

Fig. 1. *HinfI* polymorphism in porcine *LEP* gene. Lane 1, 20-bp ladder; lanes 2, 4 and 7, heterozygotes *T/C*; lanes 3 and 6, homozygotes *T/T*; lanes 5 and 8, homozygotes *C/C*.

agarose gel. Two alleles were detected: allele *T* – fragment 152 bp (not cut) and allele *C* – fragments 68 and 84 bp. Three different genotypes observed are shown in Fig. 1.

Mendelian inheritance/allele frequencies: Codominant inheritance was confirmed in selected families of different breeds as well as in the Hohenheim PiGMaP three-generation pedigrees Meishan × Pietrain and Wild Boar × Meishan.² Allele frequencies in unrelated animals of different breeds are presented in Table 1.

Table 1. Frequencies of *LEP* alleles

Breed	n	Allele	
		<i>T</i>	<i>C</i>
Meishan	7	0	1
Large White	14	0.82	0.18
Landrace	12	0.96	0.04
Pietrain	6	0.75	0.25
Black Pied Pöestice	7	0.79	0.21
Hampshire	6	0.92	0.08
Czech Meat Pig	11	0.73	0.27

Chromosomal location: The *LEP* gene has been mapped to porcine chromosome 18.^{1,3}

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References

- 1 Neuenschwander S. *et al.* (1996) *Anim Genet* 27, 275–8.
- 2 Geldermann H. *et al.* (1996) *J Anim Breed Genet* 113, 381–7.
- 3 Sasaki S. *et al.* (1996) *Mamm Genome* 7, 471–2.

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The microsatellite marker (*BFRO 002*) characteristic for different geographically remote brown trout, *Salmo trutta* L., populations

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Source/description: A polymorphic locus, characterized by dinucleotide repeat (GT)₁₄, designated as *BFRO 002*, was isolated

from a library of size-selected (100–600 bp) *Sau3AI* genomic restriction fragments from marble trout (*S. trutta marmoratus*) cloned into pBluescript II SK+ (Stratagene) vector, previously restricted with *Bam*HI, and propagated in Epicurian *Coli* Competent Cells (Stratagene). Screening of the library was performed by the Chemilluminescence Quick-Light™ Genome Mapping Probe Kit (FMC) applying (CA)_n and (GA)_n oligonucleotides as probes. DNA sequence (GenBank accession no. AF 005074) was obtained by conventional dideoxy method using DIG *Taq* DNA Sequencing Kit (Boehringer Mannheim). Primers flanking the repetitive motif were designed.

Primer sequences (5'–3')

A 10/2 F (GT-strand): ATGTTTTTGTACTGCACTATGTATT

A 10/2 R (AC-strand): GGAGATAAGAGTCAACGAGGC

(5'-digoxigenin labelled)

PCR conditions: Amplification was carried out in 10 µl containing 50 ng genomic DNA, 0.75 µM each primer, 0.2 mM dNTPs, 1.5 mM MgCl₂, 20 mM Tris-HCl, 50 mM KCl and 0.5 U *Taq* Polymerase. Thermal cycling reaction was performed under the following conditions: 3 min at 94°C followed by 29 cycles of 94°C for 45 s and 60°C for 25 s. The PCR products were run on a direct blotting electrophoresis device GATC 1500 (Gesellschaft für Analyse-Technik und Consulting mbH) using denaturing 4% polyacrylamide gel and detected by colour reaction with alkaline phosphate conjugated anti-digoxigenin antibodies.

Polymorphism: In the test material four alleles (118, 120, 122, and 126 bp; Fig. 1) were detected in 35 brown and 25 marble trout. According to the mtDNA D-loop genotyping¹ and to the geographical origin of brown trout, 14 were recognized as Danubian, 19 as Atlantic and two as Mediterranean type of *S. trutta*. The allele 118 was characteristic only for brown trout of Atlantic origin, meanwhile the alleles 122 and 126 were found in the Danubian trout population, the latter also being characteristic for marble trout. The two specimens, characterizing Mediterranean brown trout, were homozygous for the allele 120.

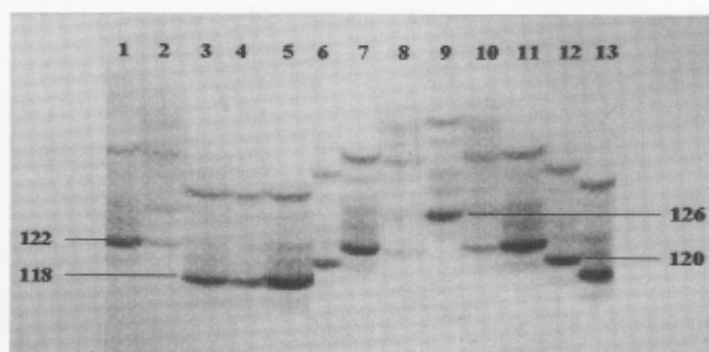


Fig. 1. Four alleles representing five different genotypes. Lanes 1, 2, 7, 8, 10 and 11, Danubian brown trout; lanes 3, 4, 5 and 13, Atlantic brown trout; lanes 6 and 12, Mediterranean brown trout; lane 9, Marble trout. Allele sizes are indicated in the margins.

Other comments: The PCR with A 10/2 F and A 10/2 R primers failed to amplify genomic DNA from rainbow trout (*Oncorhynchus mykiss*) and grayling (*Thymallus thymallus*).

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Reference

- 1 Bernatchez L. *et al.* (1992) *Mol Ecol* 1, 161–73.

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