

Conserving a single gene versus overall genetic diversity with the help of optimal contributions

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Old low input/low output breeds



- Harbour unique genetic variation
- Conservation in gene banks
 - Genetic diversity should be maximised



Maximising genetic diversity in a gene bank

- Optimal contributions is the method of choice
- Minimises $c'Ac$
 - A = numerator relationship matrix
 - Pedigree based or Molecular based
 - c = contribution vector
 - Sums to 1
 - Excluded animals have 0 contribution
- Constraints
 - No negative contributions
 - Equal contributions of selected candidates
 - Male and female contributions sum to 0.5
- Software program: Gencont



Conservation of special genes

- Often interest in specific genes
 - Coat or colour varieties
 - Curly coat in American Bashkir Curly horses
 - Poultry colour varieties
 - Elimination of specific genes
 - Scrapie sensitive alleles in sheep
 - Introgressions from other breeds
- Risk of losing other diversity when targeting a specific allele
 - Maximise diversity while constraining allele frequencies



Targeting specific alleles with optimal contributions

- Constraint on sexes: $s = Qc$
 - $s = [0.5 \ 0.5]$
 - $Q =$ two column vector, per animal $[1 \ 0]$ if male or $[0 \ 1]$ if female
 - $c =$ contribution vector
- Can be replaced by allele frequencies
 - $s = [0.0 \ 1.0]$ or $[0.05 \ 0.95]$ or $[0.5 \ 0.5]$ or any other frequency
 - $Q =$ two column vector: $[1 \ 0]$ if homozygote 1 $[0.5 \ 0.5]$ if heterozygote $[0 \ 1]$ if homozygote 2
 - $c =$ contribution vector



Does conservation of individual genes with optimal contributions work?

- Holstein population with 568 animals
 - Genotyped with 50K SNP
- Simulation of Conservation of 20 animals with equal contributions (5% each) in genebank
- Random choice of 100 loci
 - First subsequent loci with frequency 0.05/0.95; 0.10/0.90; 0.25/0.75; 0.5/0.5
- Target frequencies in genebank
 - Eliminate minor allele (0.0/1.0)
 - Original frequency
 - Maximise diversity (0.5/0.5)
 - Eliminate major allele (1.0/0.0)



Results: Genetic diversity (% fixed alleles)

- %fixed in original population: 6.1%
- %fixed in gene bank without target freq.: 10.1%
- %fixed in gene bank with target frequency 0.0/1.0

Original frequency	% fixed in gene bank
0.05/0.95	10.1
0.10/0.90	10.1
0.25/0.75	10.2
0.50/0.50	10.7

- Larger loss if target frequency differs more from original



Results: Genetic diversity (% fixed alleles)

Original frequency	Target frequency			
	0.0/1.0	original	0.50/0.50	1.0/0.0
0.05/0.95	10.1	10.2	11.2	X
0.10/0.90	10.1	10.2	10.6	X
0.25/0.75	10.2	10.2	10.2	12.0
0.50/0.50	10.7	10.1	10.1	10.8

- Larger loss if target frequency differs more from original



Practical example: Groningen White headed and B19

- Rare breed: around 60 bulls left, 98 if gene bank animals included
- Blood group B19 only known in this breed
- Should we breed for (more?) B19?
 - Do we lose other diversity if B19 is fixed?
- 42 animals with blood group known, including 14 of 98 bulls
- Other bulls genotype estimated with BLUP (Gengler et al 2007)



Allele frequencies and average relatedness

- Whole population
 - Allele frequency: 21.1%
 - Average relatedness: 0.085
 - with optimal contributions: 0.050
- Average relatedness with optimal contributions and target frequency:
 - 0.075 for 5%
 - 0.050 for 25%
 - 0.054 for 50%
 - 0.132 for 100%
- Loss of diversity when B19 animals are lost
- Loss of diversity when B19 is fixed



Conclusions

- Targeting specific alleles while conserving animals can lead to a substantial loss of diversity
- Optimal contributions restrict the loss
- The more the target allele frequency differs from the population allele frequency the higher the loss

