A cost-effective genetic tool to detect introgression in the red-legged partridge

SEVANE N.[1], ARANA P.[2], CAÑÓN J.[1], DÁVILA J.A.[3], DUNNER S.[1], FRANCESCH A.[4], GÓMEZ DE NOVA P.[3], PENA R.[4], QUENEY G.[5], FEDENCA[6]

[1] Veterinary Faculty, UCM, Spain
[2] Biology Faculty, UCM, Spain
[3] UCLM – IREC, Spain
[4] IRTA, Spain
[5] ANTAGENE, France
[6] www.fecaza.com

Consorcio *Perdiz Roja* FEDENCA-Laboratorios de Genética®

Motivation

In Southern European countries, release of captive-bred red-legged partridges (*Alectoris rufa*) is used to periodically reinforce hunting areas where wild populations have decreased. Several studies have recorded cases of artificial genetic pollution of *A. rufa* with *A. chukar*, due to better growth and adaptation performances of the latter to captivity as a result of artificial selection. Hybrids detection is crucial to avoid uncontrolled restocking which may lead to a widespread introgression of foreign species in locally adapted partridge species. However, the effort to monitor genetic quality of restocked partridges is scarce across the entire species range and the results obtained by different laboratories are often contradictory.

Aims

The aims were to develop a cost-effective medium-throughput genotyping method to allow easy introgression detection of *A. chukar* into wild *A. rufa* populations and to standardize its application among the main Spanish and French partridge laboratories.

Strategy

Four Spanish and one French laboratories analyzed 266 partridge blind **samples**:

- 68 wild red-legged partridges hunted in Spain and France
- 80 captive-reared individuals from two Spanish cynegetic farms
- 40 red-legged samples issued from specimens located in two Spanish museums
- 31 wild chukar partridges hunted in Lebanon and 7 restocked chukar from Cyprus
- 40 artificially generated hybrids *A. rufa* x *A. chukar*

Molecular **markers** used by the participant laboratories (total 57):

- *Genomic*: 34 SNPs (Single Nucleotide Polymorphism); 1 INDEL; 19 microsatellites
- *Mitochondrial*: 3 SNPs

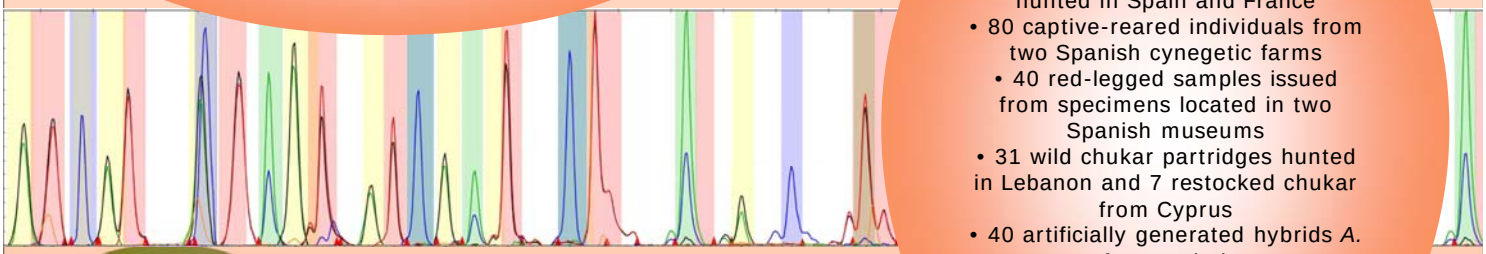

Figure 1. ABI3130 sequencer electropherogram analyzed using GeneMapper v4.0 (Applied Biosystems)

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Results

Among the SNP markers validated, a subset of twenty-three target sequences (22 genomic and 1 mitochondrial) were selected based on their species exclusivity and optimized in one multiplex reaction hybridized with Primer Extension technique (Figure 1).

Table 1 shows the theoretical detection power of the 22 nuclear markers selected.

Taking into account that all the SNPs are species exclusive (or almost exclusive), the hybridization index (HI) of an individual or a population is:

$$\mathbf{HI} = \frac{\text{nº of chukar alleles}}{\text{total nº of alleles}} \times 100$$

B1 (*A. rufa* x F1*)	**100**
B2 (*A rufa* x B1)	**99,8**
B3 (*A. rufa* x B2)	**94,7**

Table 1. Theoretical detection power of the 22 nuclear markers selected.
$B_{1\text{-}3}$ are the successive backcrosses.
*F1: *A. rufa* x *A. chukar*

Conclusions

The simple, flexible and low-cost SNP typing assay developed here allows the fast genotyping of a small number of SNPs at a reasonable price with no need for an expensive infrastructure.

This fact, along with the unification of criterion and method for hybrids detection among the main Spanish and French partridge laboratories, provides an effective tool to control the introgression of reproductive-bred individuals in hunting areas and on farms before restocking.