

# Optimising Collections and Databases for Molecular Biology.

J.F. LÓPEZ-GIRÁLDEZ<sup>1</sup>, E. GARCÍA-FRANQUESA<sup>2</sup>, J. MARMÍ<sup>1</sup> & X. DOMÍNGO-ROURIA<sup>1,3</sup>

<sup>1</sup>Unitat de Biologia Evolutiva, Universitat Pompeu Fabra, Dr. Aiguader 86, 08003 Barcelona, Spain, *Email: francisco.lopez@cefe.upf.es, xavier.domingo@cefe.upf.es*; <sup>2</sup>Hispan de Zoologia de Barcelona, Passadís Piusas s/n, 08003 Barcelona, Spain, *Email: marmic@hmc.com.es*; <sup>3</sup>Wildlife Conservation Research Unit, Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, U.K.

Public and private institutions owning natural history collections can play a key role in continuing collecting efforts. With the discovery of the Polymerase Chain Reaction (PCR) technique to amplify DNA (Saito *et al.*, 1988), the majority of samples obtained non-invasively are useful for molecular biology studies and their collection does not compromise animal conservation.

## INVASIVE SAMPLING

- Hunting and fishing
- Capture and release



- ## NON-INVASIVE SAMPLING
- Digestive and reproductive remains
  - Temporal remains
  - Carcasses
  - Road kills



## SAMPLE COLLECTORS

### PREPARATION AND PRESERVATION

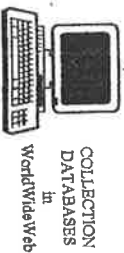
During the preparation and preservation of specimens, protocols that help maintain the presence and structure of nucleic acids for the future should be promoted. Laboratory protocols have been developed to achieve the extraction of nucleic acids from samples that had received several preservative treatments in the past. However, some of these protocols are technologically demanding. Freezing constitutes an optimal treatment in most cases but other protocols, such as preservation in ethanol and drying, are also highly successful for DNA extraction.

- Terao (blood, vert. muscle, soft tissue): Baker, 1994; Zumbo *et al.*, 1999.
- Frozen formalin: Schemm-Petermann *et al.*, 1997.
- Frozen formalin: Schuster *et al.*, 1998.
- Pinned material: Menden *et al.*, 1996; Lantieri *et al.*, 1998.
- Bone: Bardi *et al.*, 1994; Thomas & Moore, 1997; Yang *et al.*, 1998.
- Otolith: Hinchliffe *et al.*, 1999.
- Scale: Rodriguez-Robles & De Jager-Bercher, 1999; 2000.
- Hair: Clark, 1998; Femenia, 1999.
- Feather: Rodriguez-Robles, Schumann *et al.*, 1998; Bakke *et al.*, 2000.
- Eggs from study skins or mounted specimens: O'Connor *et al.*, 1998; Vigilant, 1999.
- Reddish brown study skin or mounted skin: Bouda & Brown, 1998.
- Skin: Gendron, Paves *et al.*, 1997.
- Fossilized specimens: Stoddard *et al.*, 1997; Chaffey, 2000.



### DATABASE CONSTRUCTION

The worldwide accessibility to databases of collectors and the establishment of rules for sample use are necessary steps to protect the sample and the needs of both museums and research laboratories. Collection databases should include basic natural history information to complement molecular data.



## MUSEUMS

### TECHNIQUES

Numerous techniques are available to explore DNA diversity. The selection of the technique depends on the quality of the tissue available and on the mutation rate of the DNA region under study.

- RFLP: Restriction Fragment Length
- VNTR: Variable Number of Tandem Repeats Analysis



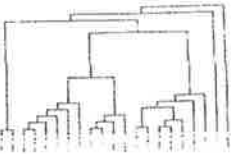
- STR: Short Tandem Repeats analysis
- DNA Sequencing
- SSCP: Single-Strand Conformation Polymorphism
- DDM: Direct DNA Sequencing
- AFLP: Amplified Fragment Length Polymorphism
- RAPD: Randomly Amplified Polymorphic DNAs



### APPLICATIONS IN CONSERVATION GENETICS

Molecular biology has already been widely used in many applications both in extant and extinct species in relation to the management and conservation of wild animals. Molecular techniques have been used to clarify:

- Phylogenetic classification.
- Taxonomic classification.
- Species identity.
- Endemism
- Population structure and relationship.
- Effective population size.
- Population expansion.
- Gene flow.
- Large scale equilibrium.
- Parentage.
- Individual identification.
- Quantitative trait identification.



## MOLECULAR LABORATORIES