

Development of a strategy for the conservation of genetic resources based on genetic and geographic data: black poplar example

<u>Weronika B. Żukowska</u>

Andrzej Lewandowski



Institute of Dendrology, Polish Academy of Sciences



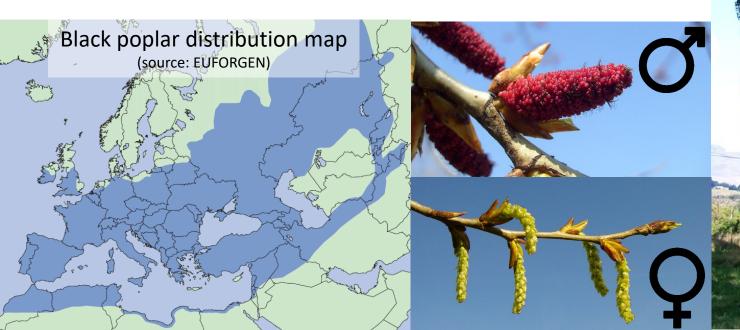
wzukowska@man.poznan.pl





Black poplar

- \checkmark one of the main riparian forest-forming species
- ✓ pioneer and dioecious; lives 200-300 years
- ✓ reproduces generatively and vegetatively
- $\checkmark\,$ high ecological and economic values
- $\checkmark\,$ used in paper industry and for plywood



Lombardy poplars – a variety of black poplar

Black poplar's

Progressive destruction of its natural habitat

Regulation of rivers

Old trees prevail

Beavers and poplar canker

Little chance of generative regeneration

Element of Nature 2000 network but not a protected species in Poland

Massive introduction of hybrid Canadian poplars that may interbreed with pure black poplar





Aims of the study



To determine the spatial genetic structure (SGS) of black poplar populations

Aims of the study



To assess their genetic variation and differentiation

Aims of the study

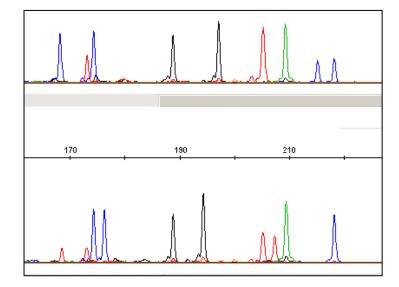


To develop a conservation strategy for black poplar's gene pool in Poland

Materials & methods

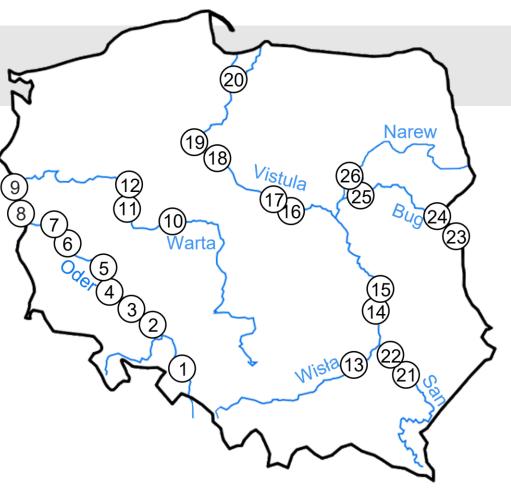
26 populations located along the six biggest river valleys in Poland (1,261 trees)

18 nuclear microsatellite markers





3	Ind	Cat	x	Υ
4	Pu01	Wi2	51.468490	21.900725
5	Pu02	Wi2	51.469125	21.901978
6	Pu03	Wi2	51.469358	21.901790
7	Pu04	Wi2	51.469250	21.901598
8	Pu05	Wi2	51.469393	21.901610



RESULTS

1000

₽ +;

STANDAR C

Clonality

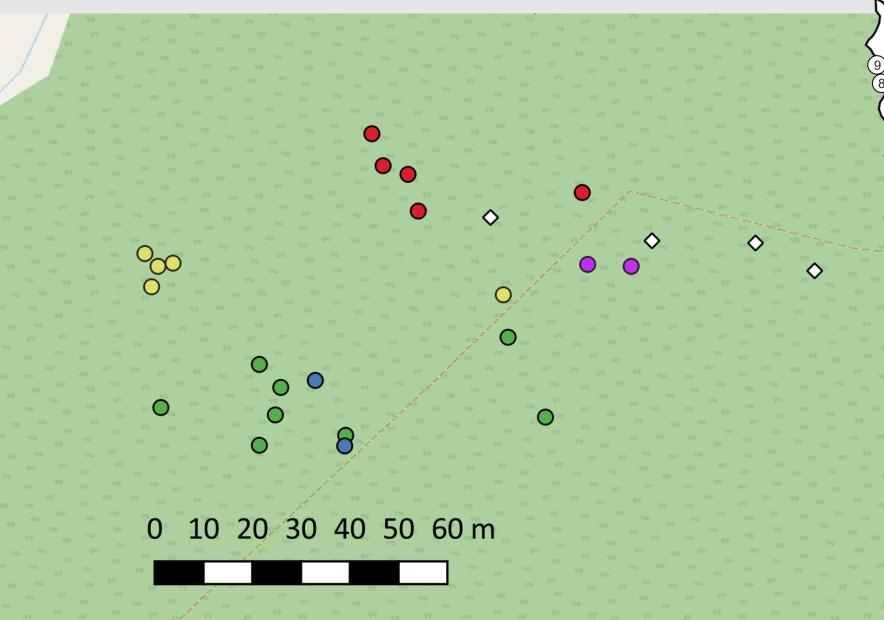
261 trees were clones

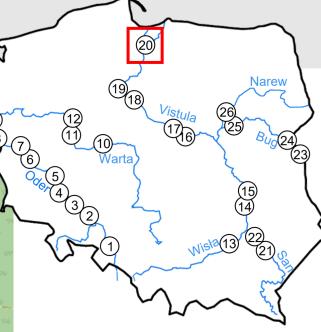
1000 (79.30%) different genotypes

River	Clonality [%]	
Oder	28	
Warta	23	
Vistula	23	
San	2	
Bug	2	
Narew	3	
MEAN	13.5	



Clonality – population Vi8 (species distribution limit!)





Genetic clones are marked with circles in the same color.

White diamonds

- unique genotypes.

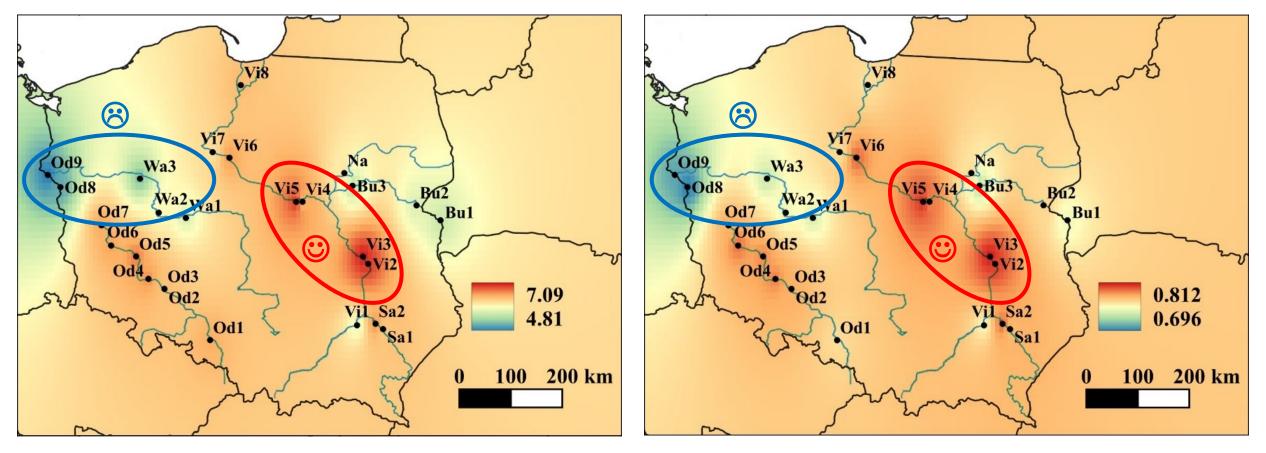
Is it a natural population?

Genetic variation

Inverse Distance Weighted (IDW) interpolation of:

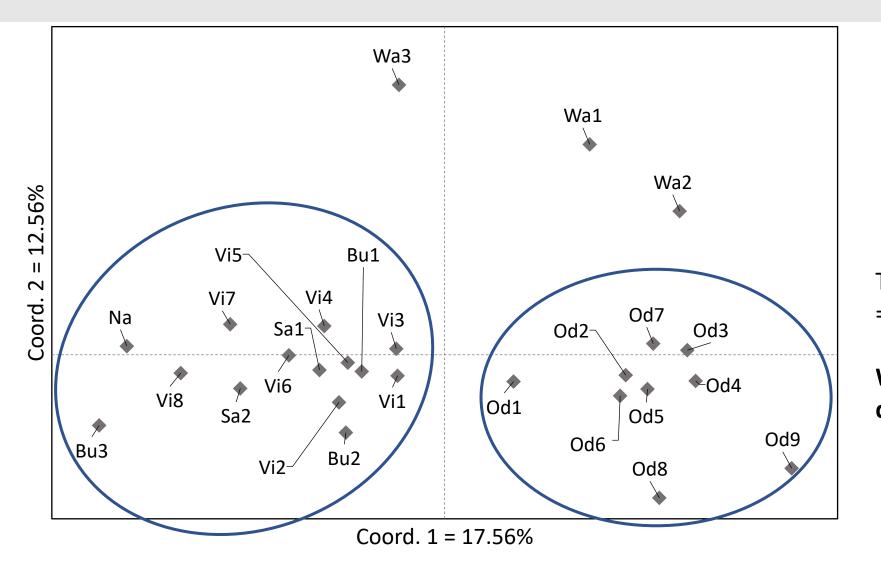
a) allelic richness values (A_R)





Genetic differentiation

(Principal Coordinates Analysis – PCoA)

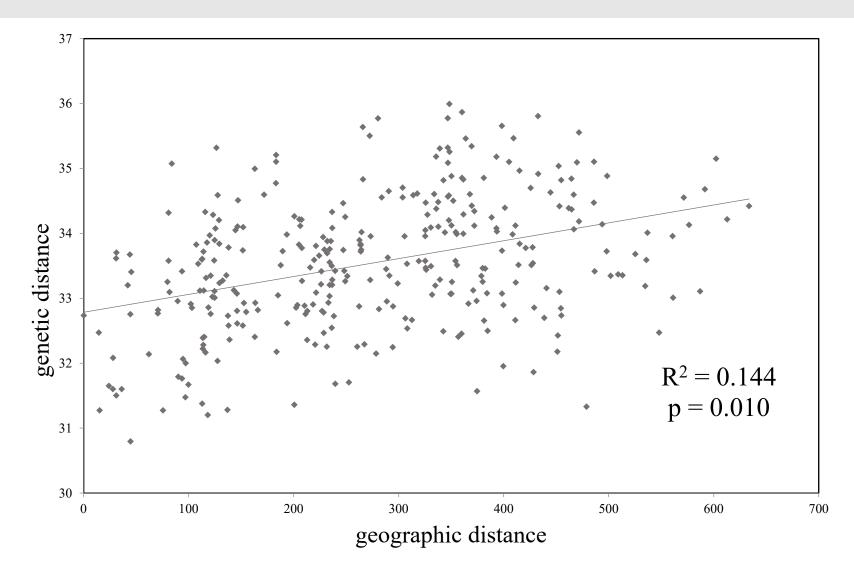


Two large genetic groups = two river basins.

Warta's populations are all different!

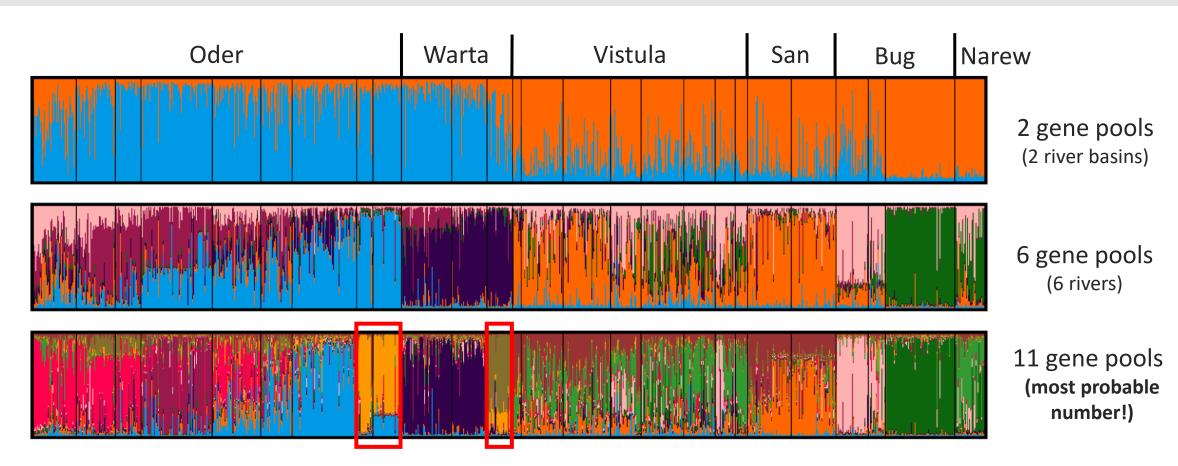
Isolation by Distance (IBD)

(Mantel Test)



The observed genetic differentiation cannot be explained only by the geographic distance.

Gene pools (Bayesian clustering)

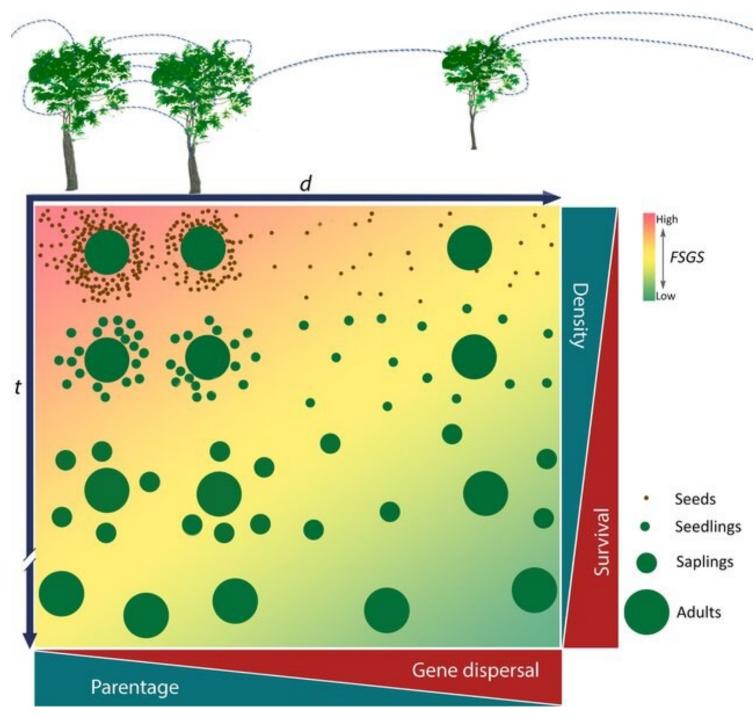


Diagrams showing the probability of a given tree belonging to different genetic groups marked with colors. Each tree is represented by a vertical line. Populations are separated by black lines.

Spatial Genetic Structure (SGS)

Schematic representation of fine-scale spatial genetic structure (FSGS) on different life stages in the space-time complex.

Pollination events (dotted lines), time (t), and distance (d). doi:10.1007/s11295-022-01550-1



Spatial Genetic Structure (SGS) cont.

Most populations showed statistically significant SGS, especially for the first two distance classes.

This means that trees located closer to each other were more genetically related.

Pop Wa2

Sp = 0.008

Distance class

Pop Wa3

Sp = 0.058

Distance class

0.16

0.12

0.08

0.04

-0.04

-0.08

-0.12

1 2 3 4 5 6

9 10

0

Such result is expected for natural populations.

0.04

0.03

0

-0.02

-0.03

-0.04

1 2 3 4 5 6 7 8

ent 0.02

coeffic 0.01

ē -0.01

9 10

Pop Wa1

Sp = 0.008

5 6 7 8

Distance class

0.03

0.02

0.01

-0.01

-0.03

1 2

3 4

gills

Ξ -0.07

0



Spatial Genetic Structure (SGS) cont.

Pop Sa1

Sp = 0.030

Distance class

1 2 3 4 5

These diagrams allows calculating the minimum distance between trees marked as seed sources to avoid close relatedness among offspring.

0.08

0.06

0.02

te 0.04

.u -0.04

-0.06

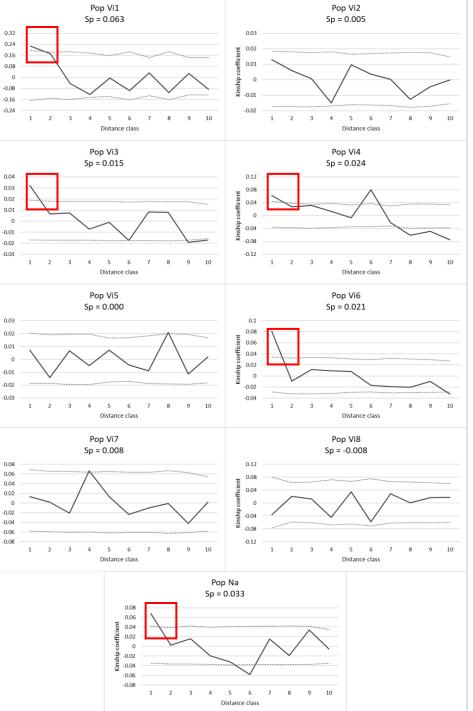
-0.08

년 -0.02

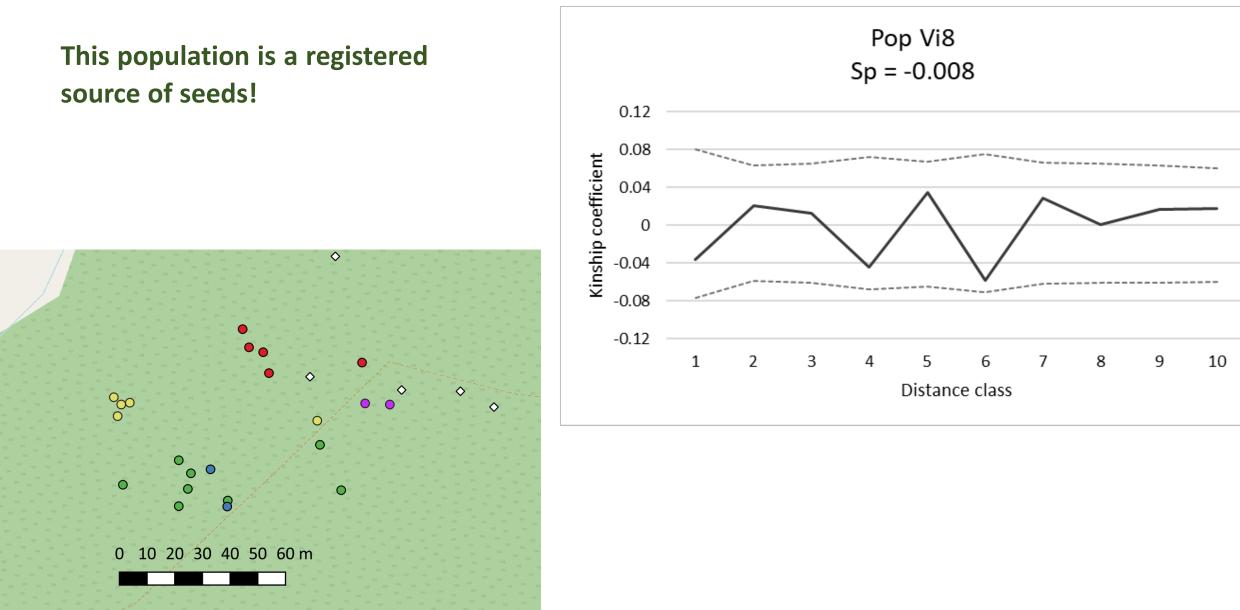
Oder – 10 m Warta – 12 m Vistula, San – 7 m Narew – 5 m



Distance class



Going back to population Vi8 (species distribution limit!)



Conclusions and conservation strategy

- 1. The results confirm the need to start activities for the protection of genetic resources of black poplar in Poland.
- 2. Given strong genetic structuring, we opt for establishing local clone archives.
- 3. If local conditions support the long-term survival of young plants, they can be planted using local seed sources.
- 4. Registered seed sources should be revised.
- 5. Populations characterized by high genetic variation and effective size accompanied by relatively low clonality should be registered as new seed sources.
- 6. Further research requires determining the adaptive potential of the populations, especially of those from the distribution limit.



Thank you for your attention ©

wzukowska@man.poznan.pl

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