practicum: Isolation of microsatellite markers. Practicum: Microsatellite markers. P - Isolation and characterization of polymorphic microsatellite loci. Genetic diversity analysis using microsatellite markers.
5. Descriptive statistics: Informativeness of a genetic marker. Descriptive statistics: Within-population diversity. L - Codominant and dominant marker data; informativeness of a genetic marker; genotype and allele frequencies; Polymorphism Information Content. Allelic richness; observed and expected heterozygosity; Hardy-Weinberg equilibrium (HWE); Shannon's information indeks.
6. Genetic distance measures: Among populations. L - Genetic distance between populations; fragment and allelic frequencies; distance measures based on evolutionary models; distance measures based on geometric considerations. Genetic distance between individuals; proportion of shared alleles distance; similarity coefficients for qualitative data; choice of an appropriate distance measure.
7. Practicum: Descriptive statistics. Practicum: Genetic distance measures. P - An example of calculation of informativeness and within-population diversity parameters using codominant and dominant marker dana. An example of calculation of genetic distance measures using codominant and dominant marker dana.
8. Multivariate methods: Introduction. Multivariate methods: Overview. L - Introduction to multivariate methods; features of multivariate data and multivariate distributions; classification of multivariate methods; dependence methods; interdependence methods. Factor analysis (FA); discriminant analysis (DA); canonical discriminant analysis (CDA); multidimensional scaling (MDS).
9. Multivariate methods: Classification methods. Multivariate methods: Ordination methods. L - Tree terminology; types of trees; UPGMA and related algorithms; Neighbour joining (NJ);

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unrooted and rooted trees; bootstrapping. Qualitative and quantitative data; principal component analysis (PCA); eigenvalues and eigenvectors; biplots; principal co-ordinate analysis (PCoA).

10. Seminar: Cluster analysis. Seminar: Principal Coordinate Analysis. S - An example of cluster analysis: Genetic relations among basil taxa. An example of PCoA: Genetic diversity of broomrape species.
11. Genetic structure: Wright's F-statistics. Genetic structure: Analysis of Molecular Variance. L - Testing Hardy-Weinberg equilibrium (HWE); Wright's F-statistics; Wahlund effect; fixation index; index of genetic differentiation; Weir and Cockerham's approach. Analysis of Molecular Variance (AMOVA) vs. Analysis of Variance (ANOVA); variance components; □-statistics; testing significance by permutations.
12. Genetic structure: A Bayesian approach. Spatial and landscape genetics: Introduction. L - Basic concepts of Bayesian statistics; linkage disequilibrium (LD); Bayesian model-based clustering method (STRUCTURE); Bayesian Analysis of Popultion Structure (BAPS). Spatial distribution of genetic variability; spatial autocorrelation; Moran's index; basic concepts of landscape genetics.
13. Spatial and landscape genetics: Basic approaches. Cultivar identification: Molecular tools for cultivar identification and pedigree reconstruction. L - Bayesian Analysis of Population Structure: Spatial clustering; TESS; Geneland; genetic barriers; Monmonier's algorithm; Wombling. Cultivar identification; genetic relationships among cultivars; pedigree analysis and reconstruction.
14. Cultivar identification: Genetic characterization of grape cultivars. Software overview. L - Molecular markers in grapes; genetic characterization of grape cultivars; genetic diversity and relationsips among Croatian grape cultivars. Overview of commonly used statistical programmes; input data; PowerMarker; FSTAT; GENEPOP; Phylip; AFLP-Surv; Micorsat; Arlequin; STRUCTURE; BAPS.
15. Seminar: Wright's F-statistics and AMOVA. Seminar: Bayesian model-based clustering method. S - An example of Wright's F-statistics and AMOVA: Genetic diversity and population structure of wild olives. An example of Bayesian model-based clustering method: Genetic structure and differentiation in hops.

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Obvezna literatura

1. Belaj, A., Muñoz-Diez, C., Baldoni, L., Porceddu, A., Barranco, D., Šatović, Z. 2007. Genetic Diversity and Population Structure of Wild Olives from the North-western Mediterranean Assessed by SSR Markers. Annals of Botany 100: 449–458
2. Belaj, A., Muñoz-Diez, C., Baldoni, L., Šatović, Z., Barranco, D. 2010. Genetic diversity and relationships of wild and cultivated olives at regional level in Spain. Sciencia Horticulturae 124(3): 323-330
3. Carović-Stanko, K., Liber, Z., Besendorfer, V., Javornik, B., Bohanec, B., Kolak, I., Šatović, Z. 2010. Genetic Relations Among Basil Taxa (Ocimum L.) Based on Molecular Markers, Nuclear DNA Content and Chromosome Number. Plant Systematics and Evolution 285(1-2): 13-22
4. de Vicente, M.C., López, C., Fulton, T. (eds.). 2004. Genetic diversity analysis with molecular marker data: Learning module. International Plant Genetic Resources Institute (IPGRI), Rome, Italy
5. Román, B., Hernandez, R., Pujadas-Salvá, A.J., Cubero, J.I., Rubiales, D., Šatović Z. (2007). Genetic diversity in two variants of Orobanche gracilis Sm. [var. gracilis and var. deludens (Beck) A. Pujadas] (Orobanchaceae) from different regions of Spain. Electronic Journal of Biotechnology 10 (2): 1-9
6. Safner, T., Miller, M.P., McRae, B.H., Fortin, M.-J., Manel, S. 2011. Comparison of Bayesian Clustering and Edge Detection Methods for Inferring Boundaries in Landscape Genetics. International journal of molecular sciences 12(2): 865-889
7. Sefc K.M., Pejić I., Maletić E., Thomas M.R., Lefort F. 2009. Microsatellite markers for grapevine: tools for cultivar identification and pedigree reconstruction. In: Grapevine Molecular Physiology & Biotechnology. K.A. Roubelakis-Angelakis editor, Kluwer Publishers, Amsterdam. Pp. 565-596
8. Štajner, N., Šatović, Z., Čerenak, A., Javornik, B. 2008. Genetic structure and differentiation in hop (Humulus lupulus L.) as inferred from microsatellites. Euphytica 161(1-2): 301-311
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10. Vaz Patto, M.C., Šatović, Z., Pêgo, S., Fevereiro, P. 2004. Assessing the genetic diversity of Portuguese maize germplasm using microsatellite markers. Euphytica 137: 63-72

Preporučena literatura

1. Frankham, R., Ballou, J.D., Briscoe, D.A. 2002. Introduction to Conservation Genetics. Cambridge University Press, Cambridge, UK
2. Gillespie, J.H. 1998. Population genetics: A concise guide. The Johns Hopkins University Press, Baltimore, MA, USA
3. Hartl, D.L., Clark, A.G. 2007. Principles of Population Genetics, Fourth Edition. Sinauer Associates, Inc., Sunderland, MA, USA
4. Karp, A., Isaac, P.G., Ingram, D.S. 1998. Molecular Tools for Screening Biodiversity: Plants and Animals. Chapman and Hall, London, UK
5. Weir, B.S. 1996. Genetic Data Analysis II: Methods for Discrete Population Genetic Data. Sinauer Associates, Inc., Sunderland, MA, USA

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