Forest Research Institute

„Characteristics of genetic diversity and differentiation of progeny and mother stands of European Beech in Poland”

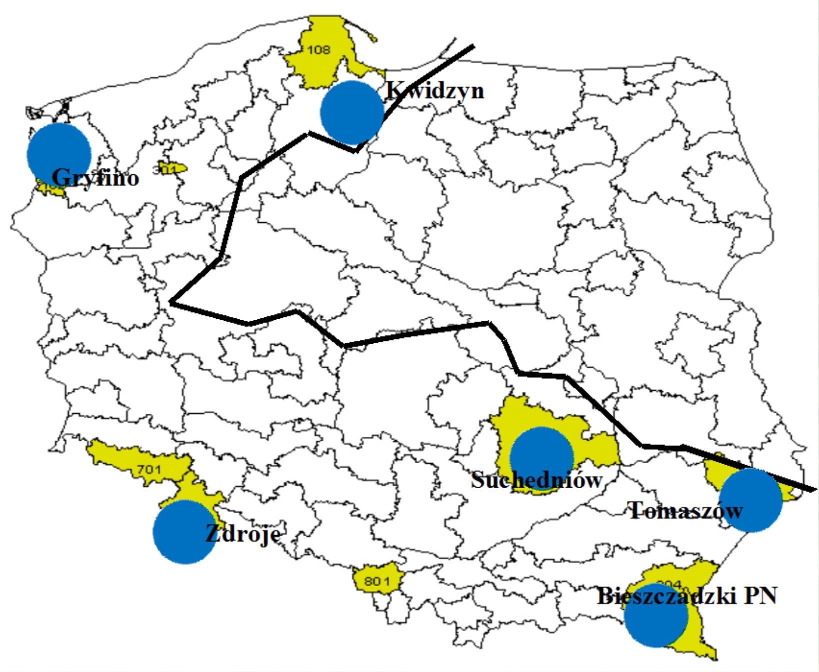
Małgorzata Sulkowska, Justyna Nowakowska

Sekocin 2010

Present genetic structure of European beech (*Fagus sylvatica* L.) populations was formed within last few thousand years influenced many different factors not only environmental (glacial epoch) and genetic (selection) but also anthropogenic. Beech is very important forest tree species in Poland and it ocupies 5,1% of forest area in Poland.

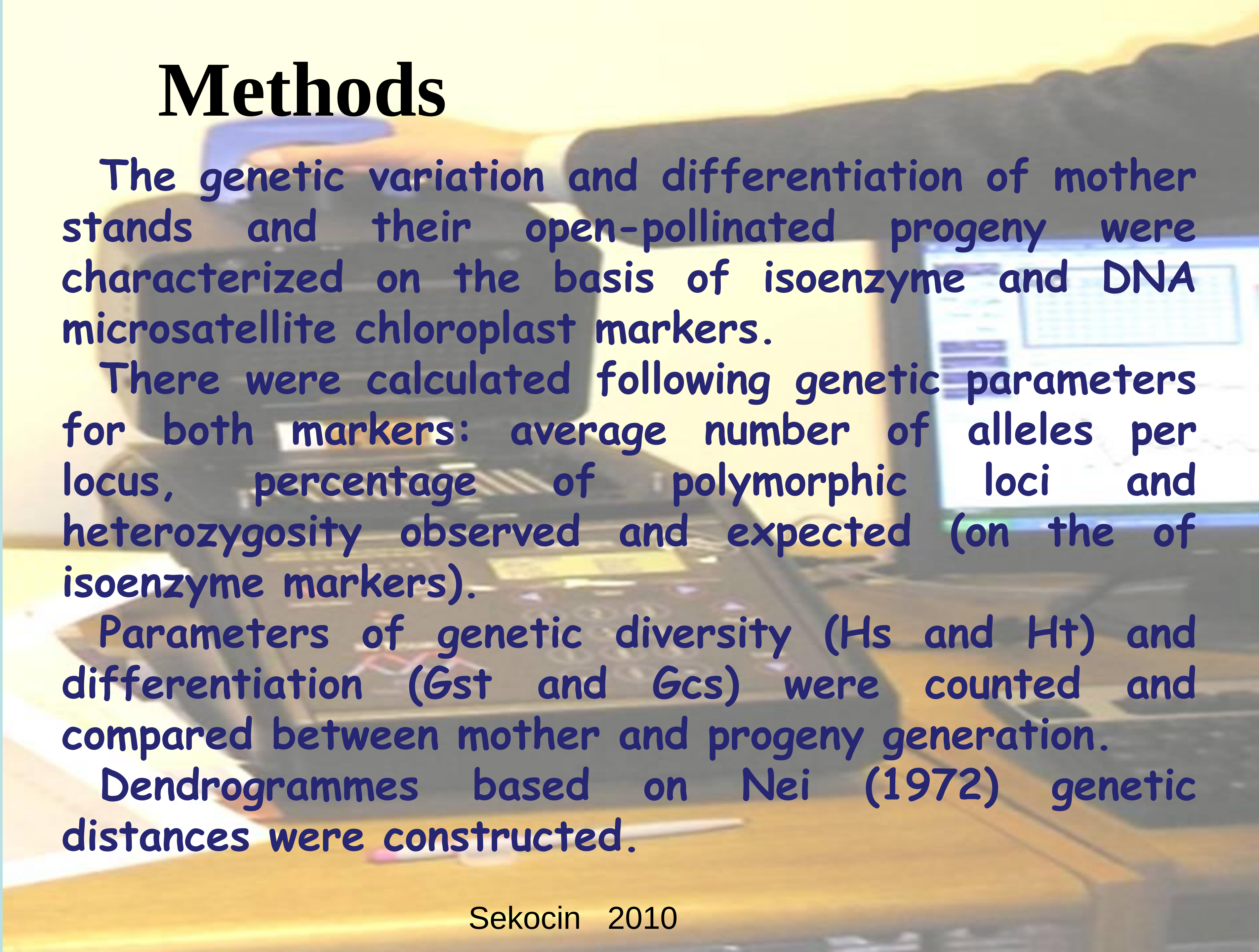
In Poland, beech attains its north-eastern limit of natural range, which is limited by: continental climate, soil conditions, winter temperatures and air humidity.

Methods



The investigated beech populations represent Beech Trial in Bystrzyca Klodzka. The were classified according to phytosociogical characteristics as the following plant associations: *Galio-odorati-Fagetum* (Gryfino and Kwidzyn), *Dentario glandulosae-Fagetum* (Bieszczadzki National Park), *Luzulo-luzuloides-Fagetum* (Suchedniów, Tomaszów), *Dentario enneaphyllidis-Fagetum* (Zdroje). The genetic structure of these populations was analyzed. Thirty individuals per one generation (mother, progeny stands) in every provenance were investigated.

Methods



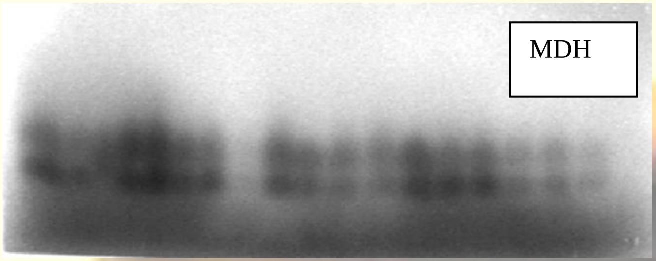
The genetic variation and differentiation of mother stands and their open-pollinated progeny were characterized on the basis of isoenzyme and DNA microsatellite chloroplast markers.

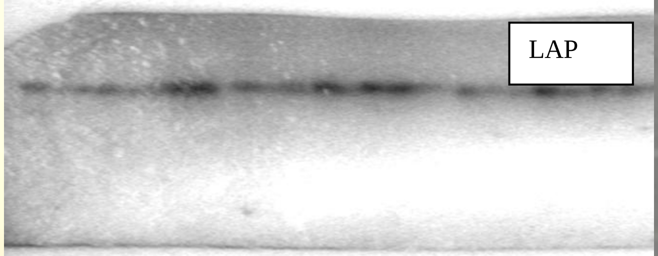
There were calculated following genetic parameters for both markers: average number of alleles per locus, percentage of polymorphic loci and heterozygosity observed and expected (on the of isoenzyme markers).

Parameters of genetic diversity (Hs and Ht) and differentiation (Gst and Gcs) were counted and compared between mother and progeny generation.

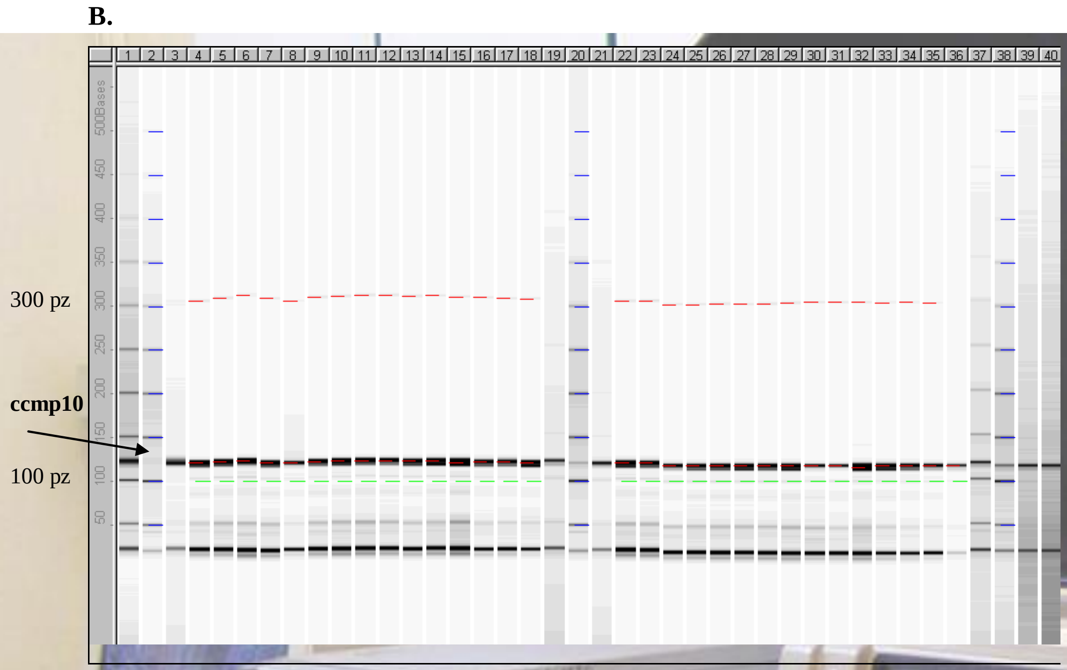
Dendrogrammes based on Nei (1972) genetic distances were constructed.

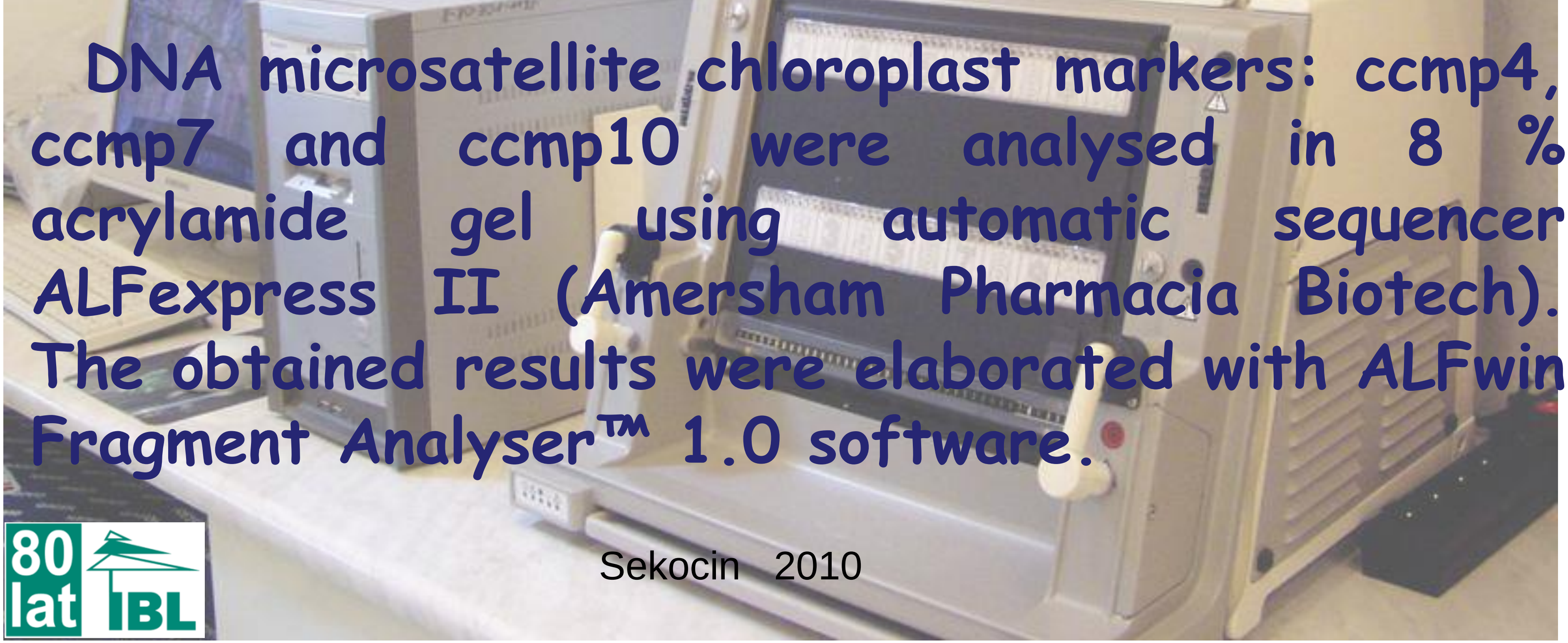
Methods





Following enzyme systems were analysed: glutamate-oxaloacetate transaminase (GOT – EC 2.6.1.1 – *Got-2*), leucine aminopeptidase (LAP – EC 3.4.11.1 – *Lap-1*), malate dehydrogenase (MDH – EC 1.1.1.37 – *Mdh-1*, *Mdh-2*, *Mdh-3*), menadione reductase (MNR – EC 1.6.99.2), phosphoglucomutase (PGM – EC 2.7.5.1), phosphoglucose isomerase (PGI – EC 5.3.1.9 – *Pgi-2*), shikimate dehydrogenase (SKDH – EC 1.1.1.25).



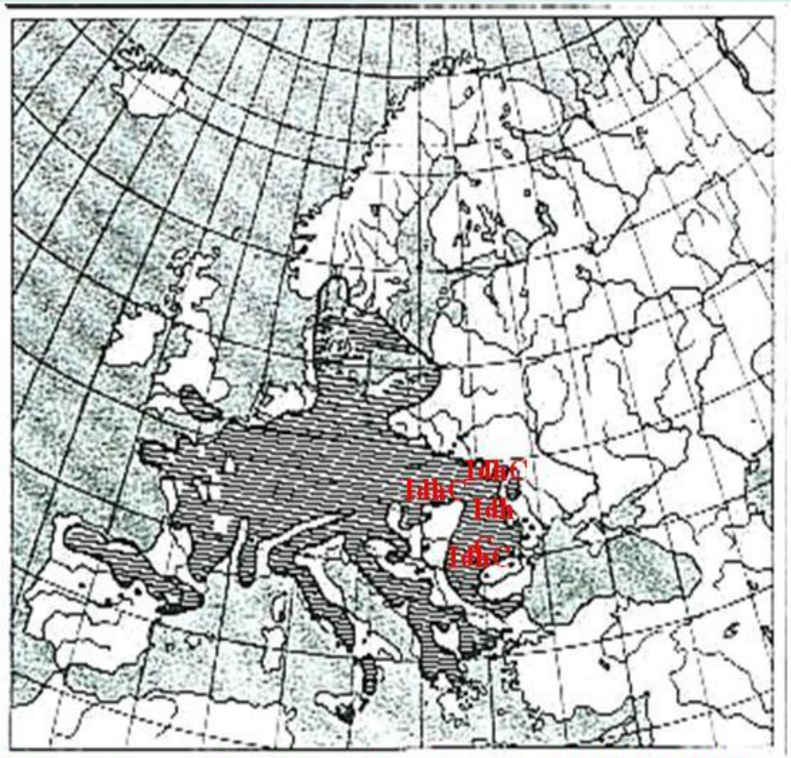


DNA microsatellite chloroplast markers: ccmp4, ccmp7 and ccmp10 were analysed in 8 % acrylamide gel using automatic sequencer ALFexpress II (Amersham Pharmacia Biotech). The obtained results were elaborated with ALFwin Fragment Analyser™ 1.0 software.

Sekocin 2010

Estimation of genetic differentiation of beech in Poland on the basis of isoenzyme analysis

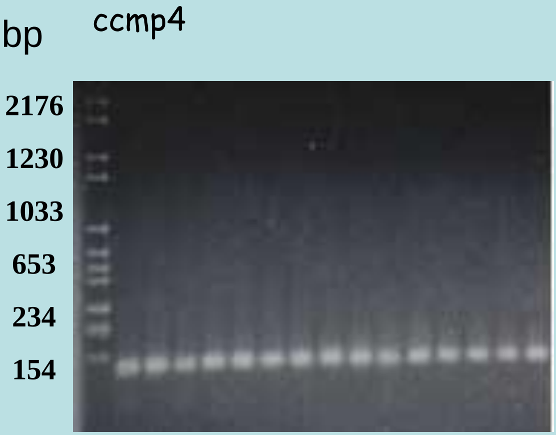
- There is slight decrease of genetic variation of beech populations towards the north of Poland, which can be explain the migration paths and selection after glacial period.
- The genetic differentiation of beech in Poland do not allowed to distinguish provenance regions
- The data showed mosaic character of species differentiation and its ecotype variation.

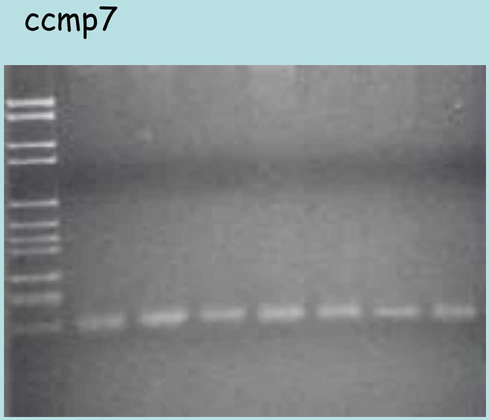


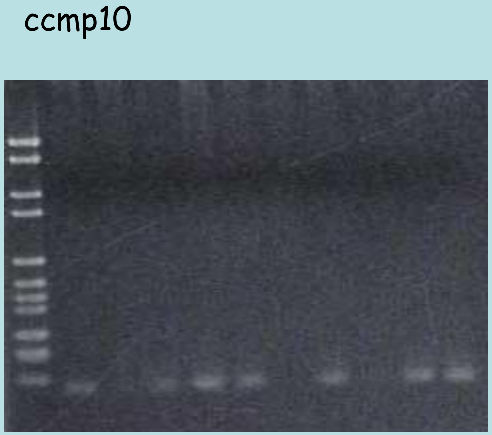
Migration path of beech on basis of Idh C allel.

Sułkowska, M. 2002: Analiza izoenzymatyczna wybranych proweniencji buka zwyczajnego (*Fagus sylvatica* L.) na powierzchni doświadczalnej w Bystrzycy Kłodzkiej. Sylwan 146 (2): 129-137.

Gömöry, D., Paule, L., Schvadchak, M., Popescu, F., Sułkowska, M., Hynek, V. & Longauer, R. 2003: Spatial patterns of the genetic differentiaton in European beech (*Fagus sylvatica* L.) at allozyme loci in the Carpathians and adjacent regions. *Silvae Genetica* 52(2): 78–83.





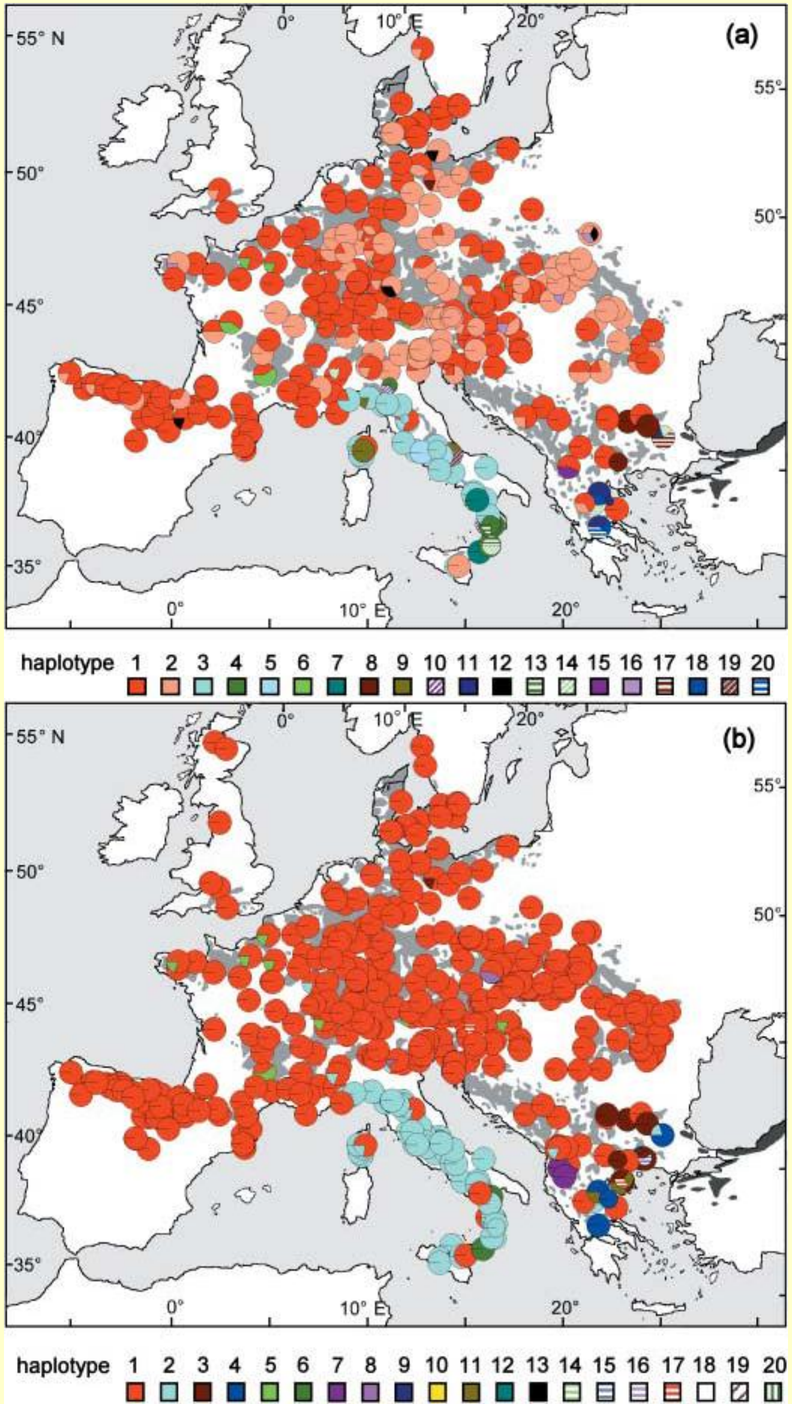


Familienstrukturen in Buchenbeständen (*Fagus sylvatica*)

Dissertation zur Erlangung des Doktorgrades, der Fakultät für Forstwissenschaften und Waldökologie

der Georg-August-Universität Göttingen

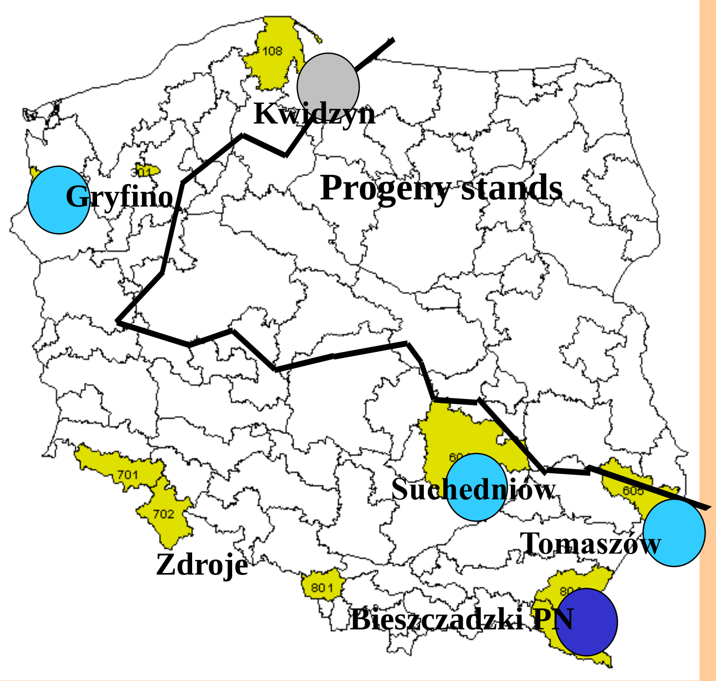
vorgelegt von, **Aikaterini Dounavi**, geboren in Athen (Griechenland), Göttingen 2000



Geographical distribution of
(a) chloroplast haplotypes detected using polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP),
(b) microsatellites (data for the Italian Peninsula were taken from Vettori *et al.*, 2004)

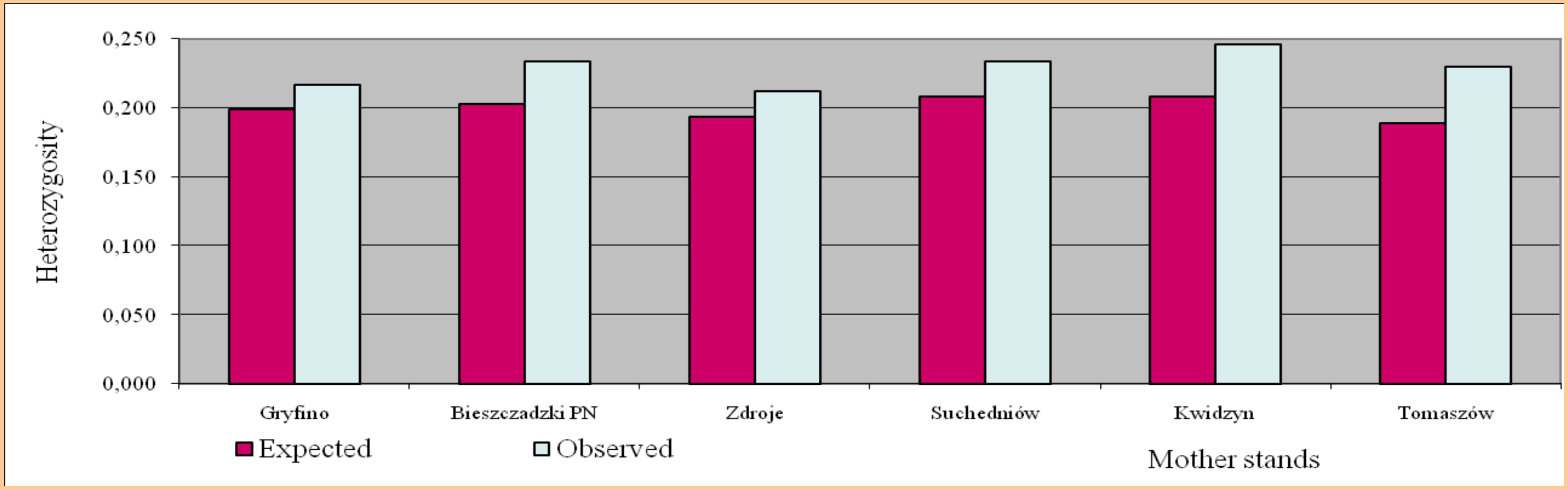
In: MAGRI, D., VENDRAMIN, G.G., COMPS, B., DUPANLOUP, I., GEBUREK, TH., GÖMÖRY, D., LATAŁOWA, M., THOMAS LITT, PAULE, L., ROURE, J.M., TANTAU, I., VAN DER KNAAP, W. O., PETIT, R.J., DE BEAULIEU, J-L 2006: A new scenario for the Quaternary history of European beech populations: palaeobotanical evidence and genetic consequences . New Phytologist 171 (1): 199-221

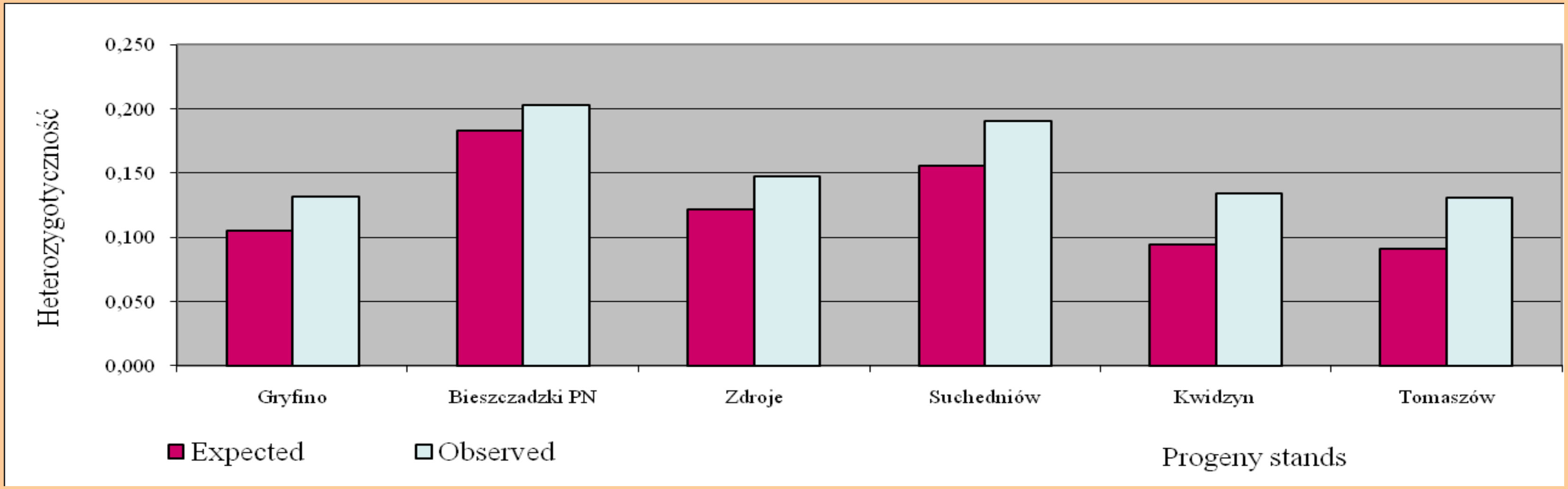
Isoenzyme markers – Average number of alleles per locus



Average number of alleles per locus ● 1,7 ● 1,8 ○ 1,9 ● 2,0 ● 2,1 ● 2,3

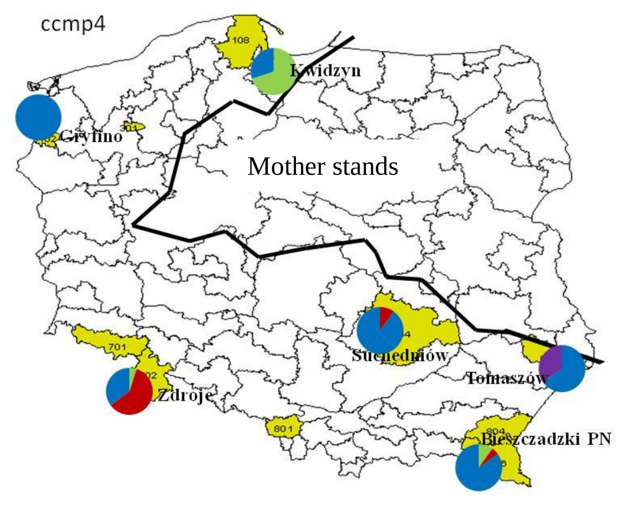
Isoenzyme markers – heterozygosity

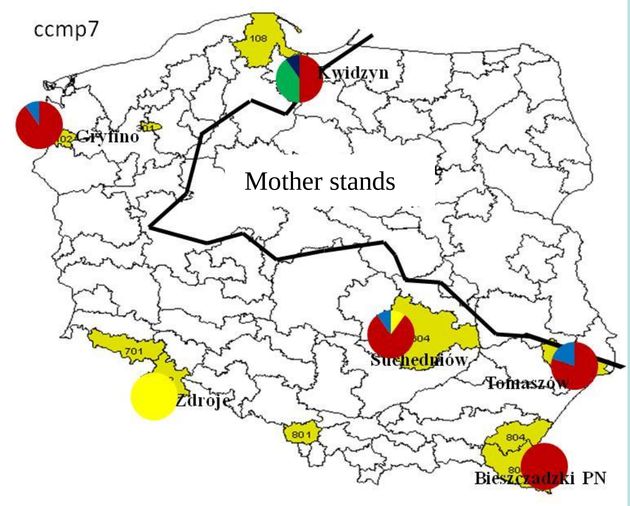


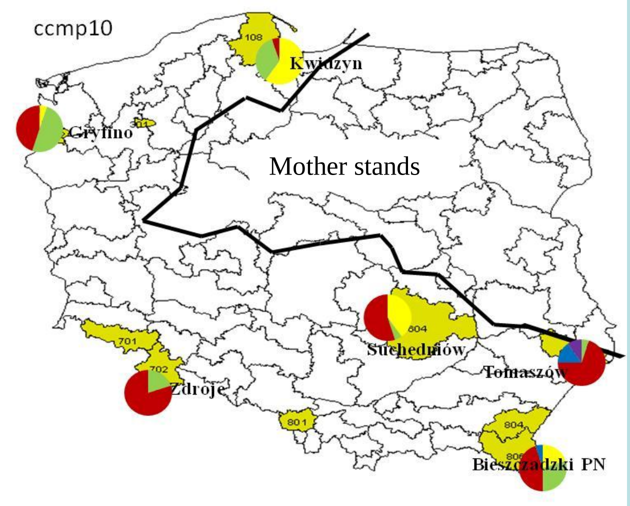


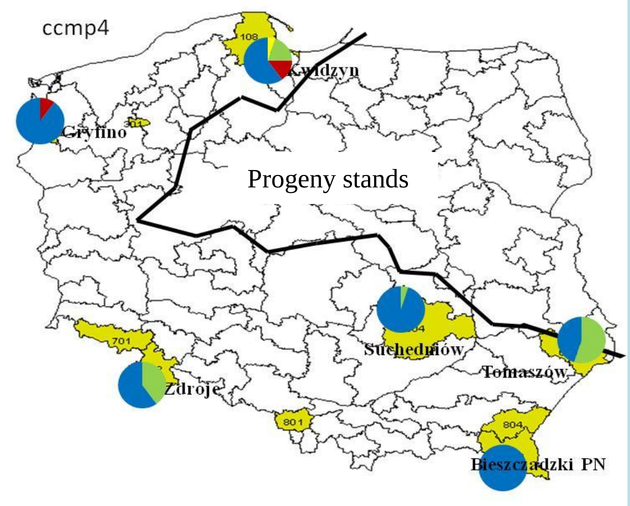
Sekocin 2010

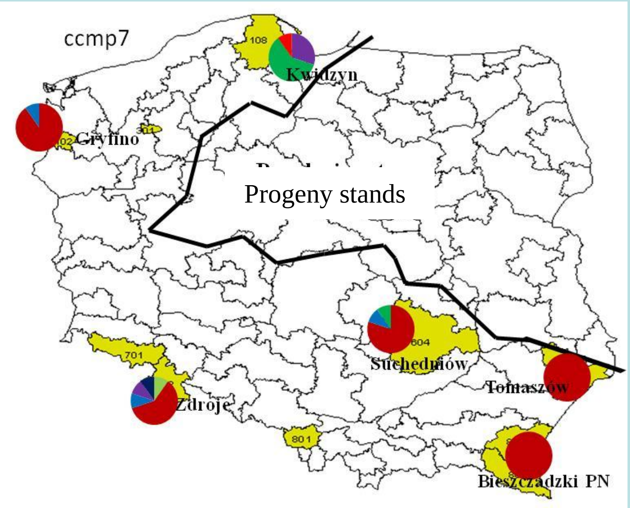
Chloroplast DNA Markers – Gene percentage of alleles

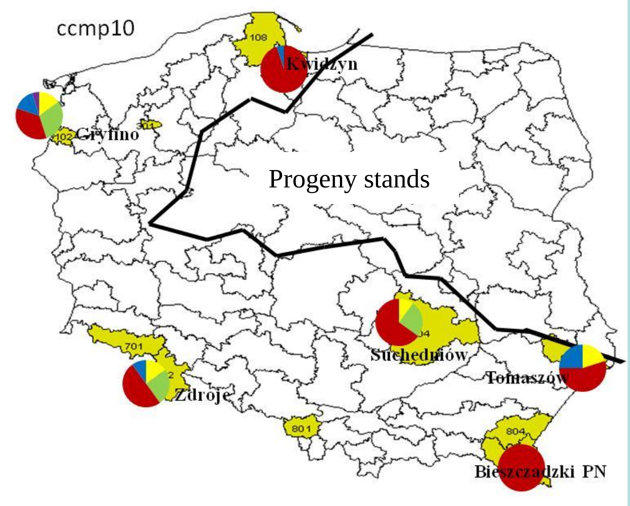












ccmp4

116	117	118	119	120
1	2	3	4	5

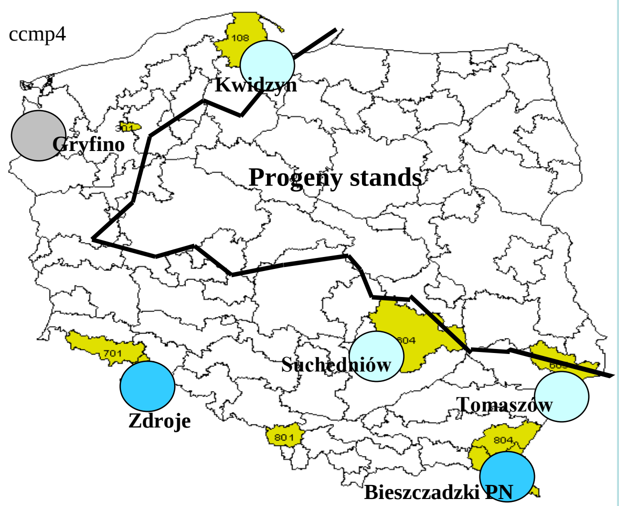
ccmp7

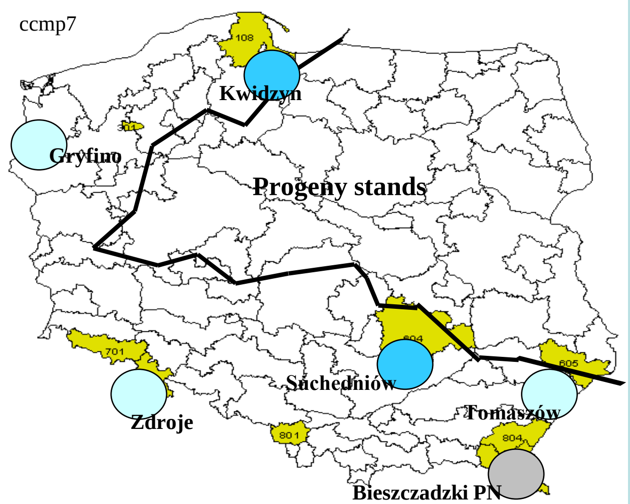
144	145	147	148	149	150	151	152
1	2	3	4	5	6	7	8

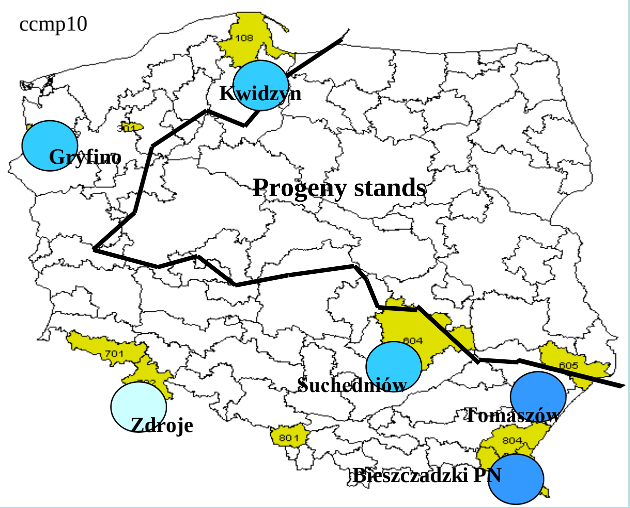
ccmp10

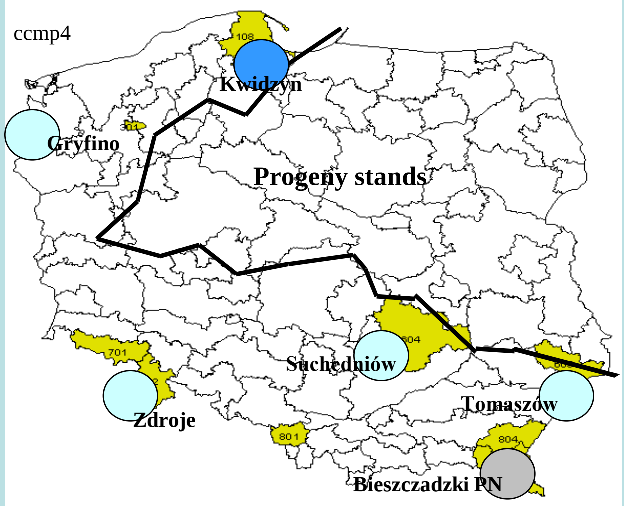
116	117	118	119	120
1	2	3	4	5

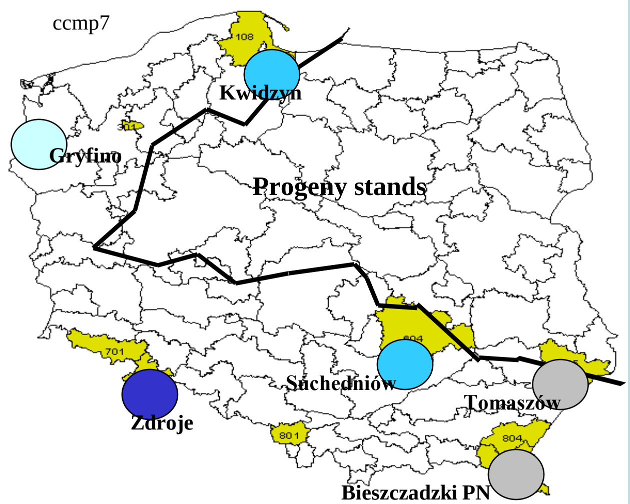
Chloroplast DNA Markers – Average number of alleles per locus

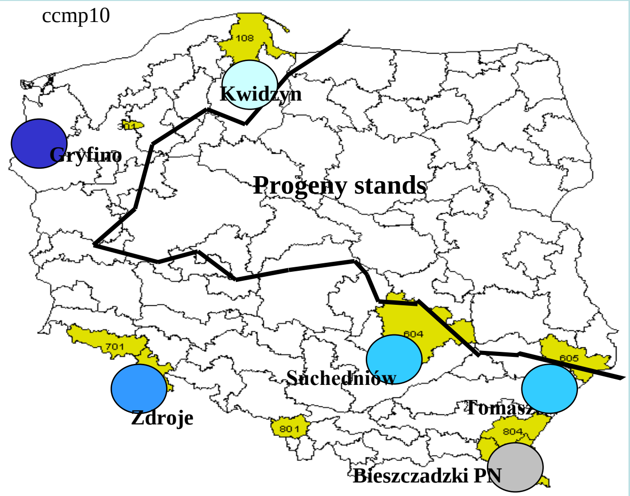

ccmp4


ccmp7


ccmp10


ccmp4


ccmp7

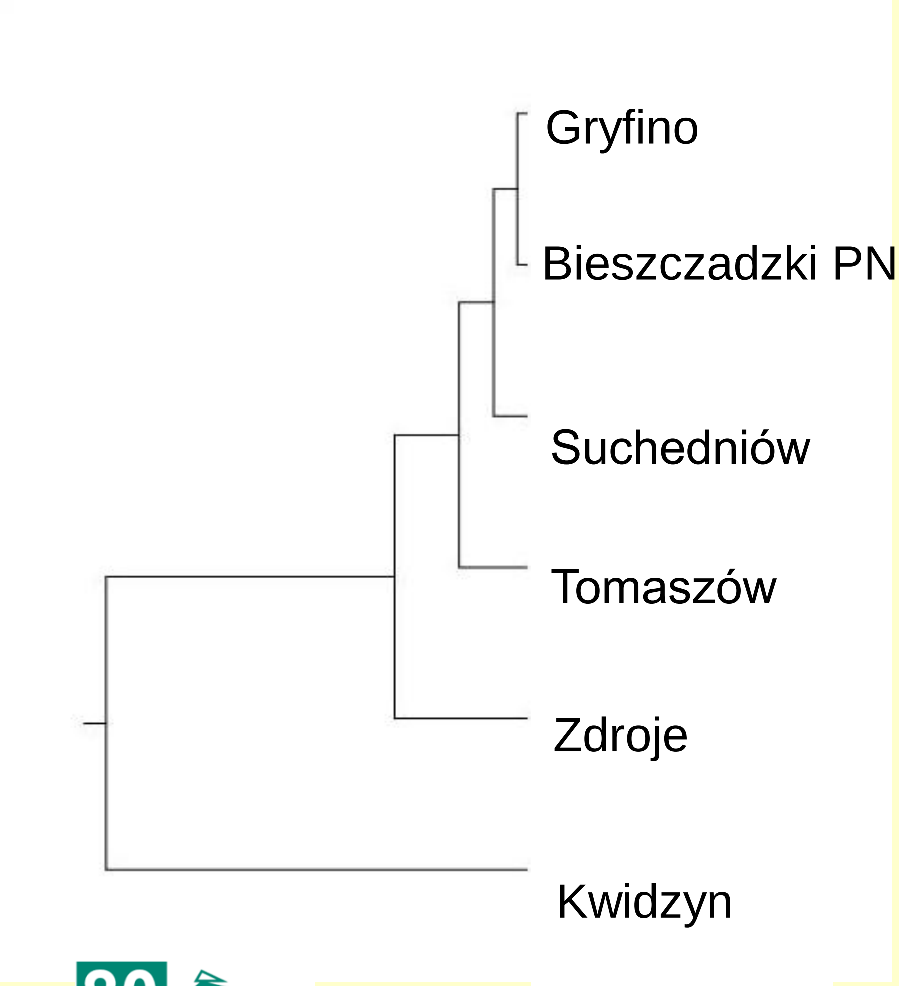

ccmp10

Average of alleles per locus ● 1 ○ 2 ● 3 ● 4 ● 5

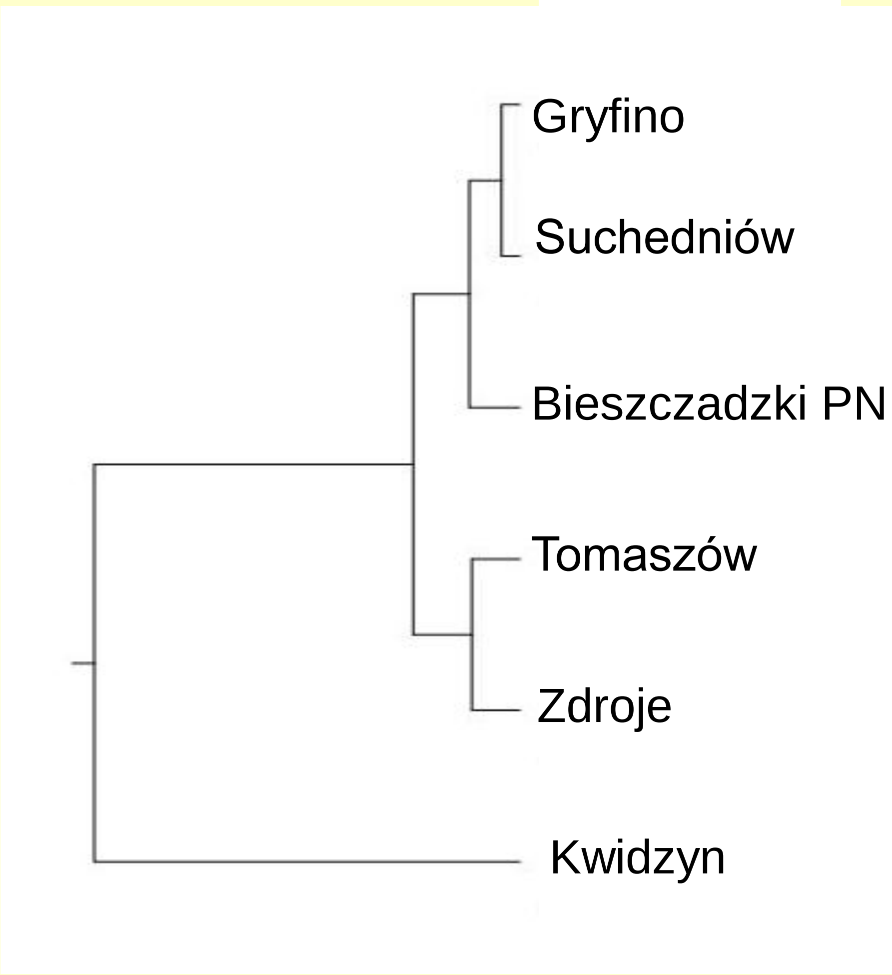
Sekocin 2010

DNA markers

Mother stands



Progeny stands



Sekocin 2010

Nei's Analysis of Gene Diversity

Mother stands

```
====================================
Locus       Ht          Hs       Gst
====================================
 ccmp4    0.5053    0.3058    0.3947
 ccmp7    0.3228    0.2667    0.1738
 ccmp10   0.6468    0.5092    0.2128
Mean      0.4916    0.3606    0.2666
St. Dev   0.0264    0.0169
====================================
```

Progeny stands

```
====================================
Locus       Ht          Hs       Gst
====================================
 ccmp4    0.3957    0.3042    0.2313
 ccmp7    0.4650    0.2767    0.4050
 ccmp10   0.5193    0.4317    0.1688
Mean      0.4600    0.3375    0.2663
St. Dev   0.0038    0.0068
====================================
```

Summary statistics

```
==============================
Locus        Hc         Gcs
==============================
 ccmp4       0.3050    0.3230
 ccmp7       0.2717    0.3103
 ccmp10      0.4704    0.1932
 Mean        0.3490    0.2665
St. Dev      0.0113
==============================
```

Ht – total heterozygosity within population
Hc – total heterozygosity within group
Hs – total heterozygosity among populations
Gst – total genetic differentiation among populations
Gcs – total genetic differentiation in groups of populations

Conclusions

- The very high inter-population diversity was shown.
- The investigations reviled the importance of using local European beech ecotypes, taking into account its plasticity, which is the best advice to obtain success in forest management and for protection of genetic resources of the species.

Thank You very much for Your attention!

And also to our colleague:

Jolanta Bieniek for her technical assistance

Sekocin 2010