Objectives, Criteria and Methods for Priority Setting in Conservation of Animal Genetic Resources

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Introduction

- The *Global Plan of Action* for Animal Genetic Resources was adopted by FAO members in 2007
  - internationally agreed framework for the management of animal genetic resources
- 4 Strategic Priority Areas
  - Inventory, monitoring and characterization
  - Sustainable use
  - Conservation
  - Policy, institutions and capacity building

Why is Conservation Important?

Livestock genetic diversity is decreasing
- ~20% of breeds at risk
- status of many others unknown

- Genetic diversity is necessary for adaptation
  - changing environments
    - production systems
    - climate
  - changing markets
- Genetic diversity is necessary for continued genetic improvement
- Cultural and historical reasons

Why is prioritization necessary?

Conservation of all breeds impossible
- Many breeds and limited financial resources
  - Food security more important in developing countries
  - Short-term economic return more important in industrialized countries

- Wholesale conservation not scientifically justified
  - Breed may have no apparent short- or long-term value
  - Breeds may be effectively the same genetically

Factors influencing conservation priority

- Risk of extinction
  - Breed Demographics
    - number and distribution
- Genetic variability (seek to maximize)
  - between and within breeds
  - molecular and quantitative genetic
- Phenotypic performance
  - genetic merit for productivity

Factors influencing conservation priority

- Unique traits
  - adaptive traits
  - interaction with environment
- Historical and cultural importance
- Practical considerations
  - species and ease of conservation
  - chance for success

Prioritization

- Decision support may be needed
  - many factors to consider simultaneously
- Objective approaches have been proposed
  - use of genetic markers to measure diversity
- Goals of presentation
  - review methods
    - particular those incorporating molecular genetics
  - suggest and discuss needs for future

Prioritization without Molecular Data

Use single criterion

- Risk of extinction

Multivariate statistical methods

- Correspondence or principal components analysis
  - reduce many variables to smaller number
- Cluster analysis
  - assign breeds to similar groups
  - choose single breed from each group
- Multivariate Index
  - assign different weights to characteristics of breeds
- Choice models (Zander and Drucker 2008)
- Geographical approaches
  - particularly valuable when no formal “breeds” exist

Prioritization with Molecular Data

- Molecular data is used to measure breed diversity and relationships among breeds
  - ↑ diversity = ↑ priority
  - ↑ distinctiveness = ↑ priority

Weitzman Method

- Among first approaches to objective prioritization for conservation
  - developed for wildlife species
- Standard for comparison of methods
- Considers diversity and extinction probability
  - ↑ diversity = ↑ priority
  - ↑ risk = ↑ priority

Weitzman's Conservation Potential

$$CP_i = -m_i z_i$$

- CP_i is the conservation potential of species *i*
  - basis for priortization
- m_i is the marginal contribution to diversity of species *i*
- z_i is the risk of extinction of species *i*
- CP_i is the amount of diversity maintained if breed *i* were made completely safe
  - z_i >>> 0 through some intervention

Weitzman's Diversity

$$m_i = V(S) - V(S \mid i)$$

- m_i is marginal diversity of species *i*
- V(S) is diversity of full set of species
- V(S | i) is diversity of set without species *i*
- m_i is maximized when species I is the most distant genetically from the set (S | i)
  - genetic distance
    - estimated with genetic markers
  - distance from most closely related member of S

Shortcomings of Weitzman's Method

- Developed for wildlife species rather than livestock breeds
  - emphasizes distinctiveness
- Does not account for heterozygosity, a standard measure of diversity
  - would favor homozygous, but distinct species/breeds
- Does not account for variation within species/breed
- Does not directly account for real or effective population size
- May produce misleading conclusions
- Computationally complex

Alternatives have been proposed for livestock

Diversity based on Kinship[1]

- Measure of similarity among members of a population (i.e. breed)
  - Considers both within and across-breed diversity
- Probability that random alleles drawn from two individuals is identical by descent
- Fraction of alleles two breeds have in common through common ancestors
- Can be estimated with polymorphic markers
- Kinship matrix for a set of breeds

[1]Eding & Meuwissen, 2001; Caballero & Toro, 2002

Kinship Matrix

$$\mathbf{K} = \begin{bmatrix} 0.6 & 0.1 & 0.1 & 0.1 \\ 0.1 & 0.3 & 0.1 & 0.2 \\ 0.1 & 0.1 & 0.2 & 0.4 \\ 0.1 & 0.2 & 0.4 & 0.5 \end{bmatrix}$$

kinship of 1^{st} breed with others

kinship of breeds with themselves

Matrix Formula

$$c_{min} = \frac{K^{-1}1_n}{1'_n K^{-1} 1_n}$$

← sum of inverse elements of kinships with all breeds (numerator)

← factor to ensure sum of 1.0 (denominator)

where,

- c_{min} vector of breed proportions
- K is kinship matrix of breeds
- n is number of breeds

Core Set Approach

- "Core set" is the set of breeds (and proportions) that will result in the minimum mean kinship
  - proportions for some breeds will (likely) be zero
- Proportions can be used to prioritize breeds for conservation
  - conserve breeds with $c_i > 0$

Attractive Features of Core Set Method

- Considers within-breed diversity
  - genetic variance of quantitative traits
- Flexible
  - Can apply "Safe set" approach
- Computationally simple
- Can directly incorporate Risk of Extinction

Compromise Needed?

- Diversity measures can be regarded as:

$$GD_T = wGD_W + GD_B$$

- Weitzman under-emphasizes GB_B (w = 0)
- Kinship approach over-emphasizes GB_B (w = 1)
- Alternatives may be more suitable (Meuwissen 2009)
  - Bennewitz and Meuwissen (2005) w = 0.5
  - Piyasatian and Kinghorn (2003) w = 0.2

Estimation of Extinction Risk

Three approaches:

1) Evaluate factors for each breed that affect extinction, use factors to assign breeds to categories based on level of risk
2) Predict population survival through mathematical modeling
3) Estimate loss of genetic variation over time

Factors Affecting Extinction Probability

- Population size
  - number of breeding females and mating patterns
- Distribution
  - number of herds and geographic range
- Social and cultural aspects
  - affection and enthusiasm of breeders
  - existence of breeding or conservation programmes
  - socio-economic factors
- Existence of formal breeding or conservation programmes
- Species fecundity

Extensions to Weitzman

- General framework is solid
  - diversity measurement not appropriate for livestock
- Factors beyond genetics and extinction risk influence priority for conservation
- Extensions to Weitzman Approach have been proposed
- "Optimal allocation" of resources (Simianer *et al.* 2003)
- Cost-Benefit approach (Reist-Marti *et al.* 2005, 2006)
- Expected utility (Simianer 2002)
  - genetic variation and special traits
- Weitzman (1998)
  - incorporate utility and conservation costs

General Observations

- Objective prioritization methods applied to most livestock species on research basis
- No application in practice
- Reasons?
  - lack of molecular characterization
  - no clear consensus on optimal approach
  - no simple comprehensive computational tools

Recommendations for Future

- Improve characterization
  - molecular for estimation of diversity
  - phenotypic for consideration of other information
- Improve population monitoring
  - identify breeds at risk
- Reach consensus on diversity measure
  - “Balanced” approaches
- Developed improved software
- Act now to conserve breeds known to be at greatest risk

Promoting diversity

Thank you