

# GENETIC VARIABILITY IN WILD AND DOMESTIC POPULATIONS OF *INGA EDULIS* MART. (*FABACEAE*) IN PERUVIAN AMAZON

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The "boom" in the loss of biodiversity in the Amazon came during the second half of the twentieth century. Recognising the potential importance of agroforestry systems for native tree species conservation, the development agencies encourage local communities to undertake additional transfers of tree germplasm from local natural stands into farmland populations. In recent years, attention has been focused on wide genus of *Inga* as potentially useful multipurpose trees in such agroforestry systems.

The objective of our study is to characterise the level and structure of genetic variation and to detect polymorphism in domestic and wild populations of *Inga edulis* in Peruvian Amazon.



**Domestic populations**  
 (agricultural and agroforestry systems, experimental fields, gardens etc.)  
 (n=201)  
 • Iquitos (n=70)  
 • Yurimaguas (n=9)  
 • Pucallpa (n=67)  
 • Selva Central (n=55)



**Wild populations**  
 (original vegetation) (n=62)  
 • National Reserve Pacaya Samiria (n=18)  
 • Reserved Zone Sierra del Divisor (n=5)  
 • Rio Utiquinia (n=12)  
 • Experimental Forest Macuya (n=26)



**Fieldwork:**  
 ✓ 11/2009 to 3/2012  
 ✓ Mature trees (Ø in 10-30 cm, height) randomly selected (distance > 200 m)  
 ✓ GPS coordinates and altitude  
 ✓ Morphological description (qualitative and quantitative parameters)  
 ✓ Voucher specimens  
 ✓ DNA sample preserved in silica gel

**Labwork:**  
 ✓ 4/2012 to 9/2012  
 ✓ Microsatellites  
 ✓ Genomic DNA extraction  
 ✓ Polymerase Chain Reaction amplification  
 • 5 loci (4) *I. edulis*, (1) *Pithecellobium elegans* (Forward oligonucleotide fluorescently labelled)  
 PCR profile: 95 ° C for 2 min; 95 ° C for 15 s, 55/59 ° C for 30 s, 72 ° C for 30 s, 30 cycles; 72 ° C for 15 min  
 Fragment sizing and visualization (Figure 1.)  
 • ABI PRISM 310 automated sequencer, ABI GENESCAN and GENOTYPER SOFTWARE

**Data analysis:**  
 ✓ Morphological structure  
 • two-sample  $T^2$  test; (ANOVA); Tukey HSD test (software Statistica 7.0 CZ)  
 ✓ Genetic structure (SSRs)  
 • Inbreeding coefficients ( $F_{IS}$ ,  $F_{IT}$ ,  $F_{ST}$ )  
 • Number of alleles per locus for the species complex ( $A$  and  $A_S$  - mean  $A$  across loci)  
 • Observed heterozygosity ( $H_0$ )  
 • Expected heterozygosity ( $H_e$  and  $H_T$  mean  $H_e$  across loci, the total expected heterozygosity for the species complex)  
 • Hardy – Weinberg equilibrium (HWE) (Arlequin 2000, for AMOVA; POPGEN for Shanon's diversity index; Test for HWE by comparing the sample with random permutations of the data)

Table 1. Results (n=201 domestic population)

Locus	Range (bp)	No. of alleles
Inga03	43 - 87	25
Inga05	119-141	9
Inga08	130 - 165	20
Inga33	143-241	22
Pel5	179 - 215	32

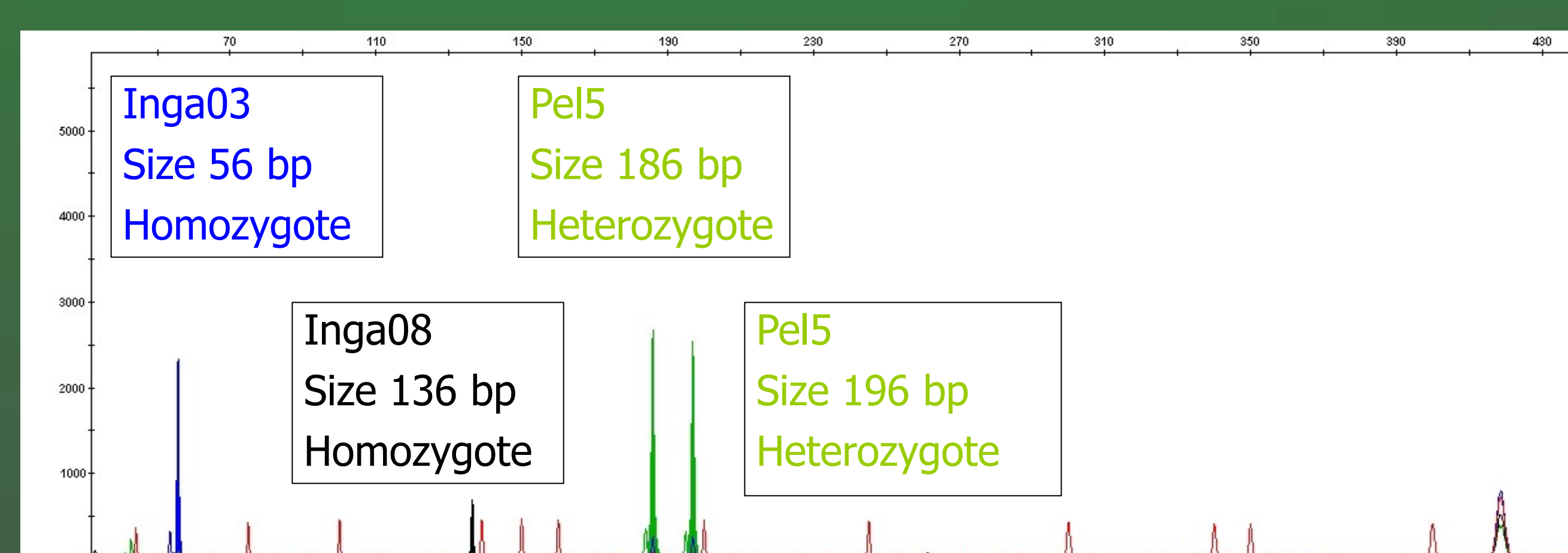


Figure 1. Example of microsatellite peaks

**First results:**  
 In the Table 1. are indicated first obtained results from the domestic population (n=201). The range in (bp) and number of alleles per each of 5 loci are indicated.

This research was financially supported by: Czech Development Cooperation Project entitled "Sustainable use of natural resources in Peruvian Amazon" Project No. 23/MZe/B/07-10; The Academy of Science of The Czech Republic and the National Council for Science, Technology and Technological Innovation, Peru, binational project entitled "Morphological and genetic diversity of indigenous tropical trees in the Amazon – model study of *Inga edulis* Mart. in Peruvian Amazon"; Foundation "Nadace Nadání Josefa, Marie a Zdeňky Hlávkových", Czech Republic