

Genetic variability of wild and domesticated populations, genetics of conservation

Modul no. 2: Conservation and Sustainable Use of Animal Genetic Resources Tomáš Urban Mendelova univerzita v Brně Agronomická fakulta





European Union

Conservation Genomics at the Population Level

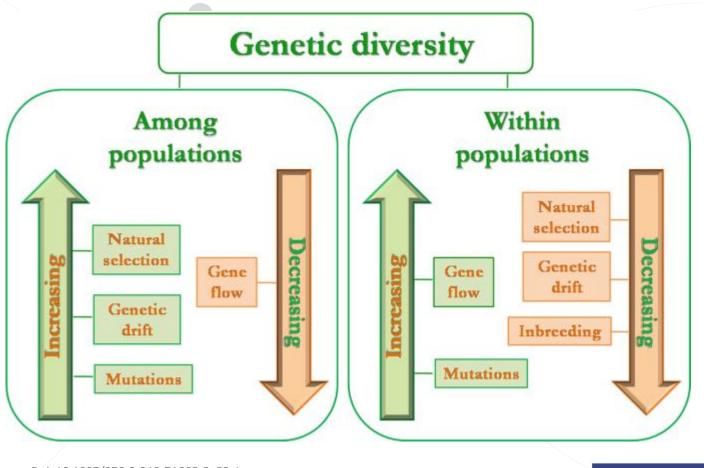
- Population level analysis of complete genomes is becoming a reality for many species.
- detecting adaptation and deleterious variation in populations and linking genetic variation to phenotypic variation.
- New technologies for data collection and application of genomic insights for biodiversity conservation will be explored. The likely impact of genomic approaches on conservation efforts over the next decade will be discussed.
- Conservation genomics/genetics includ a variety of exciting topics:
 - Application of conservation genomics to threatened species
 - Detecting adaptation in populations
 - Application of eDNA approaches
 - Linking genotypes to phenotypes for conservation
 - Detecting and understanding the effects of deleterious variation
 - Translating research into conservation efforts



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Topics of genetic diversity

Genetic diversity is a fundamental source of biodiversity which has been defined by different authors as "any measure that quantifies the magnitude of genetic variability within a population" (Hughes et al. 2008) or "the very makeup of the variation of organisms and species on Earth" (Elliott 2002). According to Ennos et al. (2000), *genetic diversity* presents "the range and sum of genetic variation within a population or populations," where the term *diversity*, which simply means the state of displaying dissimilarities, differences, or variety, has acquired an extended meaning which signifies the *sum of the* variation.



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IUCN kategorie

International Union for Conservation of Nature and Natural Resources

- IUCN List of Threatened Fauna and Flora, published every two years by the International Union for Conservation of Nature (IUCN).
- Vurnelable
 - 10% Extinction in 100 years
 - Endargened
 - 20% Extinction in 20 years or 5 generations
- Criticaly endargened
 - 50% P Extinction within 10 years or 3 generations



Our work

Data, analysis, convening and action.

Open Project Portal -



THEMES

- Biodiversity
- Business, finance and economics
- Climate change
- Freshwater and water security
- Governance law and rights
- Nature-based Solutions
- Ocean and coasts
- Protected areas and land use





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I S A G R E E

IUCN Red List



Migratory Monarch Butterfly (Endangered, A2ab ver 3.1)

What is The IUCN Red List?

Established in 1964, **The International Union for Conservation of Nature's Red List of Threatened Species** has evolved to become the world's most comprehensive information source on the global conservation status of animal, fungi and plant species.

The IUCN Red List is a critical indicator of the health of the world's biodiversity. Far more than a list of species and their status, it is a powerful tool to inform and catalyze action for biodiversity conservation and policy change, critical to protecting the natural resources we need to survive. It provides information about range, population size, habitat and ecology, use and/or trade, threats, and conservation actions that will help inform necessary conservation decisions.

Learn more about The IUCN Red List

More than 41,000 species are threatened with extinction

That is still 28% of all assessed species.

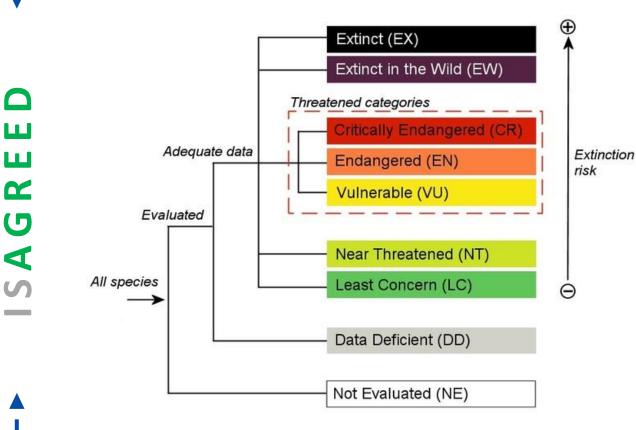


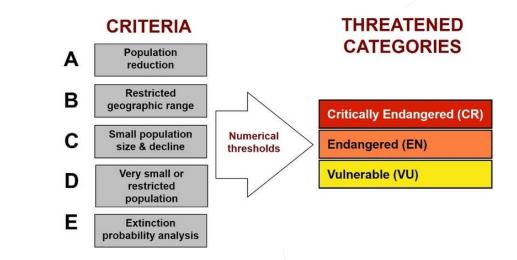




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The degree of threat according to the IUCN criteria is determined by several categories

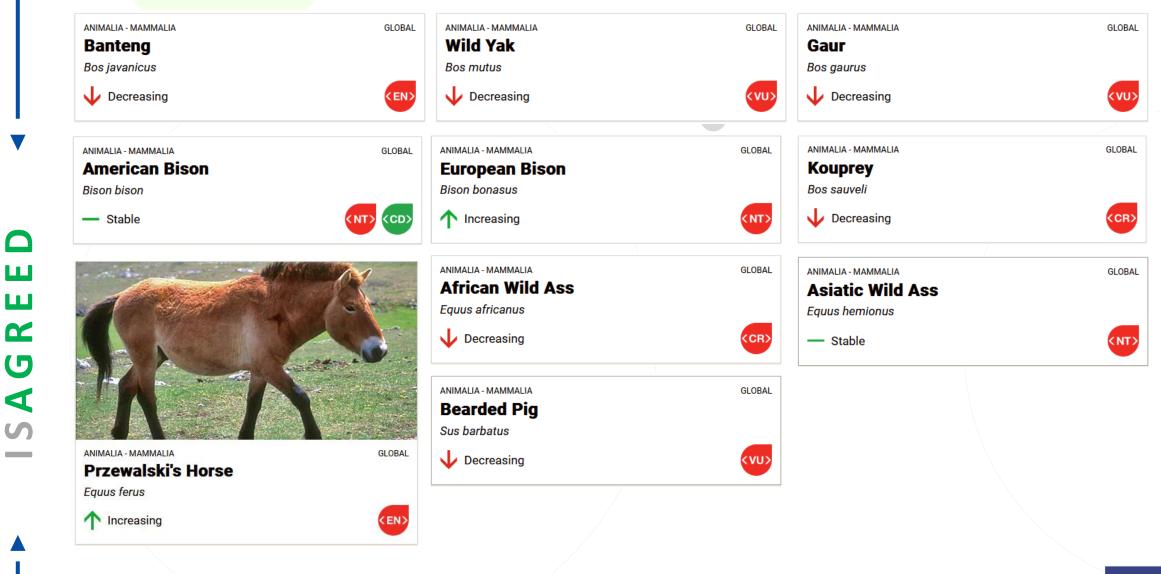




Species are assessed against five criteria (see below) based on geographic range, population size and population decline/increase, in addition to extinction probability analyses. These criteria determine which category is most appropriate for the species.



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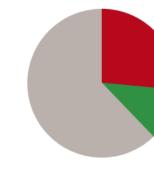


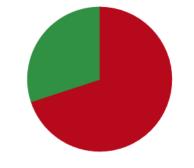
Domestic Animal Diversity Information System (DAD-IS)

 Domestic Animal Diversity Information System (DAD-IS) | Food and Agriculture Organization of the United Nations (fao.org)

Risk status of all non-extinct local Risk status of local breeds with breeds in a selected region/country

valid information on population size





SDG Region: * DAD-IS Region: * Country: All Percentage of local breeds with unknown risk status: 62,17%

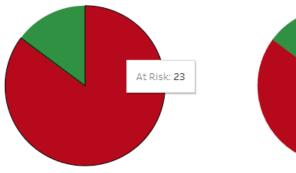
Totals:

Not at risk: 803 At risk: 1871 Unknown risk: 4 394 Proportion of countries with at least partial reporting: 41,30%

SDG Indicator 2.5.2

Regional aggregation not permissible due to less than 50% of countries reporting

Risk status of all non-extinct local Risk status of local breeds with breeds in a selected valid information on population region/country size





SDG Region: Northern America (M49) and Europe (M49) DAD-IS Region: Europe and the Caucasus Country: Czechia Percentage of local breeds with unknown risk status: 0%

Totals:

85%

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Not at risk: 4 At risk: 23 Unknown risk: 0 Proportion of countries with at least partial reporting: 100,0%

SDG Indicator 2.5.2



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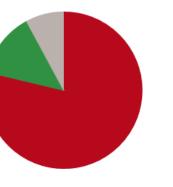
Last update: 03/02/2023

breeds in a selected region/country

Risk status of all non-extinct local Risk status of local breeds with valid information on population size

Risk status of all non-extinct local Risk status of local breeds with breeds in a selected region/country

valid information on population size





SDG Region: Northern America (M49) and Europe (M49) DAD-IS Region: Europe and the Caucasus Country: Poland Percentage of local breeds with unknown risk status: 7,874%

Totals: Not at risk: 17 At risk: 100 Unknown risk: 10 Proportion of countries with at least partial reporting: 100,0%

SDG Indicator 2.5.2 85%

Last update: 03/02/2023

SDG Region: Northern America (M49) and Europe (M49) DAD-IS Region: Europe and the Caucasus Country: Slovakia Percentage of local breeds with unknown risk status: 25,00%

Totals: Not at risk: 2 At risk: 16

Unknown risk: 6 Proportion of countries with at least partial reporting: 100,0%

SDG Indicator 2.5.2 89%

Last update: 03/02/2023





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Genetic variation in wild and domesticated populations

- Genetic diversity is the variation of heritable characteristics present in a population of one species and serves as a way for populations to adapt to changing environments. It is applicable to wild populations as well as domesticated strains, which generally have lower levels of diversity.
 - The genetic variability of wild and domesticated populations is an important topic in biology.
 - Domestication is the process by which humans have modified the characteristics of wild organisms for use in agriculture, industry, or companionship.
 - Domestication has led to a reduction in genetic diversity compared to their wild counterparts





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- Geneticists have identified low genetic variability as a concern in wild and captive populations of many species, including cheetah, Californian Channel Island fox (Urocyon littoralis), Newfoundland black bear (Ursus americanus), Gir Forest Asian lions (Panthera leo), southern koalas (Phascolarctus cinereus), European bison (Bison bonasus) and others.
- This information can be used for various conservation and management applications, including determining population units, maintaining the maximum genetic diversity in captive or wild breeding populations, and predicting adaptive responses to environmental change.





The crucial role of genome-wide genetic variation in conservation

 The unprecedented rate of extinction calls for efficient use of genetics to help conserve biodiversity.

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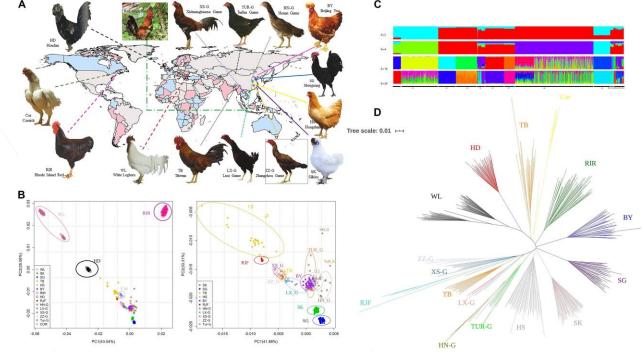
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 Several recent genomic and simulation-based studies have argued that the field of conservation biology has placed too much focus on conserving genome-wide genetic variation, and that the field should instead focus on managing the subset of functional genetic variation that is thought to affect fitness.



(A) Chicken breeds with distinct phenotypes and geographical information (Photos came from poultry genetic resources in china). (B) Principal component analysis revealing genetic differentiation of 15 populations using SNP data. Breeds which are labeled, their names are mentioned in the main text; The Commercial breeds are denoted by triangle symbols, The Chinese indigenous breeds are displayed as dots, RJFs are displayed as plus sign, Europe local breed is denoted by squares, and the rest populations are marked as asterisks; PCA was performed on the whole population, plotting the first and the second dimension revealed PCA of 15 populations. (C) The admixture plot for breeds analyzed based on different number of assumed ancestors (K). (D) Neighbor-joining tree constructed using PHYLIP.

https://doi.org/10.3389/fgene.2020.543294





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Role of Functional Genetic Variation in Conservation

- Focusing conservation efforts on presumably functional genetic variation will only be feasible occasionally, often misleading, and counterproductive when prioritized over genome-wide genetic variation.
- Given the increasing rate of habitat loss and other environmental changes, failure to recognize the detrimental effects of lost genome-wide genetic variation on long-term population viability will only worsen the biodiversity crisis.





Sustainability of Wild Populations: A Conservation Genetics Perspective

- genetics helps to understand and reduce the risk of extinction of populations and species.
- It is important to maintain genetic diversity and the health of populations in the wild to sustain healthy ecosystems.
- Genetic diversity is the range of different heritable traits within a species.
- The loss of biodiversity is a global problem, and that human population growth is having a major impact on this loss.
- If we keep taking away the natural habitats of animals, the best conservation genetic approaches will not prevent the extinction of species.







Thank you for your attention!

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