The background features a stylized illustration of oak leaves and acorns. A large, light green oak leaf with prominent veins is positioned at the top. Below it, two acorns are depicted: one is a reddish-brown acorn with a textured cap, and the other is a more detailed, brown acorn with a textured cap and a smooth, light brown nut. The entire scene is set against a light orange background with a dashed white border.

Hybridization and recruitment in a mixed stand with 3 different oak species

Klára CSEKE

Hungarian Forest Research Institute

ProCoGen Workshop

Szombathely

1st-3rd September 2014

INTRODUCTION:

The 'oak-case'









- closely related minor species within a broader species complex , but different ecological demand (Schwarz 1936, Georgescu and Moraru 1948, Georgescu and Ciobanu 1964, Magič 2000 , Požgaj 1986, Hedge és Yaltirik 1994, Mátyás 1967, Soó 1970, etc.)

↔ ecotypes of one species

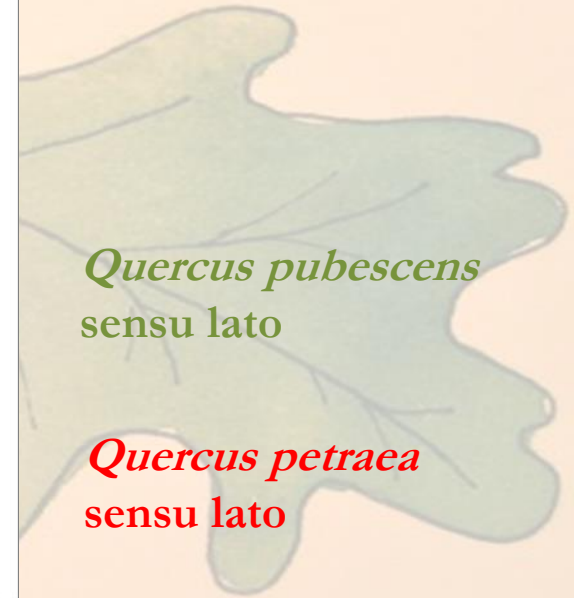
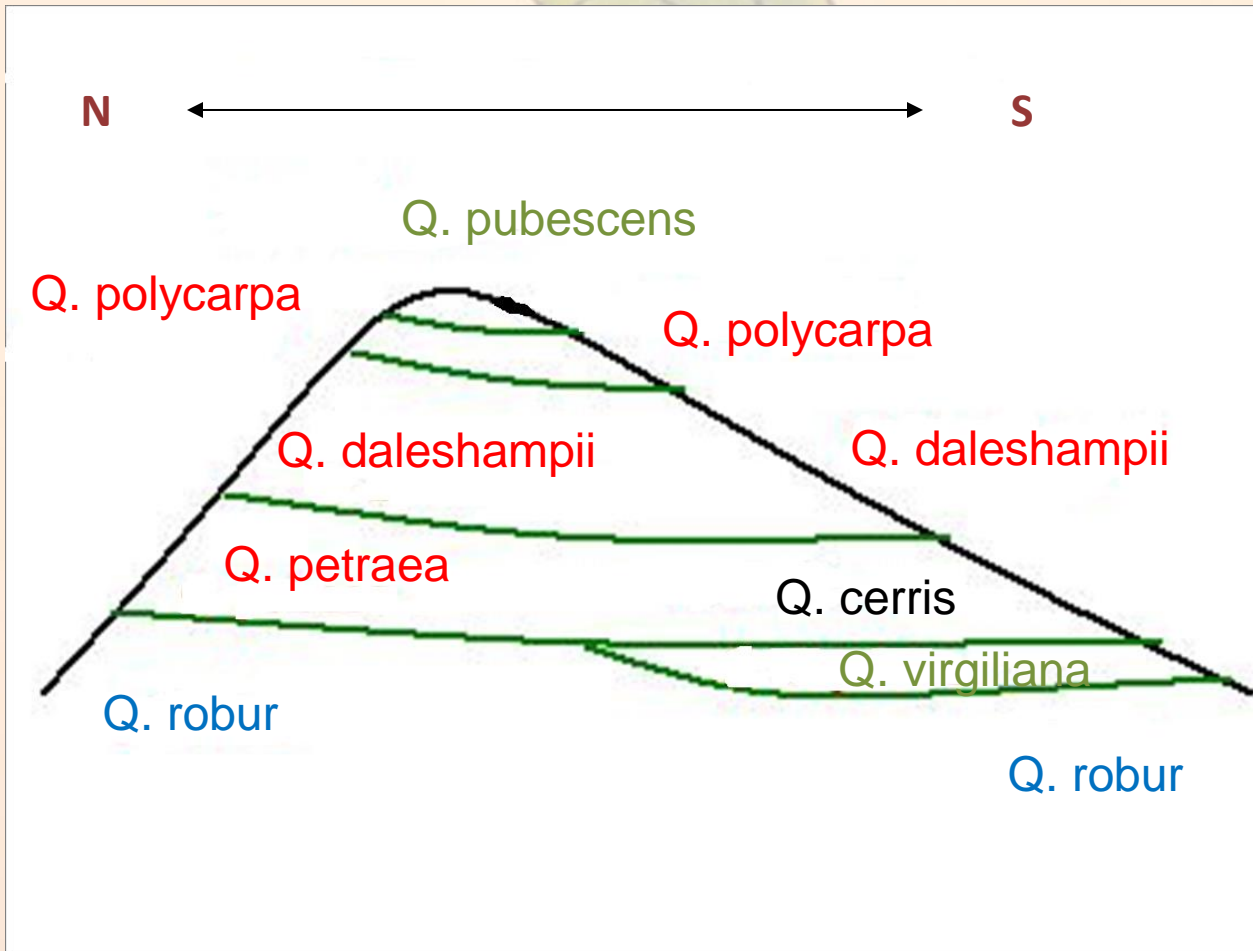
(Nixon 1993, Bussotti and Grossoni 1997, Steinhoff 1998, Kleinschmit and Kleinschmit 2000)

- supposed general hybridization (number of trees with intermediate morphology)
- accumulating 'signs' as moving south and east in Europe

White oaks in the Carpathian region

pedunculate oak complex <i>Quercus robur</i> sensu lato		sessile oak complex <i>Quercus petraea</i> sensu lato			pubescent oak complex <i>Quercus pubescens</i> sensu lato		
<i>Quercus robur</i> s.str.	<i>Quercus pedunculiflora</i>	<i>Quercus petraea</i> s.str.	<i>Quercus dalechampii</i>	<i>Quercus polycarpa</i>	<i>Quercus pubescens</i> s.str.	<i>Quercus virgiliana</i>	<i>Quercus frainetto</i>
							

A theoretical model of the ecological niches of oaks in the Carpathian Basin



Quercus pubescens
sensu lato

Quercus petraea
sensu lato

Quercus robur
sensu lato

Molecular genetic studies of European white oaks

- species and population level
 - mainly *Quercus petraea* and *Quercus robur*
 - no distinct separation

(cpDNS: Petit és mtsai 2002, Bordács és mtsai 2002; Izoenzim: Kremer és mtsai 1998, Zanetto és Kremer 1995, Le Corre és mtsai 1998, Hertel és Degen 2000; RAPD: Moreau és mtsai 1994, Bordács és Burg 1997; AFLP: Mariette és mtsai 2002; Bakker és mtsai 2001; Coart és mtsai 2002)

- fine-scale genetic studies:
 - geneflow (Streiff és mtsai 1998, OAKFLOW Projekt 2001-2005, stb.)
 - hybridization, introgression (Gugerli és mtsai 2007, Curtu és mtsai 2007, Salvini és mtsai 2009, stb.)
 - spatial genetic structure, clonal ratio (Valbuena-Carabana és mtsai 2007, Copini és mtsai 2005)



Material and methods:

Intensive study plot (ISP)

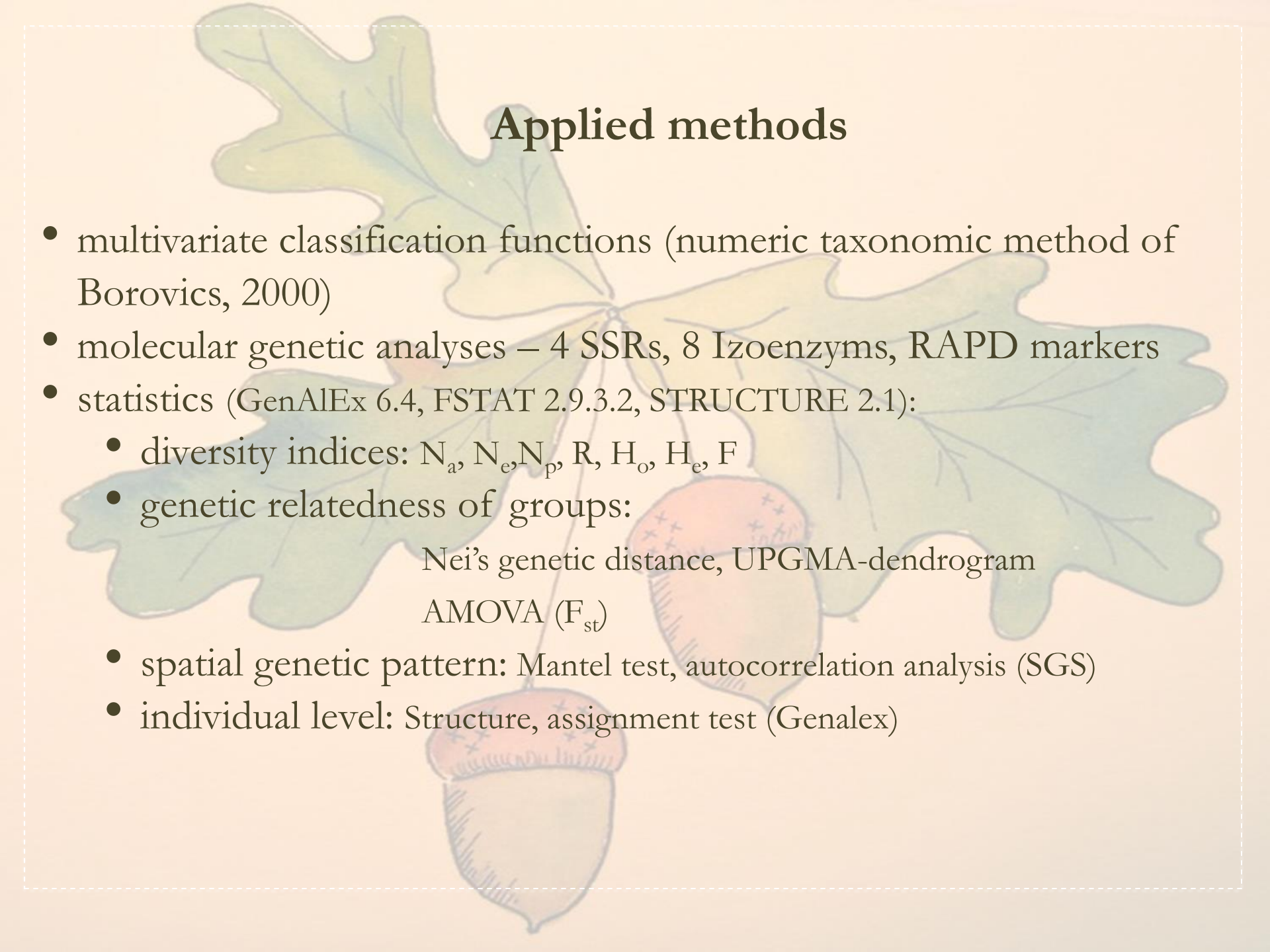
- OAKFLOW Project, 2001-2005, ISP Sopron
- xerotherm mixed oak stand, high diversity of native white oak species
- long time coppicing!
- mapping of 400 adult trees + two juvenile clumps (75 saplings) and 400 acorns from 20 mother trees



- ecological gradient
 - humid valley → warm, dry hilltop
 - *Q. robur* → *Q. petraea*, *Q. cerris* → *Q. pubescens*
 - also minor species, intermediate forms and hybrids



Applied methods

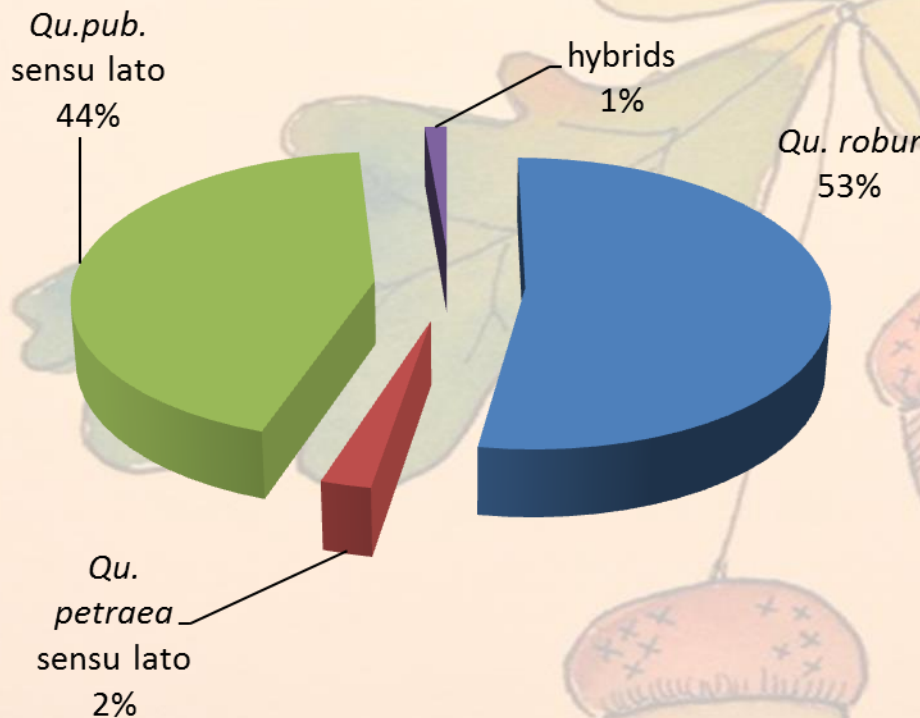


- multivariate classification functions (numeric taxonomic method of Borovics, 2000)
- molecular genetic analyses – 4 SSRs, 8 Izoenzymes, RAPD markers
- statistics (GenAlEx 6.4, FSTAT 2.9.3.2, STRUCTURE 2.1):
 - diversity indices: N_a , N_e , N_p , R , H_o , H_e , F
 - genetic relatedness of groups:
 - Nei's genetic distance, UPGMA-dendrogram
 - AMOVA (F_{st})
 - spatial genetic pattern: Mantel test, autocorrelation analysis (SGS)
 - individual level: Structure, assignment test (Genalex)

Results, conclusions



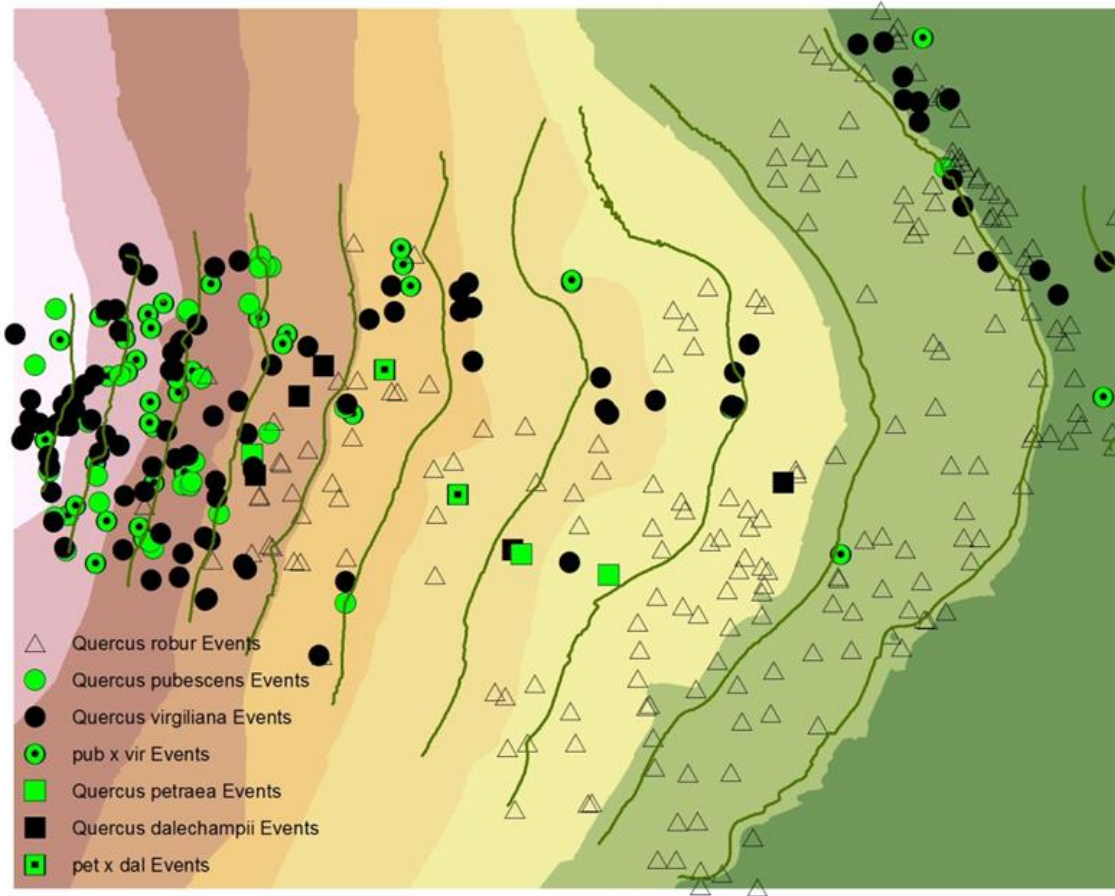
Numeric classification



Distribution of species

Taxon	number	ratio
Qu. robur	198	52,7%
Qu. petraea	2	0,5%
Qu. dalechampii	5	1,3%
Qu. petraea × dalechampii	2	0,5%
Qu. pubescens	29	7,7%
Qu. virgiliana	96	25,5%
Qu. pubescens × virgiliana	39	10,4%
Qu. petraea × virgiliana	1	0,3%
Qu. polycarpa × virgiliana	1	0,3%
Qu. robur × pubescens	2	0,5%
Qu. robur × virgiliana	1	0,3%
Total	376	100%

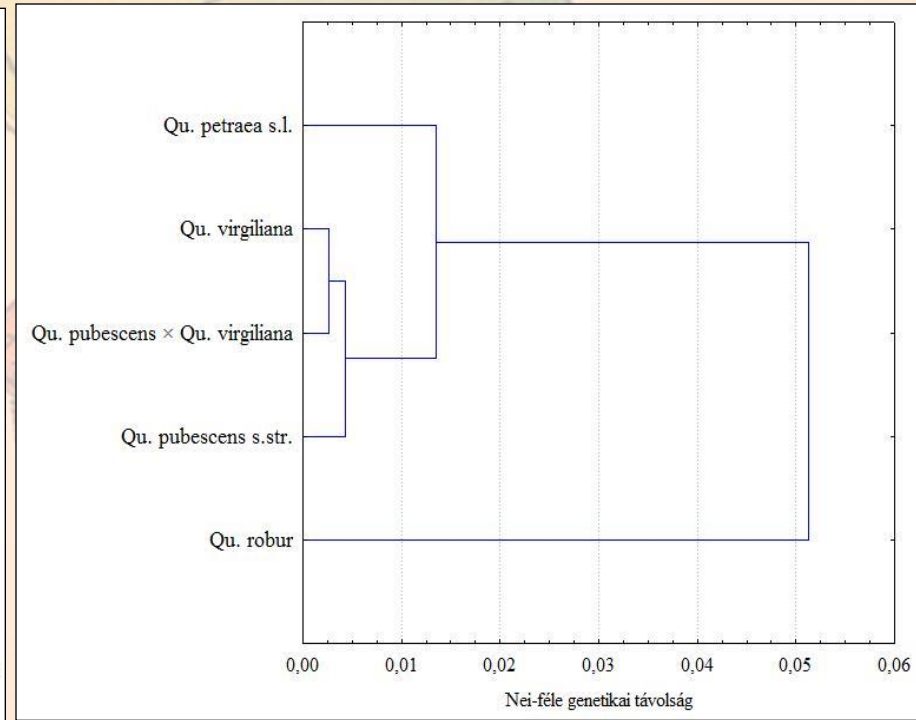
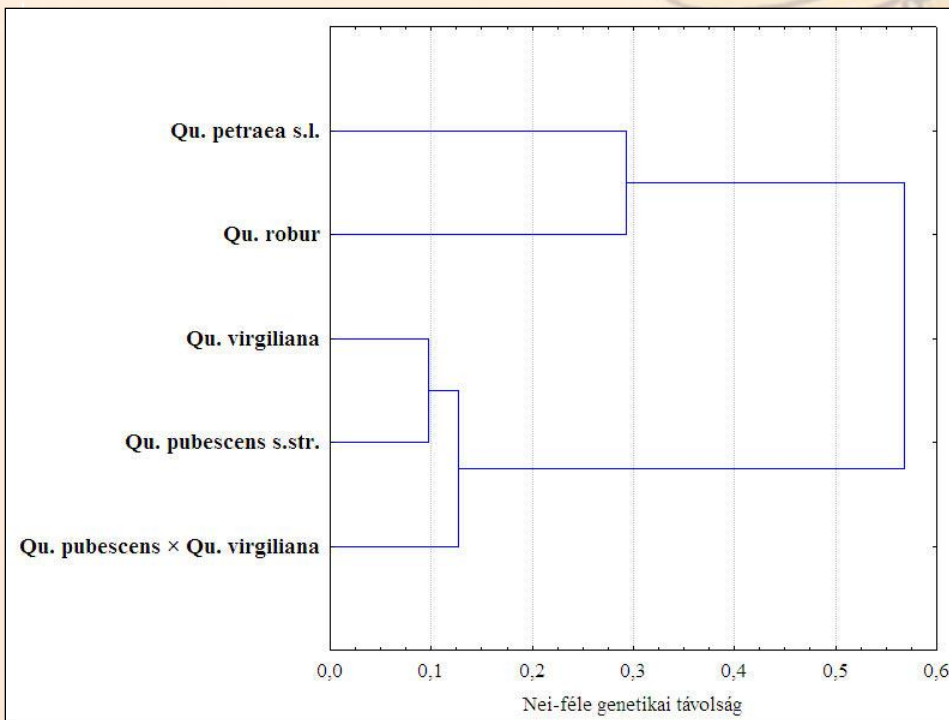
Distribution of species, ratio of clones



- along the ecological gradient
- ratio of clones 9%
 - pubescent oaks: vegetative strategy more diversified and frequent,
 - clones appeared also in the juvenile clumps

Comparison of genetic structure of the three oak groups

- no distinct separation, low between groups variability by AMOVA
- no evidence of genetic differentiation within the pubescent oak complex



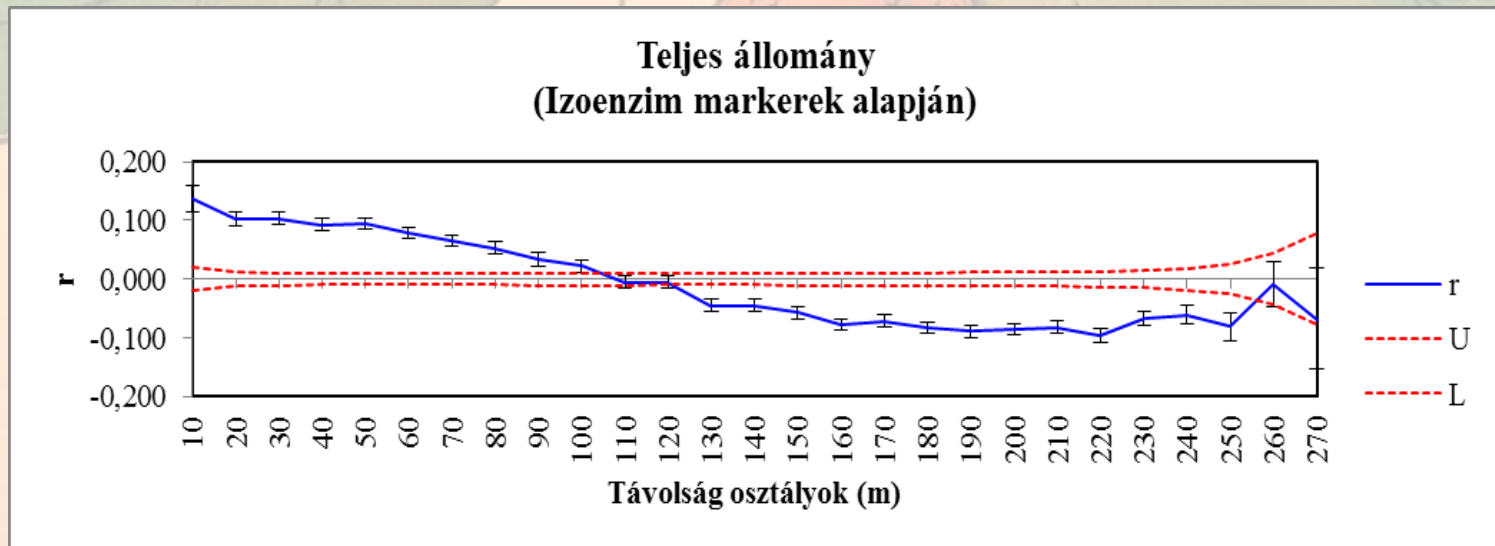
- SSR (RAPD) markers

- Isozymes

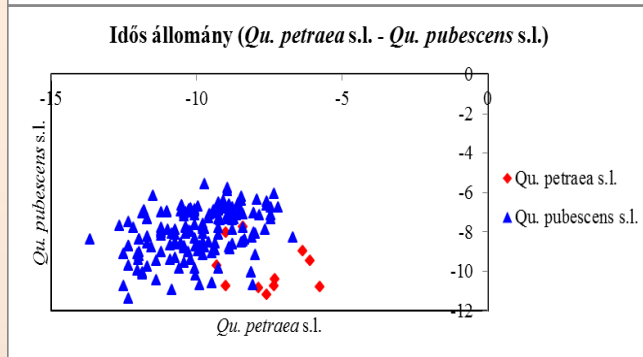
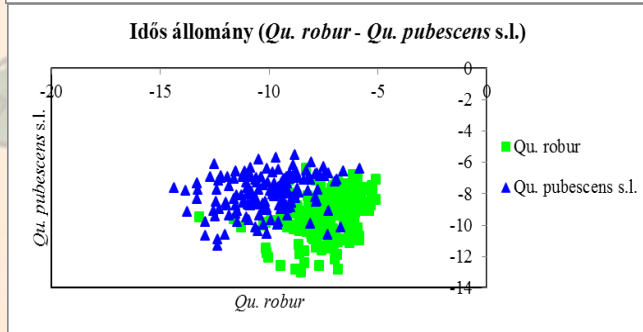
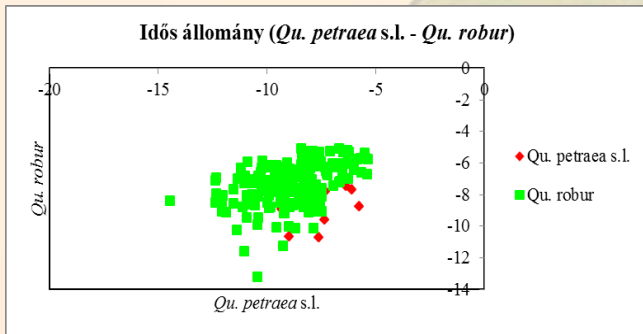
combined strategy of various different methods and aspects!

Spatial genetic structure (SGS)

- *Only a weak correlation could be identified concerning the two main oak species (pedunculate oak and pubescent oaks) groups separately.*
- *A clear spatial genetic structure was detected as the whole stand was analysed. This phenomenon could be referable also to the high number of introgressed individuals.*



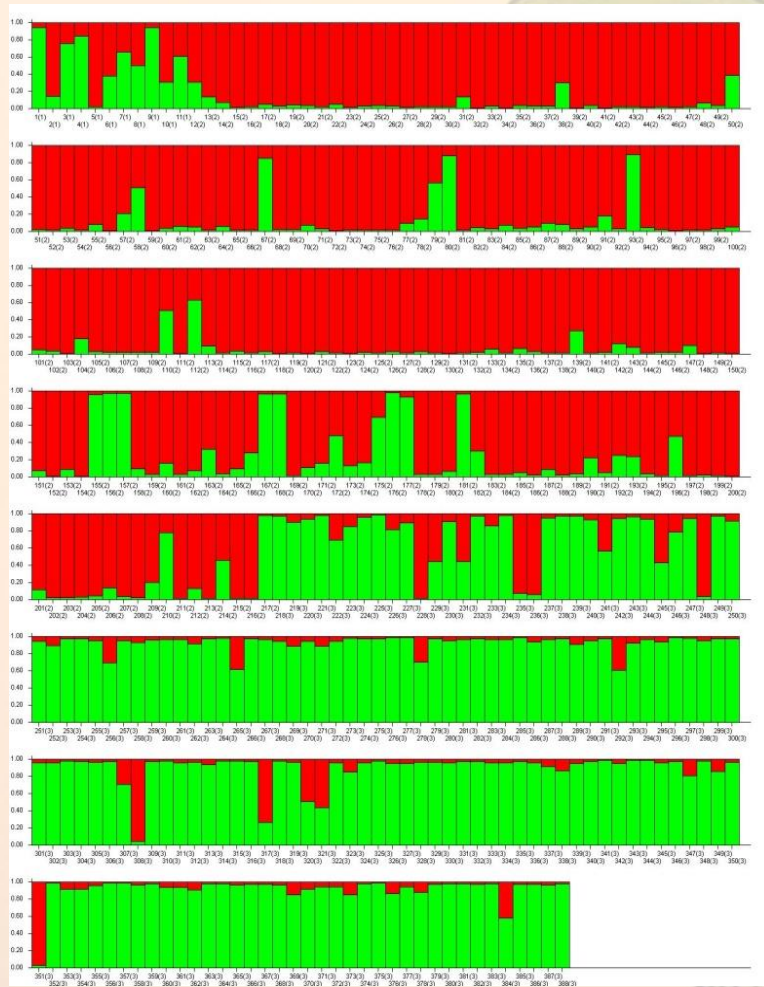
Traces of introgression: *Assignment test*

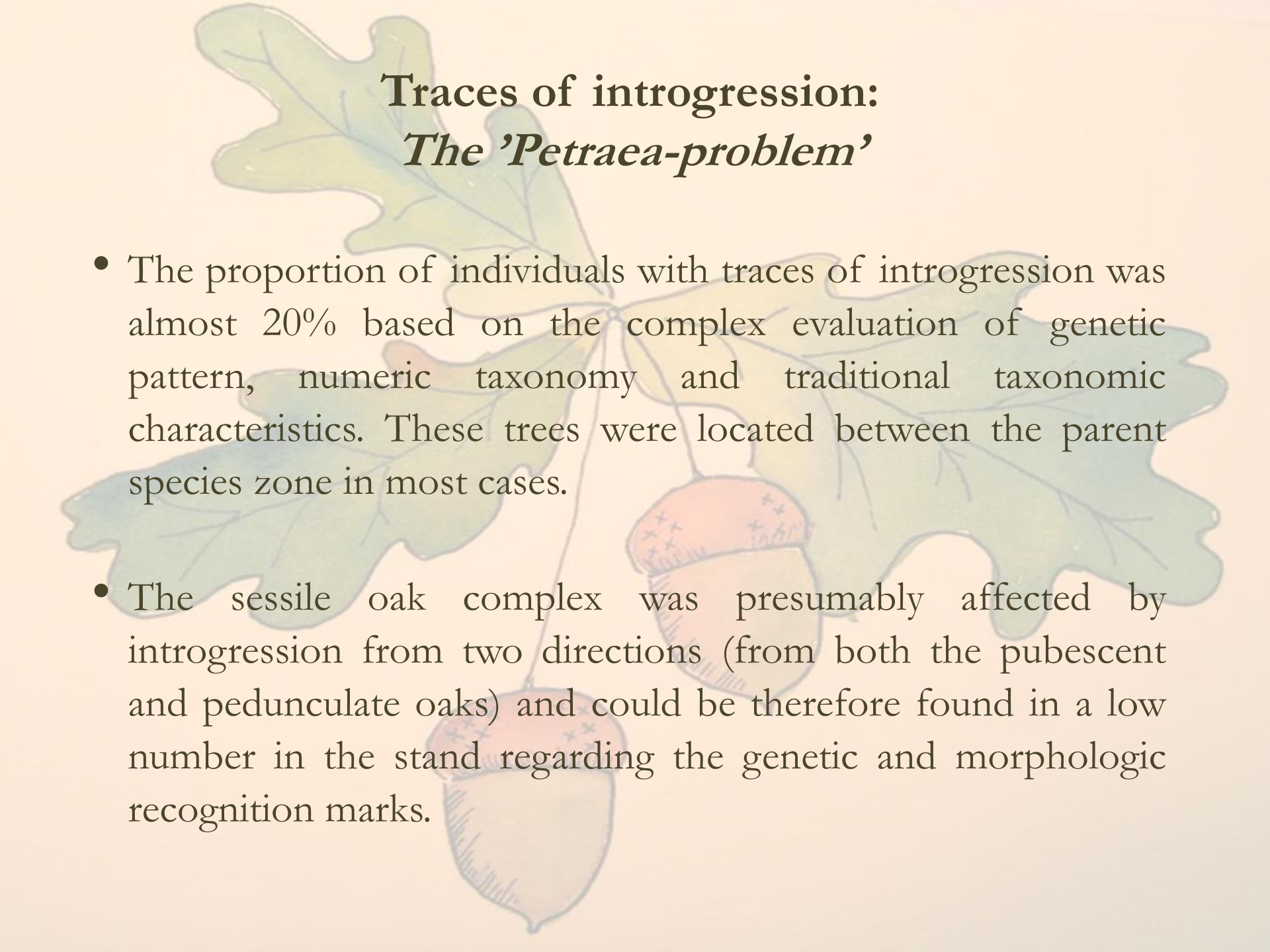


- check and rearrange previously observed groups (based on the individual genotypes)
- 15% of the individuals moved to an other species group
- mainly to the sessile oak group (43) and 65% (28) from the pedunculate oak group

Traces of introgression: *Structure K-clustering*

- two clusters:
,robur' and ,pubescens' type
- hybrid genotype ratio:10%
- homogeneous 'pubescens' cluster
- sessile oaks partly among pubescent oaks and hybrid genotypes → *affected by introgression*



The background features a stylized illustration of oak leaves and acorns. The leaves are light green with darker green veins, and the acorns are brown with a reddish-brown cap. The illustration is semi-transparent and serves as a decorative backdrop for the text.

Traces of introgression: *The 'Petraea-problem'*

- The proportion of individuals with traces of introgression was almost 20% based on the complex evaluation of genetic pattern, numeric taxonomy and traditional taxonomic characteristics. These trees were located between the parent species zone in most cases.
- The sessile oak complex was presumably affected by introgression from two directions (from both the pubescent and pedunculate oaks) and could be therefore found in a low number in the stand regarding the genetic and morphologic recognition marks.

Some other conclusions...

- In case of oak stands on mosaic sites, where different oak species are able to grow together due to the various microhabitats, hybridization could be very frequent.
- However not all the individuals with hybrid genotype showed a real transitional morphology. For taxonomic research purpose a combined strategy of various different methods and aspects should be used.
- Genetic diversity analyses without the clone genotypes showed no drastic genetic depression in the stand due to the presence of clones. Coppicing could presumably facilitate the protection of the native stand in this case. During the procedure of designation of in situ reservation sites, it is recommended to consider this possibility when the given stand is worthy of protection in the high taxonomical or morphological diversity point of view.



*Thank you for your
attention!*