

The use and integration of molecular DNA information in conservation breeding programmes: a review

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Journal of Zoo and Aquarium Research 1(2): 44–51, 2013.

Supplementary information

Useful software (Table 1) and methods (Table 2) for the integration of molecular information into conservation breeding programmes. For additional guidance on the use of molecular markers in conservation breeding programmes and conservation in general, see www.ConGRESSgenetics.eu

Table 1. Summary of the software referred to in the review: the software name and a short description on how it is useful in integrating molecular data into captive breeding programmes. Websites where the software is freely available can be found by following the hyperlink attached to each program's name.

Software	Description
GenotypeChecker (Paterson & Law 2011)	Gives a transparent overview of inconsistencies between pedigree and molecular data and allows the user to determine which of the two is erroneous.
COANCESTRY (Wang 2011)	Simulates genotype data for selection of the best estimator out of seven in a particular situation. Estimates the (molecular) relatedness between individuals.
COLONY (Wang & Santure 2009)	Implements full likelihood methods to determine the most likely pedigree for a population based on molecular data.
MOL COANC (Fernández and Toro 2006)	Provides a hypothetical pedigree for a population's founders based on molecular information.
KIN INFOR (Wang 2006)	Estimates information value of molecular data based on four values for each marker, both for estimates of pairwise relationship and estimates of relatedness.
MULTIV (Pillar 1997)	Flexibly combines different types of data, such as qualitative and quantitative data.
LDSO (Ytournal et al. 2012)	Simulates the forces resulting in certain genotypes (genetic drift, mutation etc.) and resulting in certain phenotypes (dominance, epistasis etc.)
PMx (Lacy et al. 2012)	Analyses pedigrees and provides the option to use molecular relatedness values in the kinship matrix to determine individual, subpopulation and population genetic parameters and select breeding pairs.
METAPOP (Pérez-Figueroa et al. 2008)	Software that determines ideal breeding pairs within sub-populations and migrants between them based on a kinship matrix to optimise genetic diversity maintained in the meta-population. Restrictions on e.g. migration can be made.
Uncertain Paternity Coancestry (Pérez-Enciso 1995)	Analyses a part of the pedigree, also compatible with uncertain paternities.
GENCONT (Meeuwissen 2002)	Assists in selecting individuals to increase the frequency of a trait, while selecting a set of breeders with minimum coancestry to maintain genetic diversity. Freely available by request: jack.windig@wur.nl
EVA (Berg et al. 2006)	Assists in selecting individuals to increase the frequency of a trait, while selecting a set of breeders with minimum coancestry to maintain genetic diversity.

Table 2. Summary of the methods described in the review, ordered by their use in breeding programmes. In the left column, the data used for each method (with reference to a case study), and in the right column, a short description of how these data can be used in conservation breeding programmes.

Data used	Method
Breeding to maintain genetic diversity, (based on relatedness)	
Three DNA studbooks (Henkel et al. 2011)	Breeding based on MK which is lower than average in three different studbooks differing in estimator used for founder relatedness (no founder relatedness, estimated with Q&G and allelic similarity).
Combined molecular and pedigree data (Bomcke and Gengler 2009)	Provides one value of relatedness by combining molecular and pedigree data. Pedigree data is weighed by the depth of the pedigree and molecular data by the polymorphism information content (PIC) of the markers.
Combined molecular and pedigree data (Bömcke et al. 2011)	Provides one value of relatedness by combining molecular and pedigree data. Relatedness is based on molecular information for the part measured by markers and on the pedigree for the rest of the genome.
Molecular data (de Cara et al. 2011)	Using genome-wide molecular data to determine pairs to maintain genetic diversity and heterozygosity.
Molecular and pedigree data (Engelsma et al. 2011)	Maintaining diversity by selecting a relatively small number of individuals from a population with minimum coancestry. This selection can be used for a gene-bank but also to use these individuals as founders for the next generation when fecundity is very high (see also software Gencont and EVA). Both pedigree and molecular data can be used. Molecular data contributes most by revealing when certain important diversity is missing in the selection.
Breeding to alter allele frequencies	
Pedigree (Amador et al. 2011)	Prioritises individuals for breeding on the amount of native alleles they contain based on pedigrees. With decreasing number of animals allowed to breed, the proportion of exogenous alleles removed increases, but this is accompanied by a decrease in genetic diversity.
Molecular data (Amador et al. 2012)	Similar to above, but prioritisation based on molecular data instead of pedigrees. Efficiency increases if the alleles selected for are exclusive to the native species.
Molecular data (Saura et al. 2008)	Method to determine the number of offspring from each individual needed to achieve or maintain a certain balance of allele frequencies.
Breeding to alter quantitative traits	
Combination of pedigree and molecular data (De los Campos et al. 2009)	Predicting quantitative traits in the next generation based on molecular and pedigree data separately and combined.
Combination of pedigree, morphological and molecular data (Fernández et al. 2012)	Combined strategy to increase the frequency of a qualitative trait based on morphological data while maintaining genetic diversity based on molecular and pedigree data.
Combining pedigree, molecular and performance data (Hasler et al. 2011)	Commercial method to breed for performance, while maintaining genetic diversity based on pedigree and molecular data. Also estimates genetic drift from molecular data.
Evaluation of the breeding programme	
Pedigree and neutral and adaptive molecular data	Evaluation of breeding programme based on pedigree data and both adaptive and neutral molecular data. Used to determine whether certain (MHC) genes

(Marsden et al. 2013)	were selected for, possibly because of adaption to captivity, and to produce a management plan.
Molecular data (McGreevy et al. 2010)	Evaluating the ability of a captive population to maintain genetic diversity by comparing with the wild population through molecular analysis.
Other	
Molecular data (Miller et al. 2010)	Selection of founders or individuals for reintroduction: Technique to determine a set of animals best fitting a certain genetic profile based on molecular data. This set of animals can be founders that capture the diversity of the wild population or animals fit for reintroduction.
Pedigree, demographic and molecular data (Boettcher et al. 2010)	Prioritisation of subspecies: Guidelines of the FAO to prioritise endangered livestock breeds based on demographic and genetic stability and uniqueness of the breed. Principles also apply to (sub)species.
Combed morphological and molecular data (Benin et al. 2012)	Genetic distance between populations and sub-species: Using a combined value of molecular and morphological data to determine genetic distance. Developed for strains of wheat to determine combining abilities between different lines; can potentially assist in genetic rescue.
Group-pedigree and demographic data (Wang 2004)	Group genetic management: Determining immigration rates in group-managed species based on population size, historical immigration rates and founder number.

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