ISAGREED

Fundaments of genetic variability assessment in AnGR.

Modul no. 2: Conservation and Sustainable Use of Animal Genetic Resources

Luboš Vostrý

Czech University of Life Sciences,

Fakulty of Agrobiology, Food and Natural Resources

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

ISAGREED

Co-funded by
the European Union

Genetic variability

- Genetic variability is the variability of alleles and genotypes occurring in the studied population.

- Genetic polymorphism constitutes a significant part of intrapopulation genetic variability. ➡ Genetic variability is conditioned by the existence of genetic polymorphisms.

- Genetic polymorphisms change the evolutionary potential of populations due to their ability to respond to short-term selection pressures

Co-funded by the European Union

Factors affecting genetic variability

- Historic and current effective population size
- Bottle Neck

Co-funded by the European Union

Factors affecting genetic variability

- Historic and current effective population size
- Bottle Neck
- Breeding program
- Natural selection

Co-funded by the European Union

Factors affecting genetic variability

- Historic and current effective population size
- Bottle Neck
- Breeding program
- Natural selection
- Different intensity of mutations
- Imigration or Emigration between populations
- Interaction between the mentioned factors

ISAGREED
Co-funded by the European Union

Genetic variability

Origin and sources of genetic variability

- Genetic variability – the existence of multiple alleles of many genes
- Source of genetic diversity - gene polymorphism
- Creation of genetic variability - mutation x maintenance in the population = selection
- The advantage of polymorphic genes – they give rise to a large number of variants of different genotypes

Co-funded by the European Union

Genetic variability

Origin and sources of genetic variability

- Genetic variability – the existence of multiple alleles of many genes
- Source of genetic diversity - gene polymorphism
- Creation of genetic variability - mutation x maintenance in the population = selection
- The advantage of polymorphic genes – they give rise to a large number of variants of different genotypes

- Genetic variability is primarily due to the large amount of genetic information encoded in DNA molecules (deoxyribonucleic acid) present in the nuclei of cells in the form of chromosomes.

ISAGREED
Co-funded by the European Union

Methods of assessment of genetic diversity

- Pedigree analysis
  - Pedigree completeness
  - Probability of the identity by descent
  - Probability of gene origin
- Molecula genetic methods
  - Polymorfic information index
  - Observed and expected heterozygosity
  - Wright's fixation indexes

Co-funded by the European Union

Methods of assessment of genetic diversity

- Basic indicators of genetic diversity assessment include:
  - Inbreeding coefficient
  - Relatedness coefficinet
  - Effective population size

- These indicators can be used both in pedigree and molecular genetic methods

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

Co-funded by
the European Union

Pedigree analysis

Pedigree completeness

- Basice parameter for the study of genetic variability.
- Level of completeness of the pedigree determines the accuracy of the estimated following parameters.
- Statement:
  - Percentage representation of known ancestors in individual generations
  - The higher the values in most generations bring higher the accuracy of the analyzed coefficients.

ISAGREED

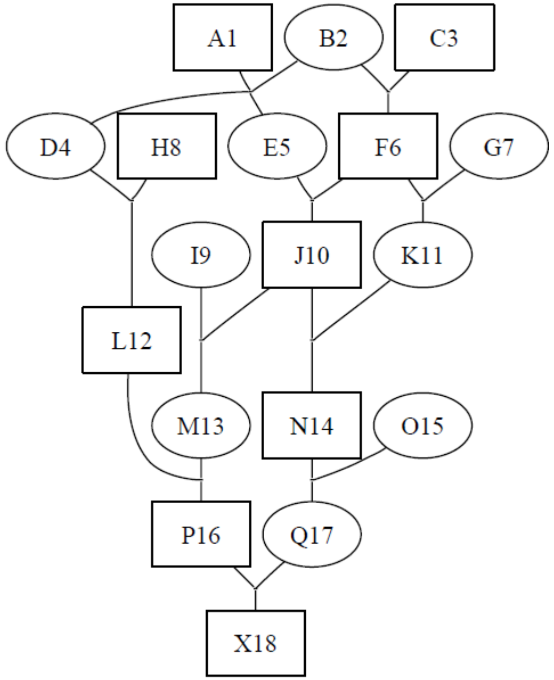
Co-funded by the European Union

Pedigree analysis

- Probability of the identity by descent
  - Individual inbreeding coefficient (F_X)
  - Relationship coefficient (R_{XY})
  - Effective populataion size (N_e)

Co-funded by the European Union

Inbreeding coefficient



Inbreeding coefficient (F_X) is the quantitative measue of inbreeding and it is defined as:

Malécot G (1948), as a probability that two homologue genes in a individual are identical by descent (autozygous).

Autozygosity is the state of the genotype where two alleles are (IBD).

Identity by status

A_1A_2

Identity by descents

A_3A_3

Co-funded by the European Union

Relationship coefficient (R_{XY}; Wright, 1922)

R_{XY} , after Wright, is the correlation between genetic (additive) values of two individuals (correlation between breeding values of two individuals).

$$R_{XY} = \frac{\sum[(1/2^{n})(1+F_{A})]}{\sqrt{(1+F_{X})(1+F_{Y})}}$$

$$R_{XY} = 2\ f_{XY} / \boxed{[(1+F_X)(1+F_Y)]^{0.5}}$$

Co-funded by
the European Union

Effektive population size

Effective population size – is the size of ideal (Wright-Fisher) population that will result in the same amount of genetic drift as in the actual population considered.

$$N_e = \frac{1}{2\Delta F} = \frac{4\,N_m + N_f}{N_m \times N_f}$$

N_m – number of mating sire
N_f – number of mating dam
ΔF – rate of inbreeding in one generations

Co-funded by the European Union

Pedigree analysis

- Probability of gene origin
  - Effective number of founders (f_e)
    - The number of equally contributin founders that would be expected to produce the same genetic diversity as in the populations under study.
  - Effective number of ancestors (f_a)
    - The minimum number of ancestors explaining the genetic diversity in population under study.
  - Founder genome equivalent (f_g)
    - The effective number of founders with the non.random loss of founder allels that would be expected to produce the same gentic diversity as in population under study

Co-funded by the European Union

Genetic diversity and founders

- Maximizing the preservation of genetic variability within a closed population is possible when an identical or larger number of offspring from each basic ancestor are mated.

- A large number of offspring minimizes the random loss of genetic variability that occurred in the generation of the basic ancestors.

- The equal representation of basic ancestors in offspring generations reinforces the genetic variability found in each basic ancestor that has not been eliminated from the progeny population if additional alleles of the basic ancestors are present in multiple individuals.

Co-funded by the European Union

Molecular genetic methods

Polymorfic information content

- It is presented as a criterion of variability (informability) of the analyzed loci
- It is mainly used in linkage disequilibrium analysis

Observed and expected hetorozygosity

- study intra-population variability and F_X status in the population
- based on the ratio of these two quantities, the loss/increase of variability in the population is evaluated

Wright's fixation indexes

F_{IS} – reduction in heterozygosit of an individual due to non-ranom mation within its subpopulation

F_{ST} – Fixation index, reduction in heterozygosity of a sub-population due to random gentic drift

F_{IT} – reduction in heterozygosit of an individual due to non-random maitng & population subdivision relative to totoal population, overal inbreeding coefficient

ISAGREED
Co-funded by the European Union

ISAGREED

Partners:

Slovak University of Agriculture Nitra

Mendel University in Brno

Siedlce University of Natural Sciences and Humanities

Czech University of Life Sciences Prague

Thank you for your attentions!

This presentation has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. *2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation - Inovácia obsahu a štruktúry študijných programov v oblasti manažmentu živočíšnych genetických a potravinových zdrojov s využitím digitalizácie"*. The European Commission support for the production of this presentation does not constitute an endorsement of the contents which reflects the views only of the authors, and the Commission cannot be held responsible for any use which may be made of the information contained therein.

Luboš Vostrý
vostry@af.czu.cz

ISAGREED

Co-funded by
the European Union