RESEARCH REGARDING THE NEW BIODIVERSITY INDICATORS IN GENETIC DIVERSITY OF THE REGION -COUNTRY HATEG

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Abstract

The present research started in June 2009 by identification of the species and breeds in the livestock of the 11 villages and 1 town existing in the Hatseg Land area. We use the modern genotyping tool for the study of zootechnical biodiversity- molecular biology tests- based on identification, amplification and characterization of nucleic acid, revolutionized the conservation of indigene animal genetic resources, gene assisted selection, pathology diagnostic and food traceability. The original Tipy Fix methods – internatinal patented by Prof.Brem - that were used in Romania (using for the first time in Romania by the researchers of CSCBA) to reveal DNA polymorphism are described as their applicability in species identification and meat traceability. Vulnerability of farm animal breeds is caused by the lack of interest apart breeders for one breed. In Hatseg land area the main mean of reducing biodiversity in farm animals is the crossbreeding. It was analysis the prion protein for scrapie resistance genotyping *as codon*-amino acid at codon 136, 154, 171 from 5 known haplotypes resulting PrP Genotype .In results of analysis in Hateg country 41 the probes present the arginine (R) at codon 171 of the prion protein who confers resistance to the structural change of prion scrapie.We presented biodiversity indicator for domestic animal in Hateg country,

Keywords: zootechnical biodiversity, Tipy Fix methods, prion protein, genotipying

Domestic animals most productive characters and performance-growth rate, resistance to disease is transmitted as quantitative traits with multiple genes. Relations between variants of different molecular markers and phenotypic expression of many quantitative characters have been demonstrated in many animal species. Markers-assisted selection MAS is the selection process we can use for future breeding nominated on genotypes identified by their association with neutral molecular markers. Specific analysis has been made in sheep, pigs and cattle. Based on these results we can achieve a study can be exploited by animal owners and OJRSA. Making a complex study of livestock biodiversity specific area of project monitoring domestic animals in the 12 villages: Baru Mare, Densuş, Pui, Rîu de Mori, Sarmisegetuza, Sălaşul de Sus, Santamaria Orlea, Toteşti, Bretea Română, Răchitova, General Berthlot. . Indicators of biodiversity components are classified according to their specific field orientation. For example:

- Domain of specific genetic diversity with two indicators:
  - Genetic diversity of domesticated animals
  - Ex situ collections of genetic material
- Domain of field-protected areas within three specific indicators:
  - Share of coverage of protected areas within
  - Duplication of biodiversity protected areas
  - Effective management of protected areas
- Domain of scope change the status of species
  - Red List Index

-Domain of species abundance and distribution range of species selected
  - Planet Index
  - Overall indicator of wild birds
- Domain of selected Biomass, the ecosystems and habitats
  - Forest cover and forest types

- Coverage of habitats

-Domain of the action-range of the invasive species

- Indicator of invasive species

- Domain for application of ecosystem integrity

-Index of ecosystem integrity

-Domain of the Biodiversity for food and medical

-Index of nutritional status of biodiversity

STATE OF KNOWLEDGE PROBLEM

The management of global animal genetic resources it was subject FAO since 1992 (FAO, 1992). The creation of improved breeds in terms of the breeder does not mean one is better adapted genofond biological needs of species, breeds and varieties of domestic animals. Therefore the development of the livestock must be implemented conservation national strategies of animal genetic resources. The animals farm there is a large reduction in genetic diversity through the disappearance of the total population (races, local sub-breeds) and the loss of genes on chromosomes in the bosom of a population following a stringent selection or genetic mutations. Half of the existing local breeds in Europe 90 years ago have disappeared. More than half of the 877 races that appear in the database of the European Association for Animal Production are threatened with extinction, in various forms.

MATERIAL and METHODS

The research team used the tools of classical and modern livestock biodiversity monitoring: assessment by means of direct analysis and molecular tests based on identification amplification and characterization of nucleic acids, which have revolutionized the conservation of animal genetic resources for assisted selection of genes, diagnostic pathology and food traceability. Original method Typi Fix - internationally patented from Prof.Brem - was first used by researchers in Romania CSCBA to discover DNA polymorphism and its applicability in the identification and traceability of meat species biodiversity. By this method one can follow the following aspects - determination of individual identity of animals in animal cells and finished products, control of paternal or maternal origin, detection of genes that influence the quality of raw material (meat and milk in our case) consangvinităţii determination, analysis determination of genetic variability, etc

REZULTS and DISCUTIONS

Determination of genetic diversity terrestrial livestock

This index is part of the component of biodiversity indicators proposed by the FAO, but was determined first in the region studied in this research. According to this indicator research team calculated Hateg country, taking into account the specific structure of each indicator, is the contact area, indicating key indicator of determining why, current status, presentation pointer

Contact area: state of components of biodiversity,
Key Indicator: Trends in genetic diversity
Reason determination the indicator:

More than 35 species of birds and mammals have been domesticated for use in agriculture and food production, there are now more than 7,000 recognized breeds.

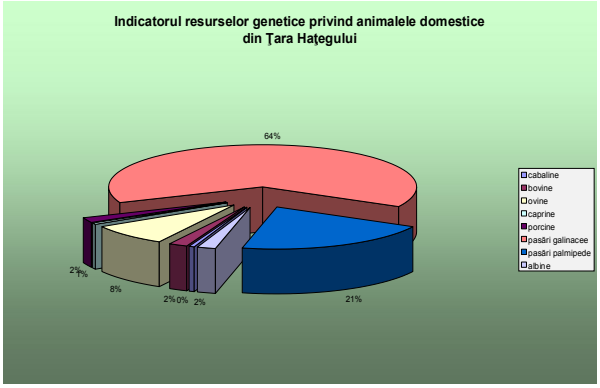
Retention of livestock is an important activity for ensuring human consumption. Livestock also provide a range of services which include ecosystems. Grazing stimulates plant growth removes excess biomass, and contribute to the conversion of nutrients and seed dispersal. Value of animal genetic resources goes far beyond their current use because they offer options for the future, a race and a population that is of little importance today can be extremely valuable in future

Current status:

In the absence of direct measures at the genetic status of populations and national races provide the best indication of trends in diversity. The indicator is made based on official data submitted by the specialized authorities in the project area (12 localities), which must be included in-Domestic Animal Information System (DAD-IS), maintained by the Food and Agriculture Organization of the United Nations (FAO). DAD-IS covers more than 30 species of domestic animals used for food and agriculture and includes data on population size and structure. DAD-IS data collection began in 1987 in Europe. Since 1996, DAD-IS was always open to all country with online. However, to achieve this indicator were regional information needs, which were collected from: Baru, Hateg, Santamaria

Orlea, Sălaşu de Sus, Pui, Toteşti, Densuş, Rau de Mori, General Berthlot, Rachitova, Sarmisegetuza

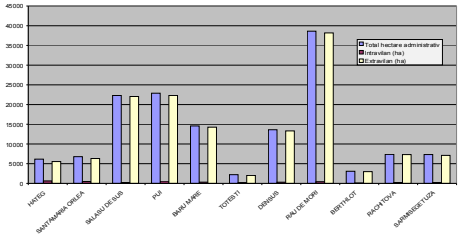
Indicator presentation:



Indicator of genetic diversity terrestrial livestock in Hateg Country

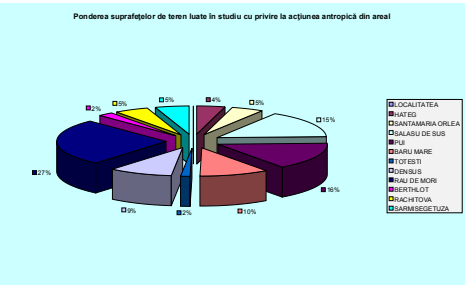
Interpretation of indicator:

Depending on the weight species (breeds) of domestic animals at regional level, the indicator shows the share of genetic biodiversity in the area under study. According to this indicator is observed that the relationship between avian species genetic resources is detrimental to domestic mammalian species.



Following the analysis of this indicator suggest reconsideration the high proportion of domestic animals, considering the load of animals per hectare, found in reiteration.

We believing that is very important to know zonal need to correlate the number of animals or hectares area for pasture. Also be exploited pastures in the area because these areas are not exploited by the existing potential



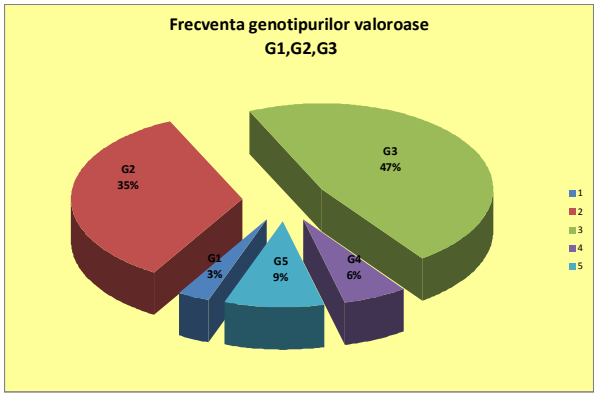
Monography on the species and the localities shows that the number of large animals (cattle, horses) varies by location, being influenced by the share of agricultural land.

In the farming farm animals is directly proportional to the agricultural area of the city, although according to the load per hectare should take this into account

In U.E. particular emphasis is placed on selecting genotypes resistant prion diseases, since 2003 has been initiated such a European program to define sequences characteristic amino-acids of scrappy. 15 genotypes were defined, which are considered reliable in diagnosing the disease, genetic mutations affecting the sequence 136, 154, 171. It was identified ARR / ARR genotype, which determines resistance to scrappy. The research team collected samples from animals in the area to identify valuable genotypes in order to preserve the gene bank. Prions are highly mobile proteins which normally are particularly worrisome because they are resistant to most forms of disinfection. They retain their power even after infestation normal sterilization processes, such as radiation, heat and ionization. In fact, prions are not destroyed even at temperatures higher than the boiling point. The testing laboratories of scrappy prion, is still some infections after total time of exposure to dry heat at a temperature of 360 degrees C. They are also impervious to freezing or drying. Many of the reasons they are so hard are undoubtedly related to their unusual composition. Prions do not have genetic material and consist entirely of protein. They are composed of a complex combination of thousands of amino acids. Since some sterilization processes - such as radiation ionozante - works by destroying the genetic material of microorganisms, prions can not be annihilated by these measures. Prions only attacks the nervous system, immune system it can affect their infectious power can not be destroyed by different modes of sterilization, freezing, drying, or high temperatures. Proteins form prions differs little from a normal protein. They produce a series of chain reactions that causes normal proteins to change shape. The analytical results of samples taken from the project area 41 samples had arginine (R) at codon 171 of prion protein, which confers resistance to structural changes of scrappy. Also present alanine (A) at codon 136 confers

resistance to structural changes associated with scrappy. The results of country analysis shows evidence Hateg 86 alanine (A) at codon 136 that confers resistance to scrappy prion structural changes. The presence of glutamine (Q) or histidine at codon 171 may send some characters of resistance to scrappy that was not detected in these samples. The analytical results from 90 samples the presence of glutamine (Q) in codon 171 of prion structural changes that confer resistance to scrappy prion. But classes G5-5 genotype 4 samples were detected with G4 genotype (ARR / VRQ) and 5 evidence-G5 (VRQ / ARQ), which are capable of prion disease. Owners were notified and they took the decision to isolate those animals and not use them for breeding.This way it is posible to make the selection of individuals with the most valuable genotypes resistant to diseases such

In November were collected other samples, which revealed other valuable genotypes in the Hateg country area.



Valuables genotypes frequency

The test results from 122 samples the presence of glutamine (Q) at codon 171 of prion resistance to scrappy prion structural changes. But G4-5 genotype classes were detected in 8 samples G4 genotype (ARR / VRQ) and 12 samples with-G5 (VRQ / ARQ), which are likely to prion disease. The parameters it was notified and they took the decision to isolate those animals and not use them for breeding. At the conclusion of the research we propose a new indicator, which integrates the health indicator of biodiversity-field.

Determination of genetic diversity of resistance to scrappy

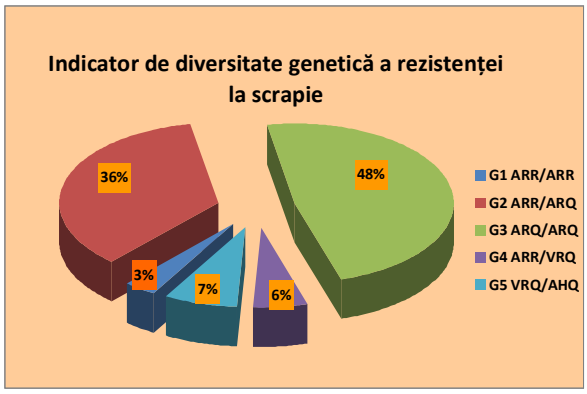
Contact area: state and trends of components of biodiversity,

Key Indicator: Trends in genetic diversity of resistance to scrapie

Reason determining indicator: selecting a core of prion disease-resistant animals

Current status: 188 sheep resistant to scrapie

Presentation indicator in the herd studied



Conclusion:

Preliminary studies shows the status of zoo technical biodiversity of studied area and have fired a warning about the shortage of domestic animals

- animal breeds have been identified specific area, such as Transylvania Pinzgau, identified animals is characterized by a high variability of traits due to lack of training and a systematic selection.
- in the village of Sălașu de Sus buffaloes number declined from 200 animals in 2006 to only 8 buffalo in 2009.
- determine livestock biodiversity using instrumental TypiFix ™ molecular genetic analysis system is a modern method, which has the advantage that is fast, single-step collection and preservation of biological tissue samples, can be a primary method of identification and conservation of animal biodiversity.

-were analyzed and identifiedλ valuable genotypes, which confer resistance to scrappy. In the future it is possible to create free herds by selecting animals. All genotypes identified will be introduced valuable gene bank.

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