



The reintroduction of the Iberian lynx in Spain and Portugal

A conservation success despite extreme genetic erosion

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Iberian lynx decline and fragmentation

s. XVI-XIX

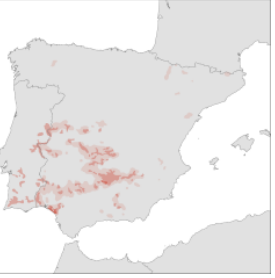
Clavero &
Delibes, 2013

Sierra Morena (SMO)
53 ind.
18 territorial females

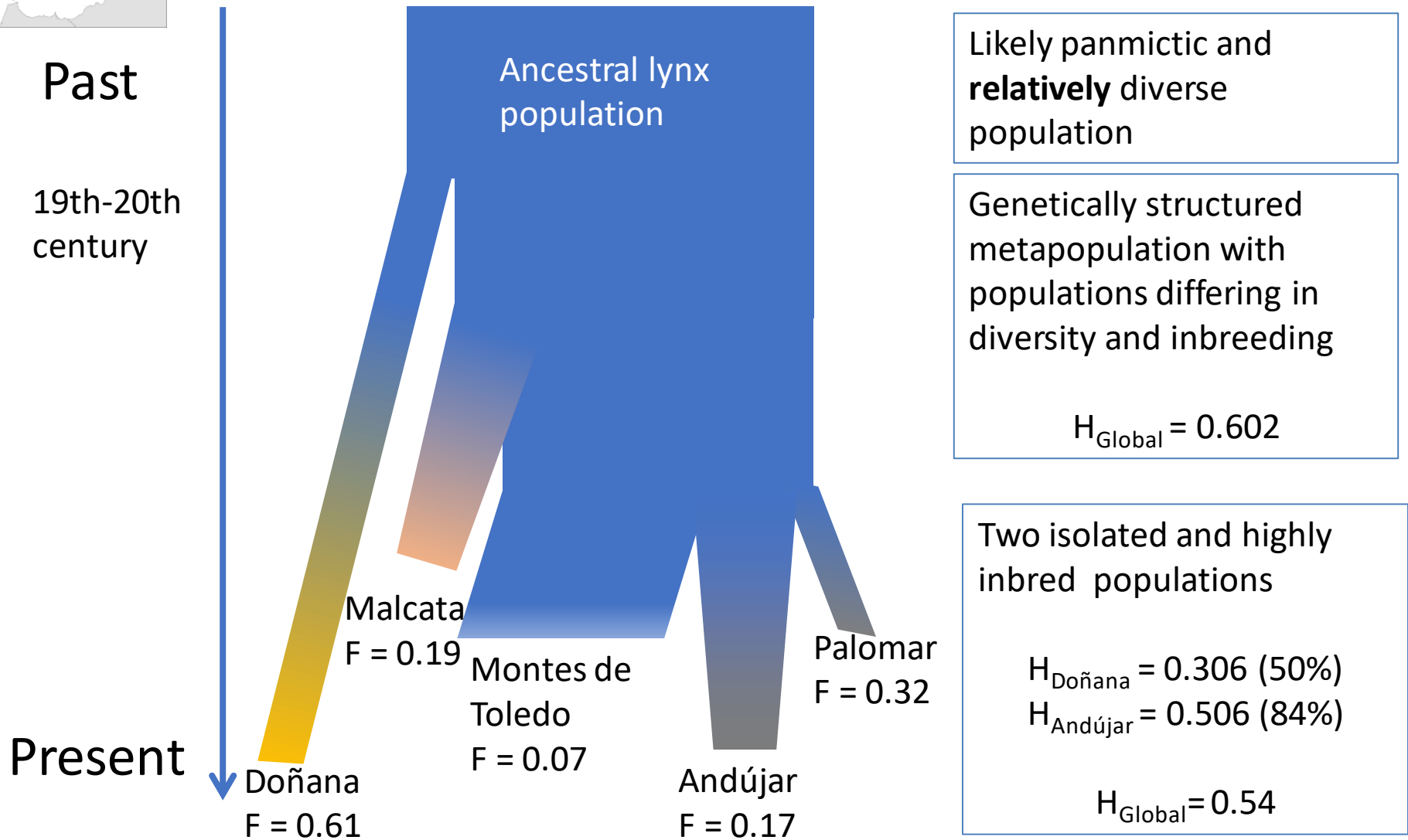
2002 census

Doñana (DON)
41 ind.
9 territorial females

1960
1980
2002



Genetic history: recent erosion



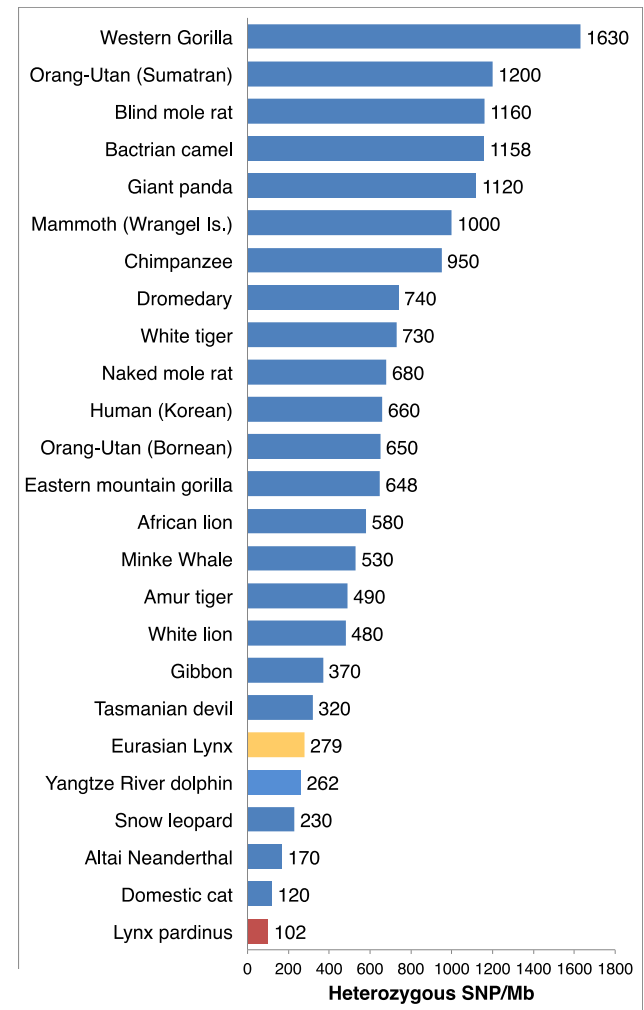
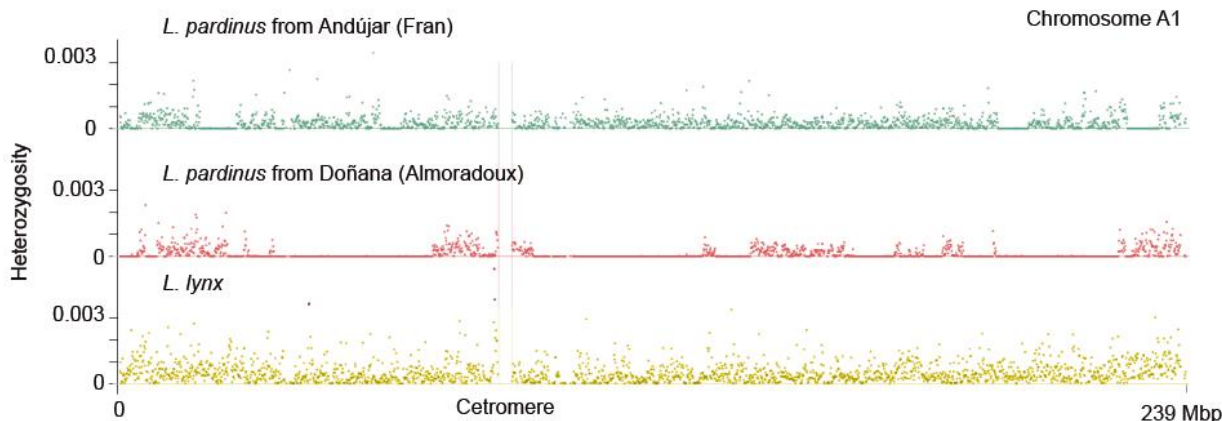
Casas-Marcé M, Marmesat E, Soriano L, *et al.* (2017) Spatio-temporal dynamics of genetic variation in the Iberian lynx along its path to extinction reconstructed with ancient DNA. *Molecular Biology and Evolution* **34**, 2893–2907.

Extreme genetic erosion in remnant populations

- Among the lowest species-wide genetic diversity ever reported
- High recent inbreeding
- Small effective size
- Most dramatic in small and isolated Doñana population
- High genetic differentiation: **Fst=0.22**

	Doñana	Andújar
F_h	0.47	0.06
F_{roh}	0.32	0.16

	Ne
DON	8.4 (4.9-13.7)
SMO	18.6 (15.0-23.3)



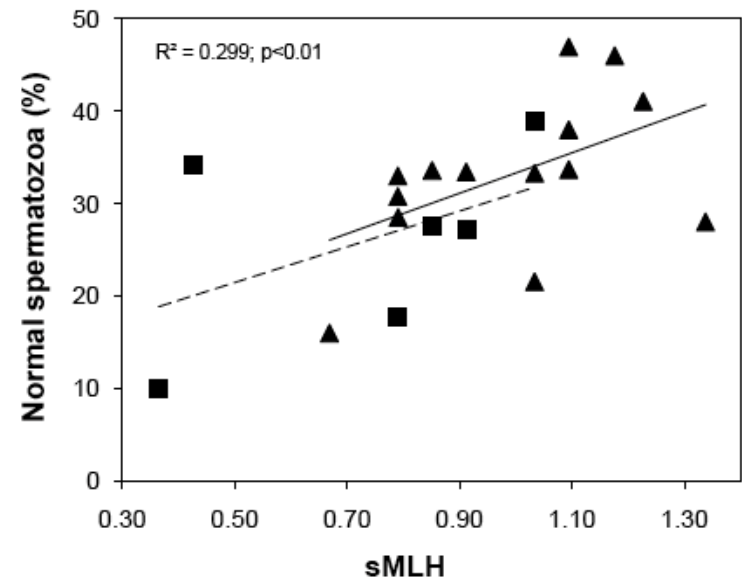
Abascal *et al.* (2016) Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biology* 17, 251.

Impact on fitness?

- High incidence of genetic? disorders
 - Membranous glomerulonephritis (Jiménez et al., 2008)
 - Lymphoid depletion (Peña et al., 2006)
 - Idiopathic epilepsy (Minguez et al., 2021)
 - Cryptorchidism (Martínez, et al., 2013)
 - High susceptibility to infectious diseases
- High rate of non-traumatic mortality
 - Feline Leukemia Virus epidemics in 2007 (12 infected, 7 died)
- Recent reduction of average litter size in DON
 - 1993-2001: 3.1 kittens (n=18, SE= 0.18, range=2-5)
 - 2006-2008: 2.2 (n=9, SE= 0.15, range=2-3).

Palomares F (2012) Possible extinction vortex for a population of Iberian lynx on the verge of extirpation. *Conservation Biology* **26**, 689-697.

Heterozygosity-fitness correlations for semen quality



Ruiz-Lopez MJ, *et al.* (2012) Heterozygosity-Fitness Correlations and Inbreeding Depression in Two Critically Endangered Mammals. *Conservation Biology* **26**, 1121-1129

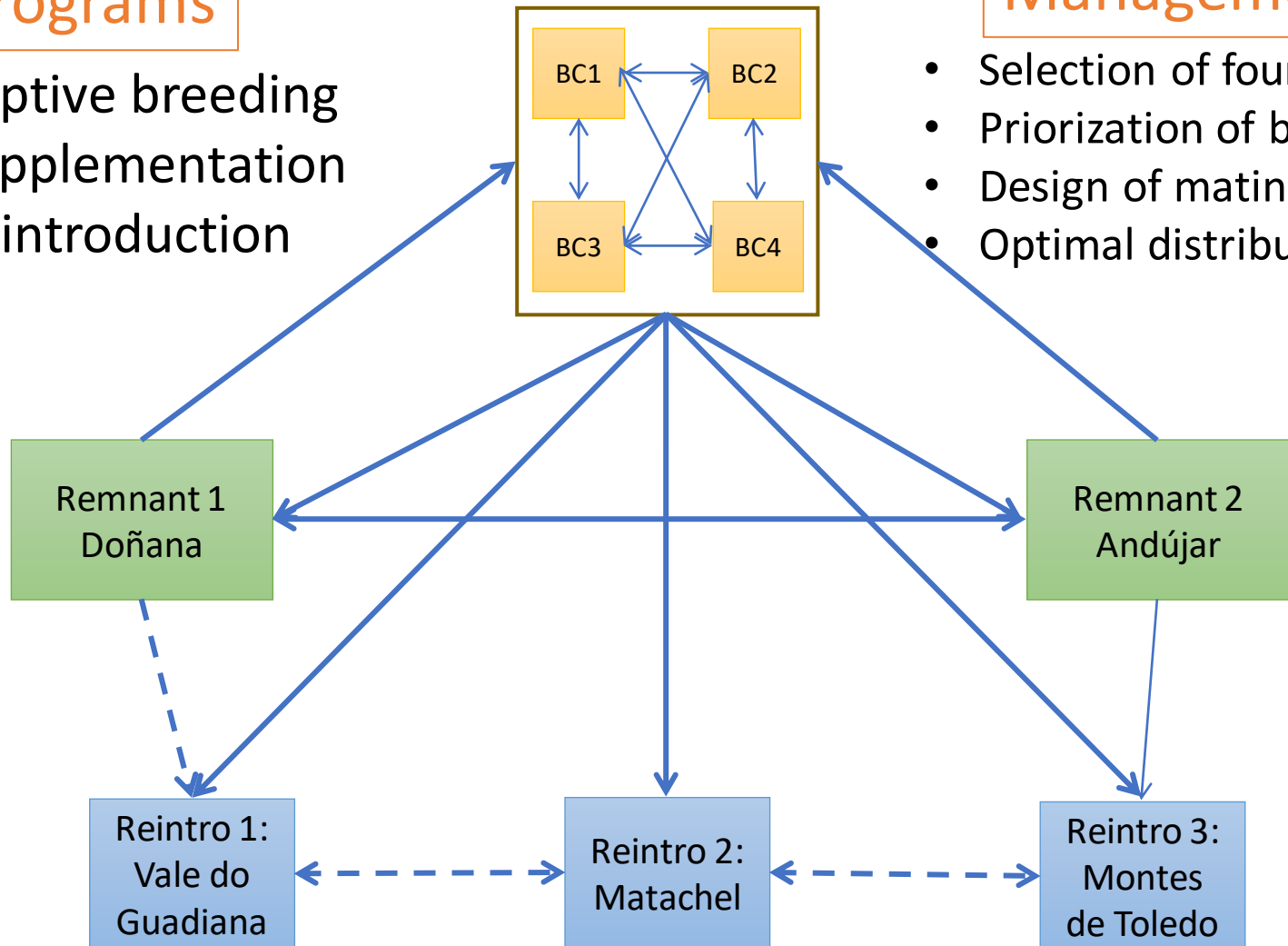
Iberian lynx conservation

Programs

- Captive breeding
- Supplementation
- Reintroduction

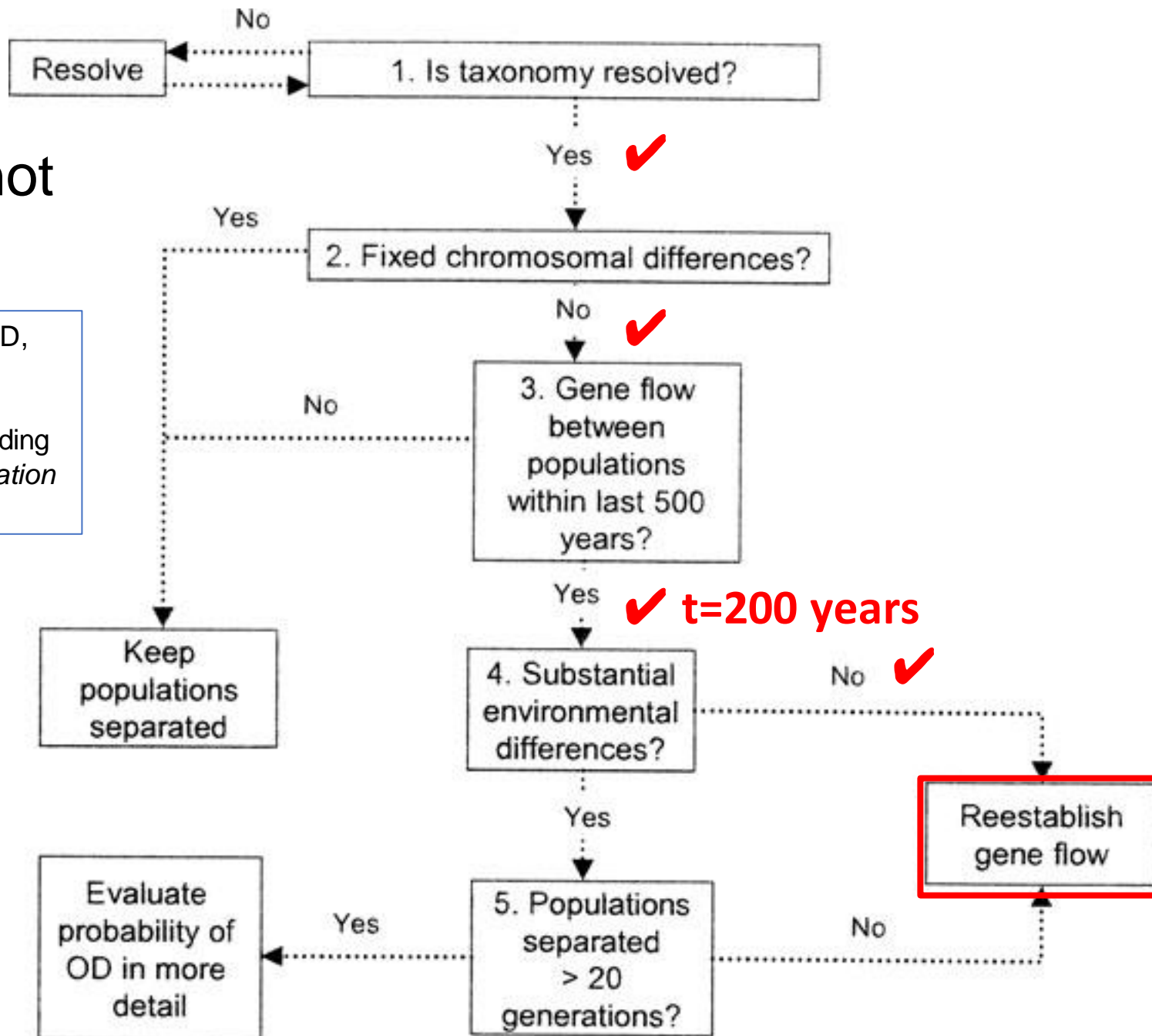
Management

- Selection of founders
- Priorization of breeders
- Design of matings schemes
- Optimal distribution

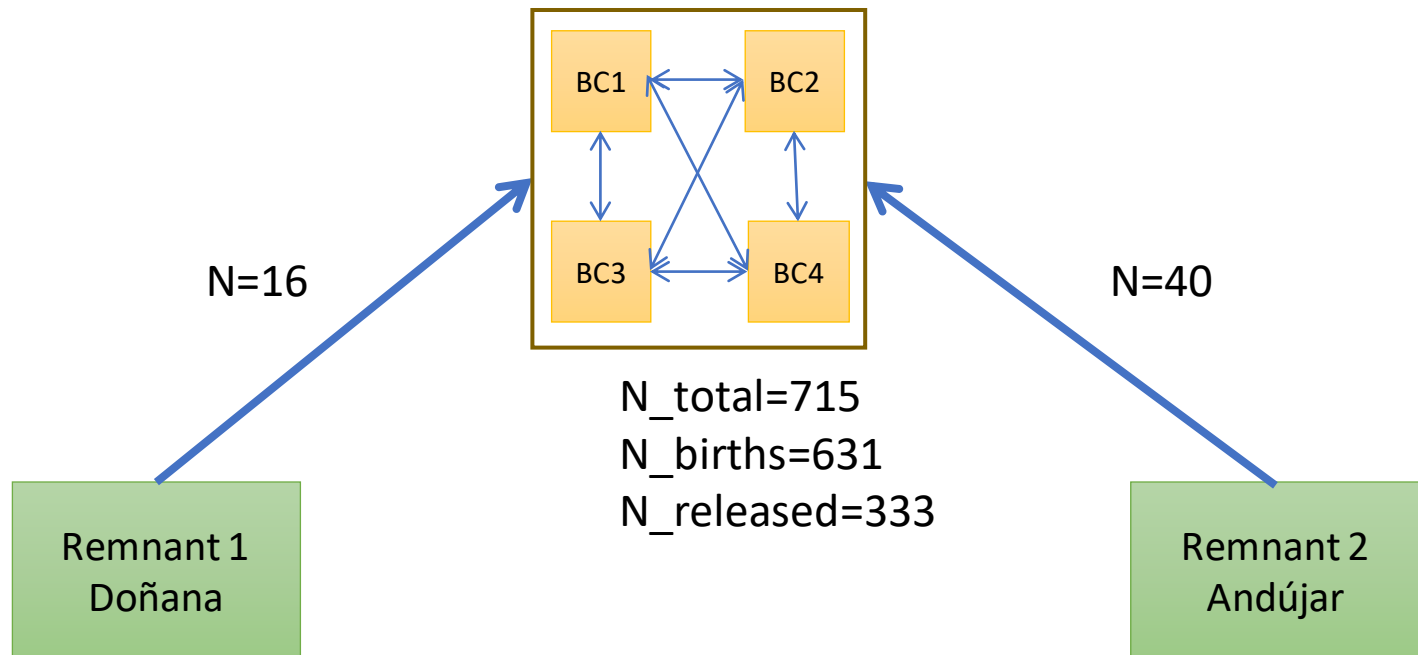


To mix or not to mix?

Frankham R, Ballou JD, Eldridge MDB, *et al.* (2011) Predicting the Probability of Outbreeding Depression. *Conservation Biology* **25**, 465-475

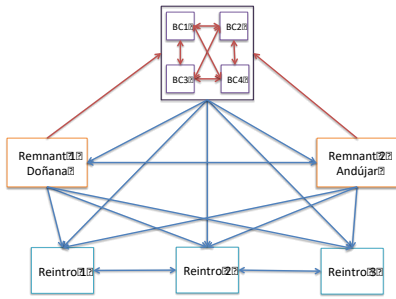


Captive breeding (2005-2021)



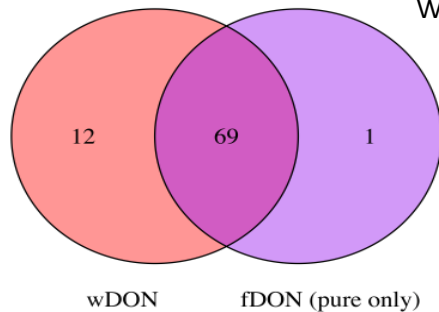
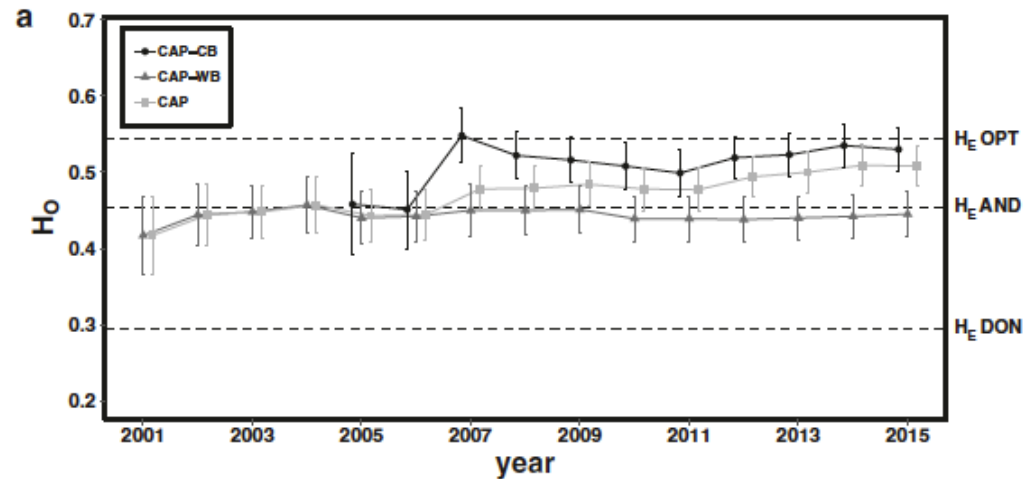
- Current status (2021): N_living=144; N_rep=95; N_cubs=48
- 20-25 attempted matings per year
- 30-45 kittens per year surviving > 2 months (avge = 39,5)
- Most are liberated at reintroduction sites since 2012
- Genetically managed based on minimum kinship

Genetics of captive population



Wilcoxon signed rank test with continuity correction

	wDON (N=50)	fDON_pure (N=9)	v	p
H_0	0.313	0.358	150	0.056
H_E	0.294	0.300	244	0.945
AR	2.250	1.944	36	0.012



wDON vs. fDON (pure only)

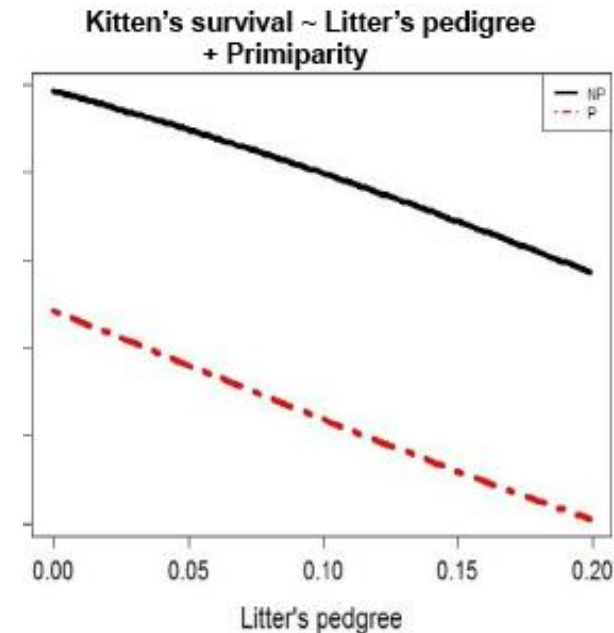
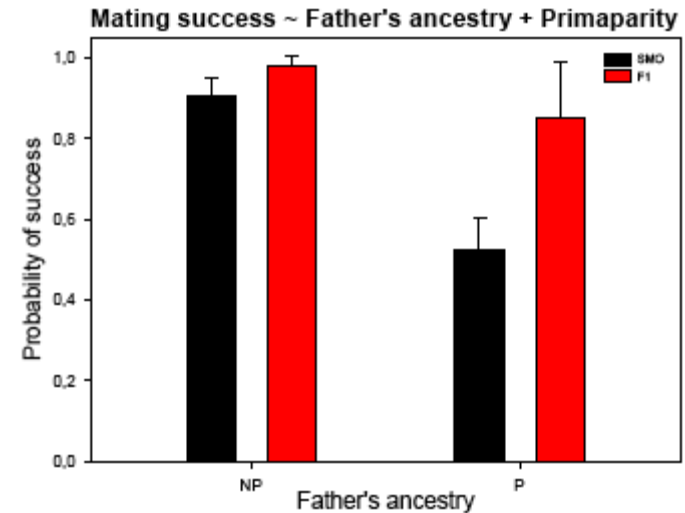
$$F_{ST} = 0.005$$

Kleinman-Ruiz, et al.. 2019. Genetic evaluation of the Iberian lynx ex situ conservation programme. Heredity 123 (5):647-661.

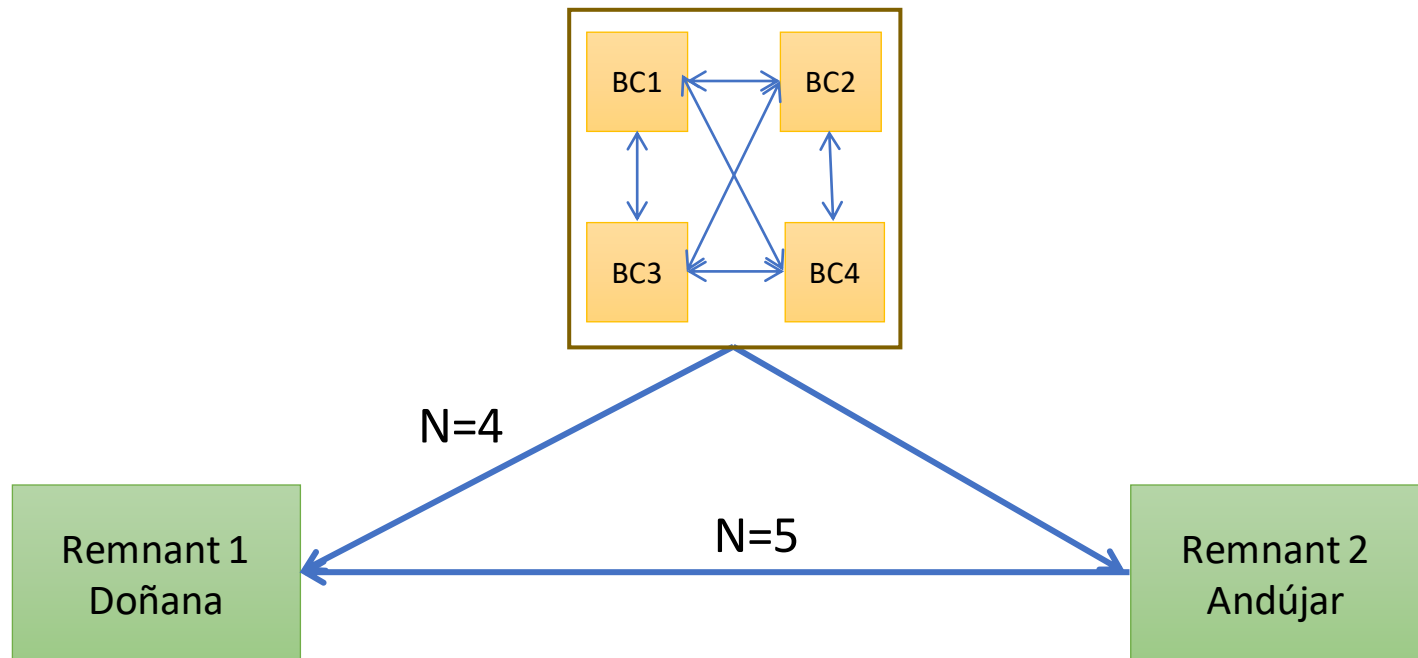
- Founders capture most of the genetic variation in the two remnant populations
- Genetic diversity in captivity higher than in remnants and close to maximum possible, due to the mixing of the two stocks and to genetic management

The fitness consequences of genetic management

- Captive-born lynxes are less inbred than wild-born lynxes
- Should result in higher reproduction and survival of released animals
 - Evidence of increased mating success of F1
 - ID for early survival
- Accumulating data from released animals suggests so
 - High survival rate
 - Large litter size

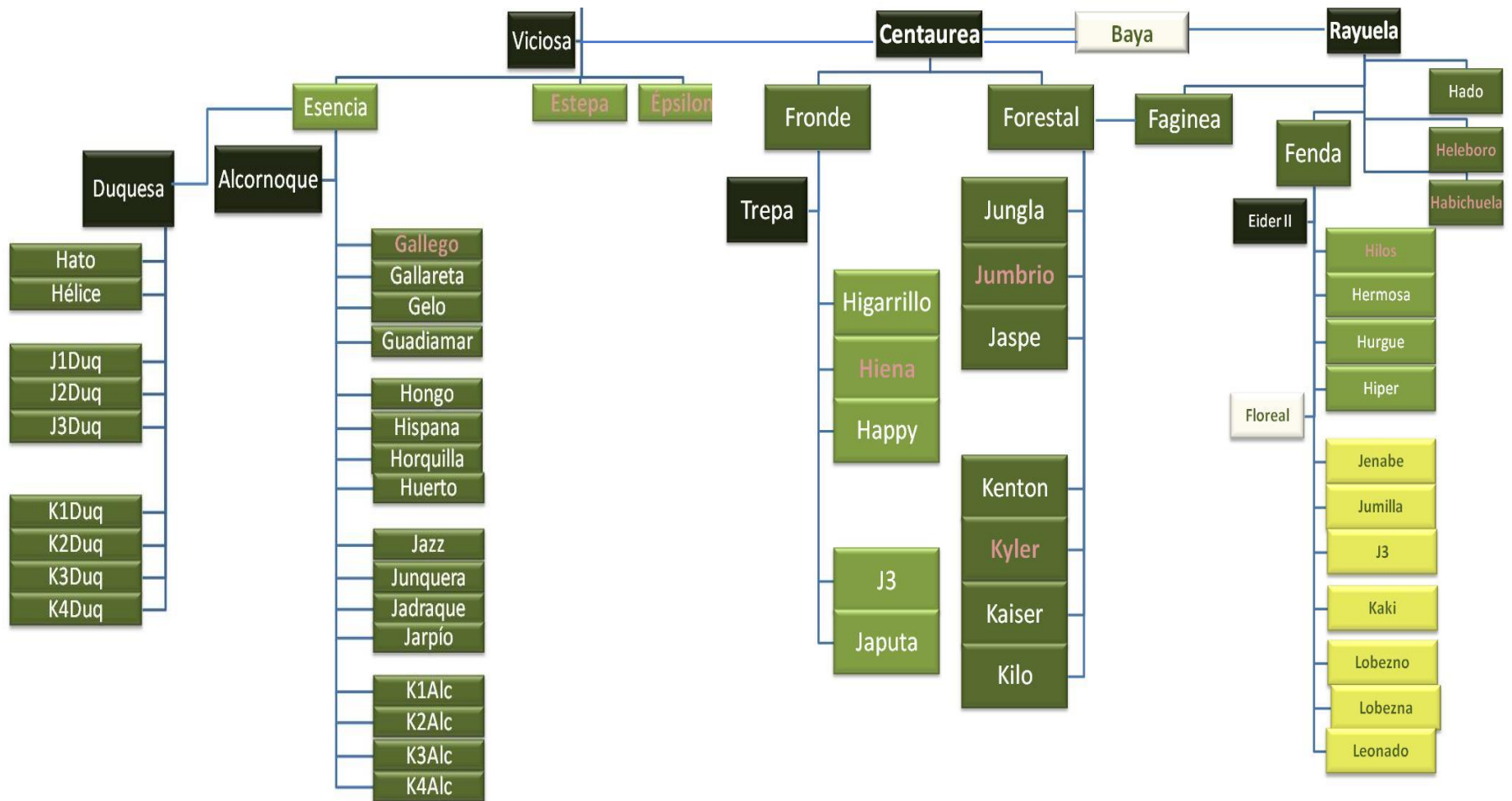


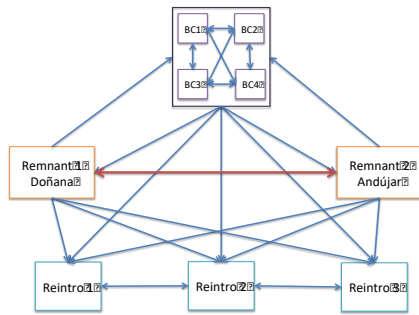
Translocations for genetic reinforcement



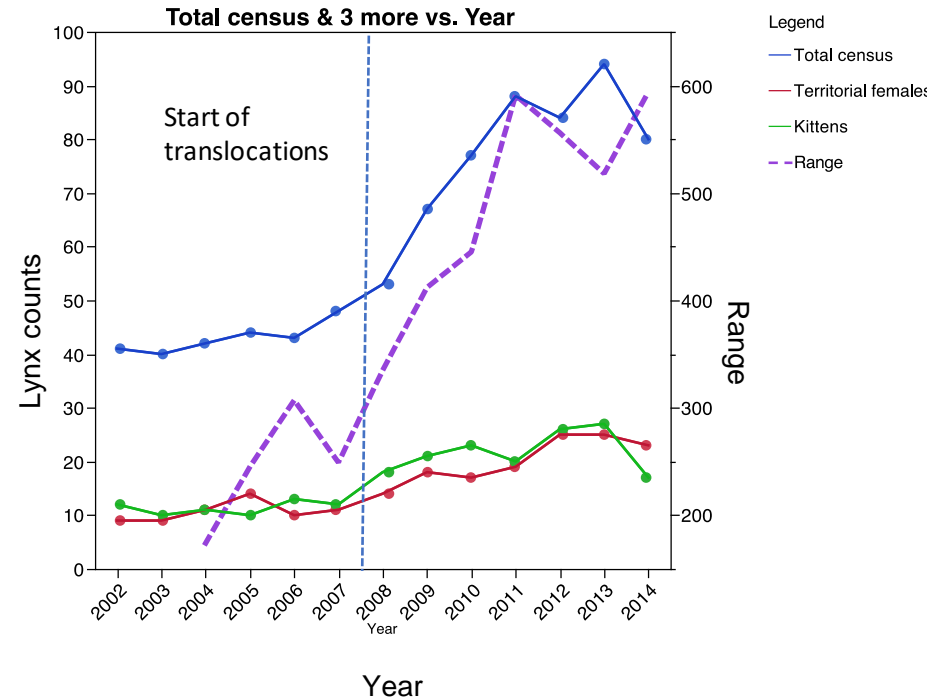
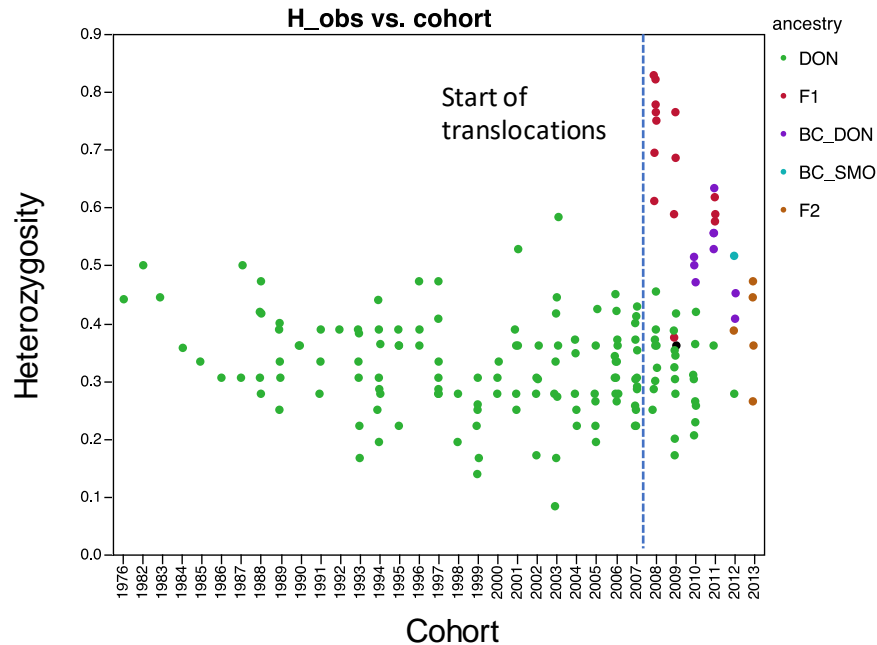
- Nine individuals released 2007-2019
 - Only three with reproduction confirmed
- Huge impact of first male released, Baya

The extense progeny of Baya (2008-2014)



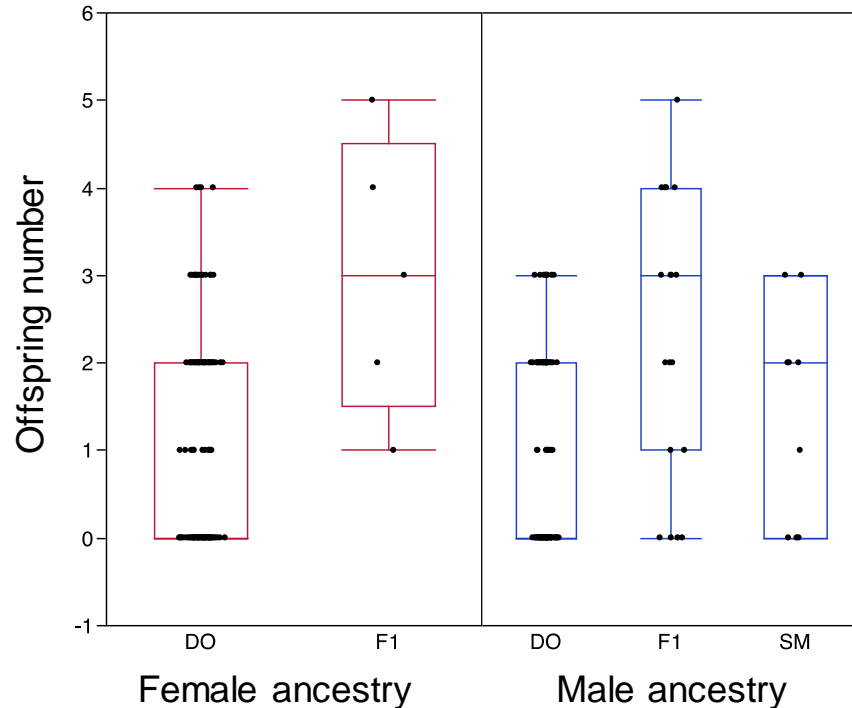


Genetic rescue in Doñana



- Following translocations:
 - Genetic diversity has increased
 - The population has increased

Reproductive output by parent ancestry



Mating success

Source	DF	L-R ChiSquare	Prob>ChiSq
Rabbit abundance	1	17.324142	<.0001*
Male ancestry	2	8.5441719	0.0140*
Female ancestry	1	3.7862033	0.0517

- Males:
 - F1 > SMO \approx DO
- Females:
 - F1 > DO

Offspring number

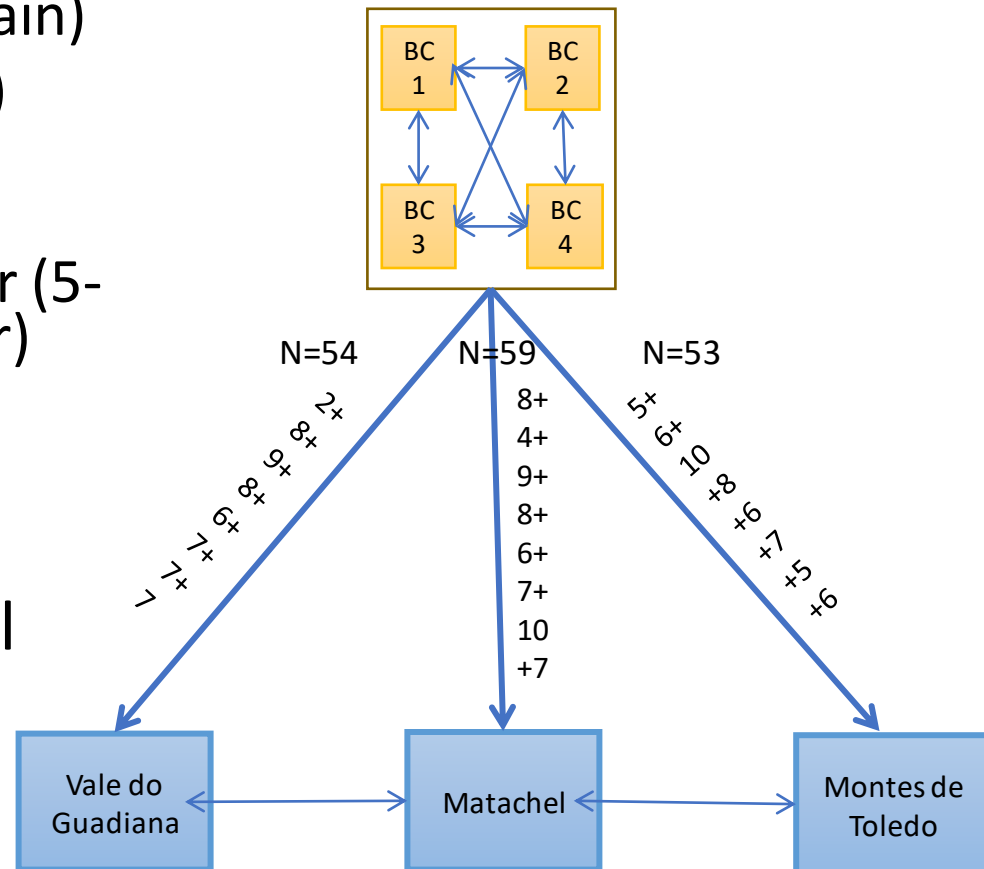
No significant results

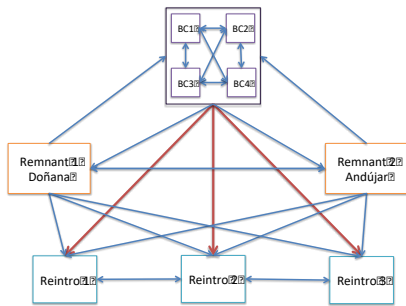
- Based on kittens observed with females within 9 months following reproduction

Reintroductions

- Areas starting in 2015:
 - Sierra Morena Oriental (C-LM, Spain)
 - Montes de Toledo (C-LM, Spain)
 - Matachel (Extremadura, Spain)
 - Vale do Guadiana (Portugal)
- Captive-born animals
 - 30-45 lynx released per year (5-10 animals per site and year)
 - >300 animals released from captivity by 2021
- Survival >70%
- Reproduction achieved at all sites since year one
 - >300 cubs born in 2021

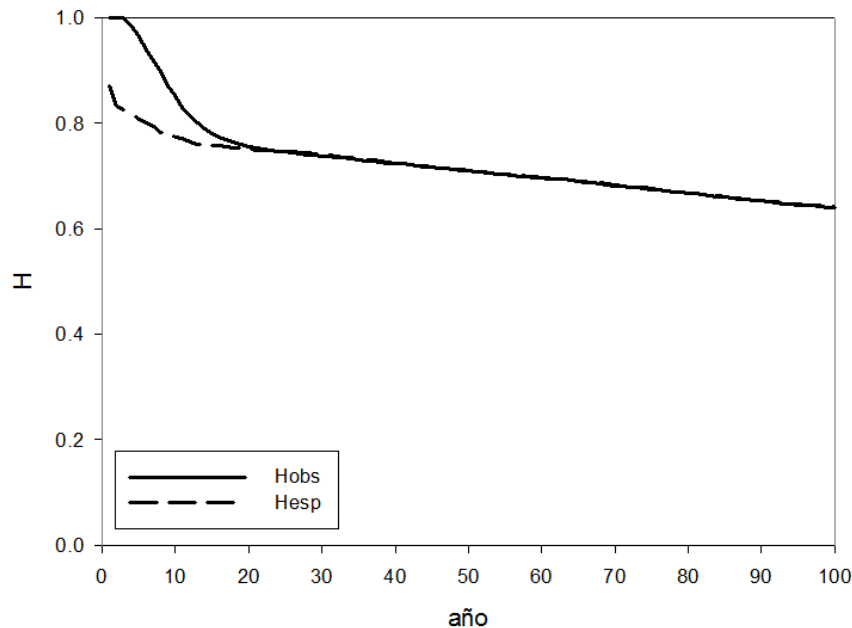
LOS LUGARES CON MAYOR POBLACIÓN





Genetic erosion in reintroduced populations

- Reintroduced populations will accumulate inbreeding and lose diversity very fast during the first few generations (founder effect)
- They will continue to do so at lower rates as long as they remain small and isolated

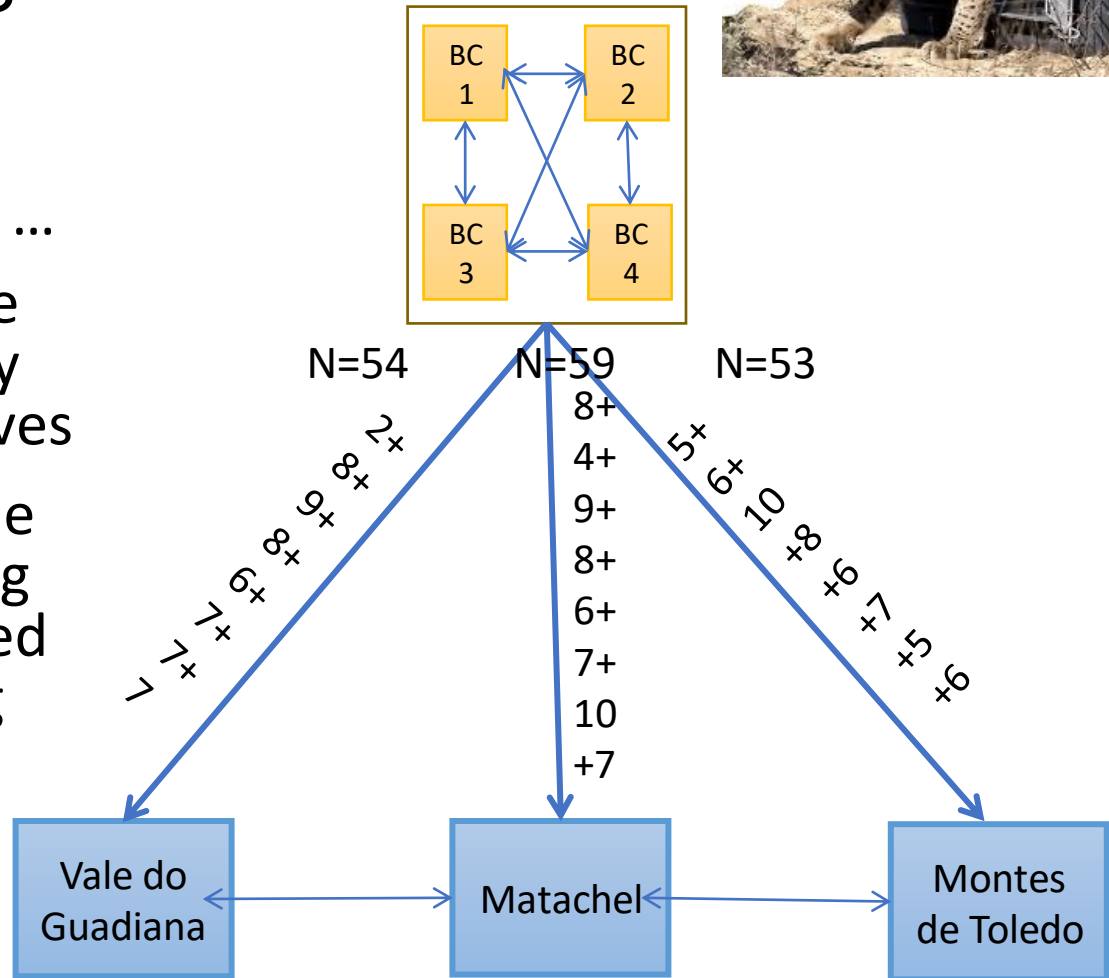


- Favourable scenario
- CC: 30 females
- Census \approx 300
- $\Delta f \approx 0.25$ in 20 years
- $H_t/H_o \approx 70\%$ in 100 years

Based on spatially-explicit individual-based simulations

Genetic management of reintroductions

- Impossible to select breeders or design matings in the wild, but ...
- Released animals can be selected to be minimally related among themselves
- Serial releases create the opportunity for selecting individuals to be released based on MK to existing
- **Requires intensive individual-scale monitoring** to yearly update census and genealogy





lynxconnect

LIFE “Lynxconnect” (2020-2025)



- “Creating a genetically and demographically functional Iberian Lynx (*Lynx pardinus*) metapopulation)” (LIFE19NAT/ES/001055)
- 18.754.029 euros (60,67% funded by UE)
- 21 partners
 - Public agencies, ONGs, CSIC, ...
- It includes an intensive individual-based genetic monitoring and management program assisted by molecular markers

Beneficiario coordinador:



Socios beneficiarios:





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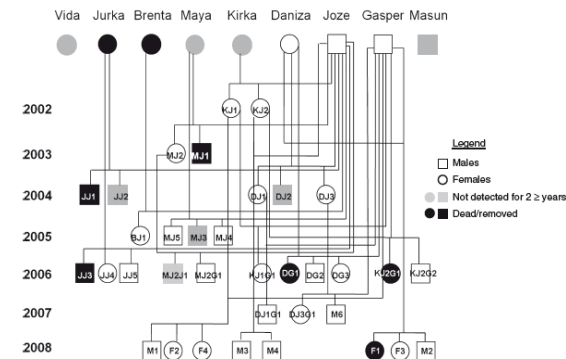
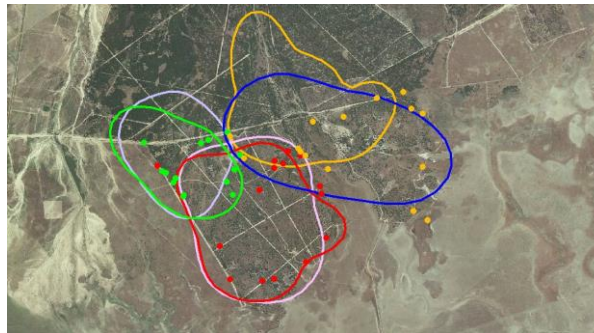
Intensive individual-based genetic monitoring: census and genealogies

• Goals

- Census of individuals
- Geo-referenced: territories, movements, immigrants,...
- **Genealogies**
- **Genetic parameters**

• Methods

- Intensive sampling of faeces
- Individual identification
- Parentage assignment
- Kinship estimates

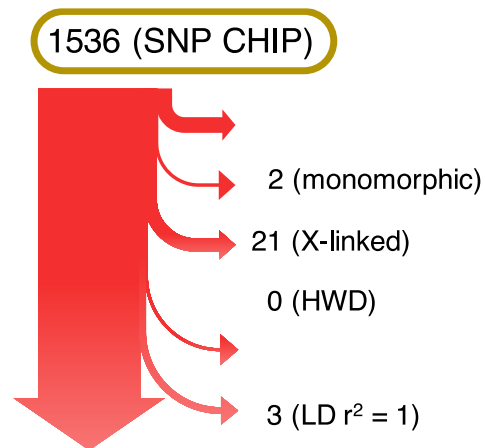


Monitoring: novel SNP markers

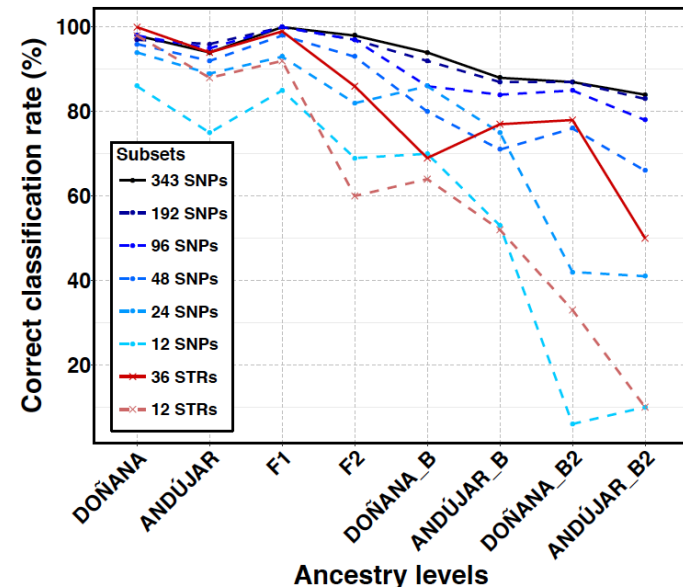
- Novel and more powerful panel of molecular markers for:
 - Population genetics,
 - Non invasive genetic monitoring
 - Genetic management

Marker	Size	PIDs	PnE	PWR FS-HS
SNPs	343	4.7×10^{-71}	2.5×10^{-29}	> 0.999
	192	2.5×10^{-43}	8.8×10^{-18}	0.998
	96	2.4×10^{-22}	2.4×10^{-09}	0.945
	48	1.4×10^{-11}	4.7×10^{-05}	0.741
	24	3.7×10^{-06}	6.9×10^{-03}	0.488
	12	1.9×10^{-03}	8.3×10^{-02}	-
Micros	36	1.2×10^{-09}	5.6×10^{-06}	0.750
	12	9.7×10^{-05}	1.8×10^{-03}	0.503

Individual identif. Parentage assignment Kinship estimation

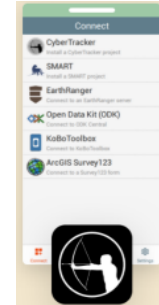


Kleinman-Ruiz *et al.* (2017)
 Novel efficient genome-wide
 SNP panels for the
 conservation of the highly
 endangered Iberian lynx.
BMC Genomics **18**, 556.



Workflow of genetic monitoring

Field

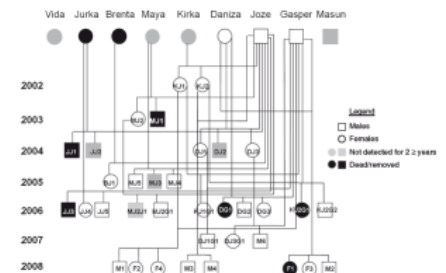
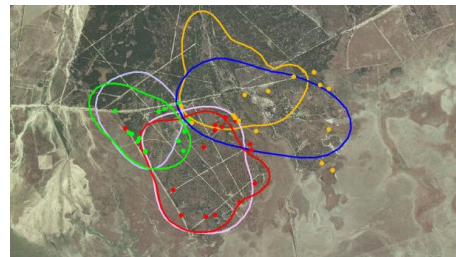
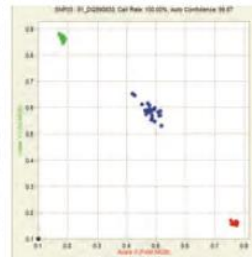
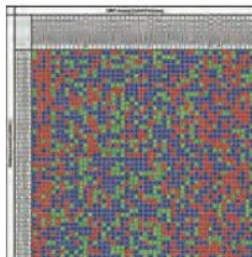


Laboratory



Highly informative SNP panels (Kleinman-Ruiz et al., 2017)

Computer



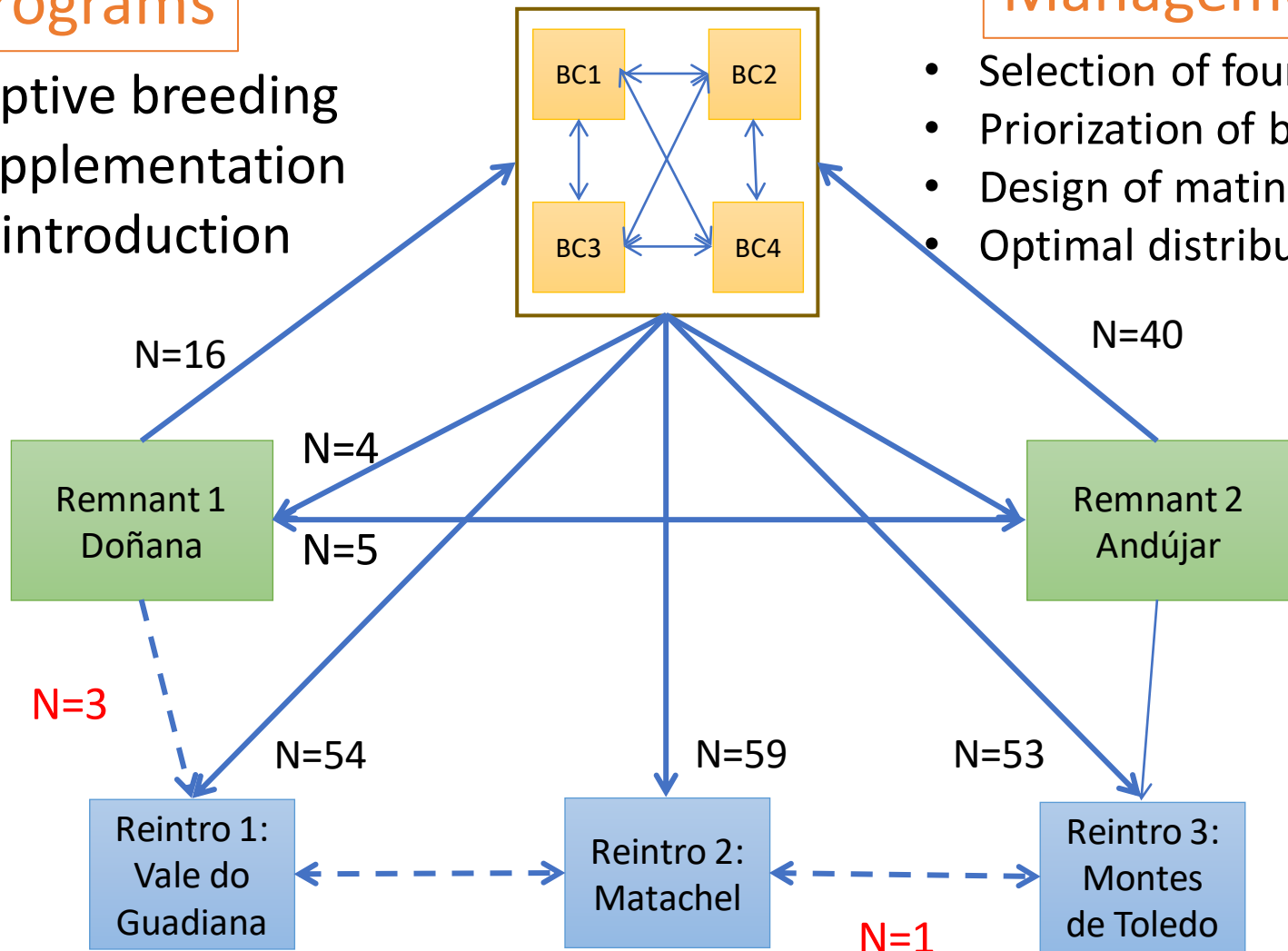
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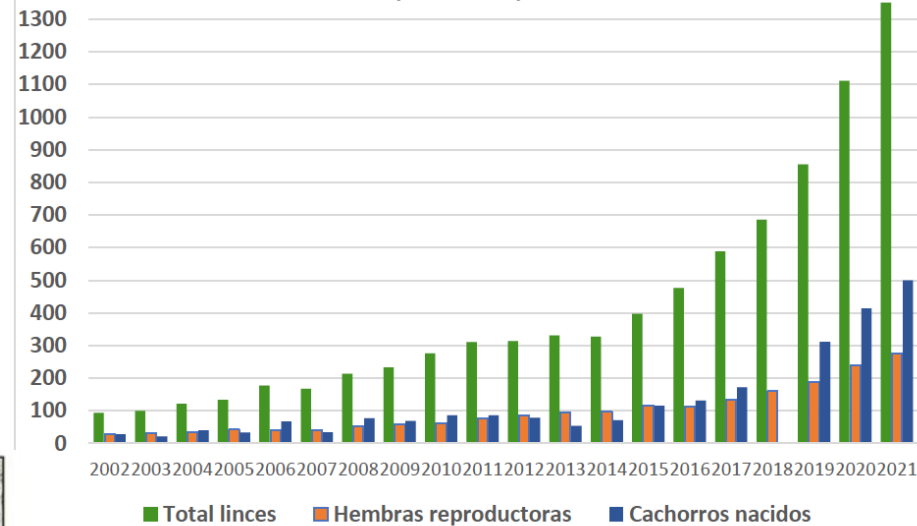


Status 2021

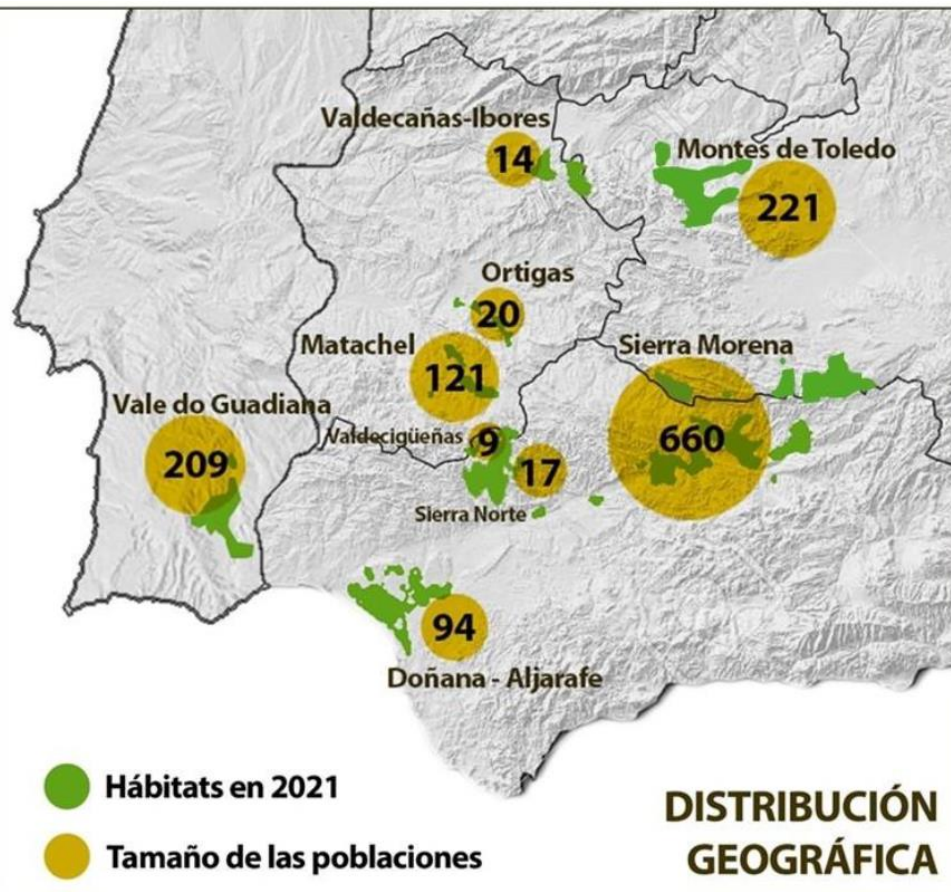


2002 → 2015 → 20??

Evolución de la población de lince ibérico en España y Portugal (2002-2021)



- 1.365 individuals
 - 865 >1-year-old
 - 277 territorial females
 - 500 cubs born
- 5 populations >20 ind
 - 2 remnants
 - 3 reintroduced

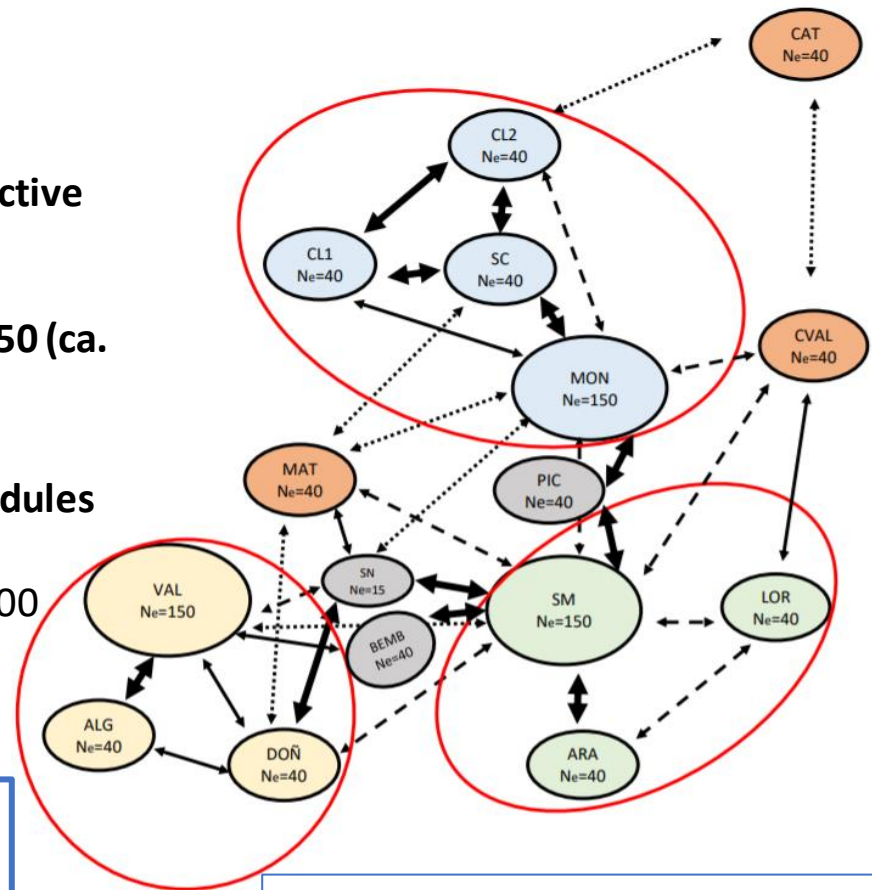




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Metapopulation Ne: FCS and genetic viability

- **Migration rates** must be between **1-4 migrants/generation**
- **8 additional populations** must be created.
- All populations must be of **$N_{ex}=40$ (50 reproductive females)**
- At least **three populations** should reach **$N_{ex}=150$ (ca. 190 reproductive females)**.
- Viable scenario with **three well connected modules**
- A sum of **$N_{ex} \geq 865$** is needed, which implies 2,200 mature individuals \approx **1,100 breeding females**.



- Focus reintroduction efforts in well-connected populations.
- Increase the target to 50 reproductive females.
- 1100 breeding females as FRP for demographic plus genetic viability

Laikre, L., F. Olsson, E. Jansson, O. Hossjer and N. Ryman (2016). "Metapopulation effective size and conservation genetic goals for the Fennoscandian wolf (*Canis lupus*) population." *Heredity* 117(4): 279-289.

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Dank je!

