

# The joint research project GENMON: Implementation of long-term genetic monitoring in beech and spruce stands in Germany

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## INTRODUCTION

Genetic diversity represents the basis for adaptability and survival of tree species in changing environmental conditions. Global warming will cause extreme weather events in the future. To gain information about the long-term development of the genetic systems of forest tree populations there is an urgent need to establish a monitoring system for forest genetic resources. After testing a concept, developed on behalf of the Federal-State-Working Group for Forest Genetic Resources in Germany (Kätzel et al. 2005) and in a pilot study (Konnert et al. 2011), the experiences were used to implement the joint project „GenMon“. The main goal of forest genetic monitoring is to assess the genetic variation and the status of the genetic system of different populations as well as its dynamics in time and space on the basis of criteria, indicators and verifiers.



FIGURE 1: Location of monitoring plots for spruce (dark green) and beech (light green)

## MATERIAL AND METHODS

- ✓ Plot establishment following a defined plot design:
  - 14 monitoring plots in *Fagus sylvatica* L.
  - 10 plots in *Picea abies* [L.] Karst.
- ✓ 16 neutral microsatellite markers were used to analyze the genetic structures at the population level in both species.
- ✓ At least 250 adult trees, 400 individuals of natural regeneration and 400 seeds were genotyped in each population to study reproduction processes.
- ✓ Phenological observations of bud flushing, flowering, fructification and vitality are performed every year.
- ✓ Data of all plots are stored in a database, which in this initial step is used to calculate genetic diversity in adult stands and their progenies, to describe and to compare the current genetic state of the populations.
- ✓ Furthermore, the selection of individuals suitable for the development of adaptation-relevant markers was facilitated.

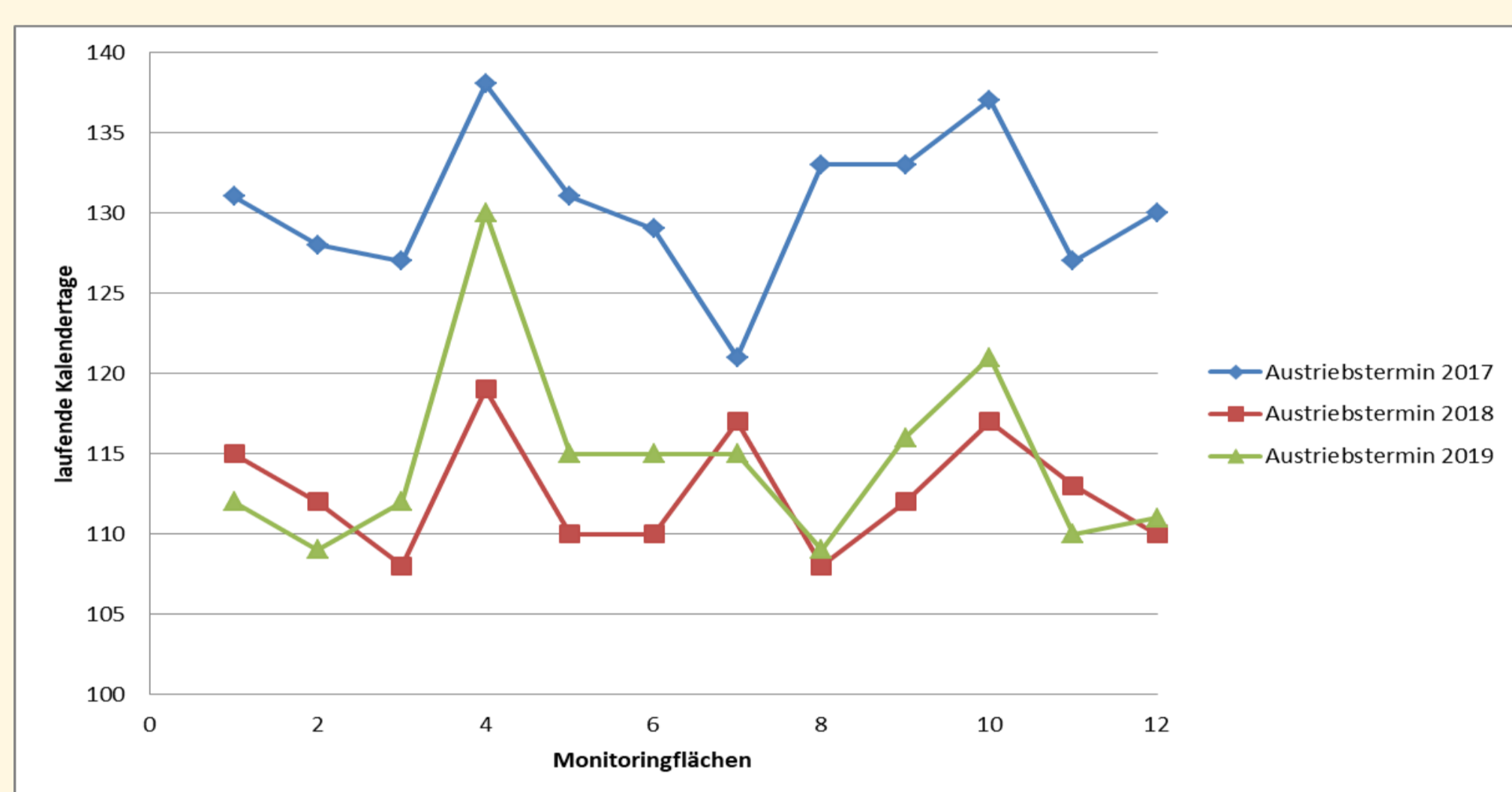


FIGURE 2: Mean flushing dates for 12 beech monitoring plots. Mean values were assessed from 20-30 trees per plot. Overall, in 2018 dates were reached 18 days and in 2019 16 days earlier than in 2017.

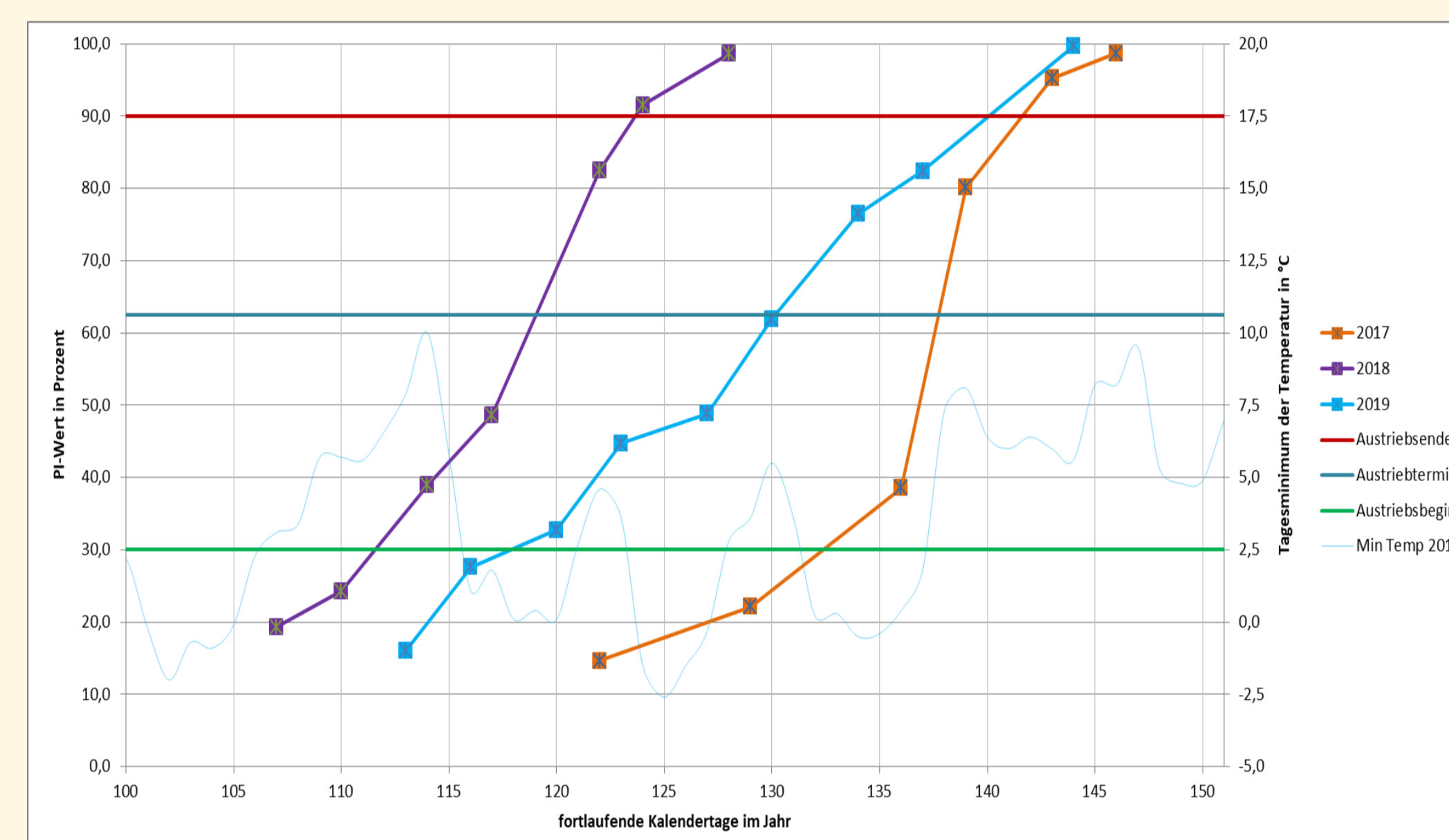


FIGURE 3: Flushing phenology of the beech plot BY1 at 1050 m a.s.l. in the Bavarian Alps. The phenological index is the share of the tree in a certain phenological stage and was assessed 5-7 times per year in 2017, 2018 and 2019. Mean values from 20 observed trees are presented.

In the year 2017 the flushing date was reached at day 137, in 2018 at day 118 and in 2019 at day 130.

In the year 2019 two frost events happened: one between day 124-127 and the second between day 133-135. The first event happened before and the second after flushing. Both events flattened the curve, but only the second one caused severe damage to the foliage.

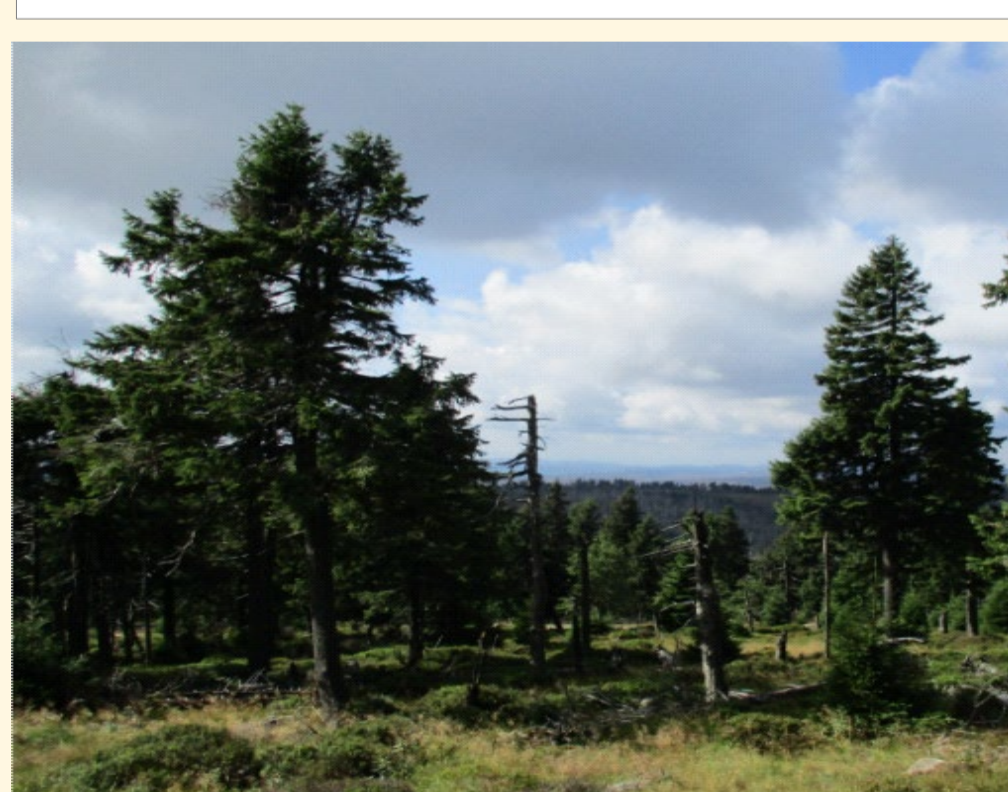
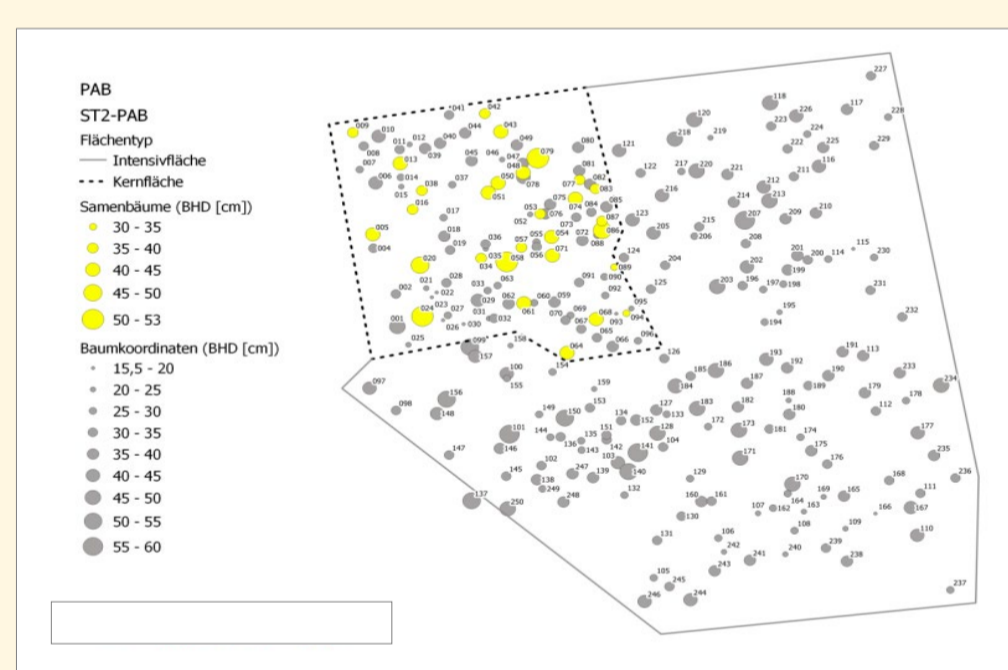


FIGURE 4: Spruce at the timber line in Central German stand „ST2-Brocken“ (top: distribution and diameter of trees; below: part of the stand with low density of trees)

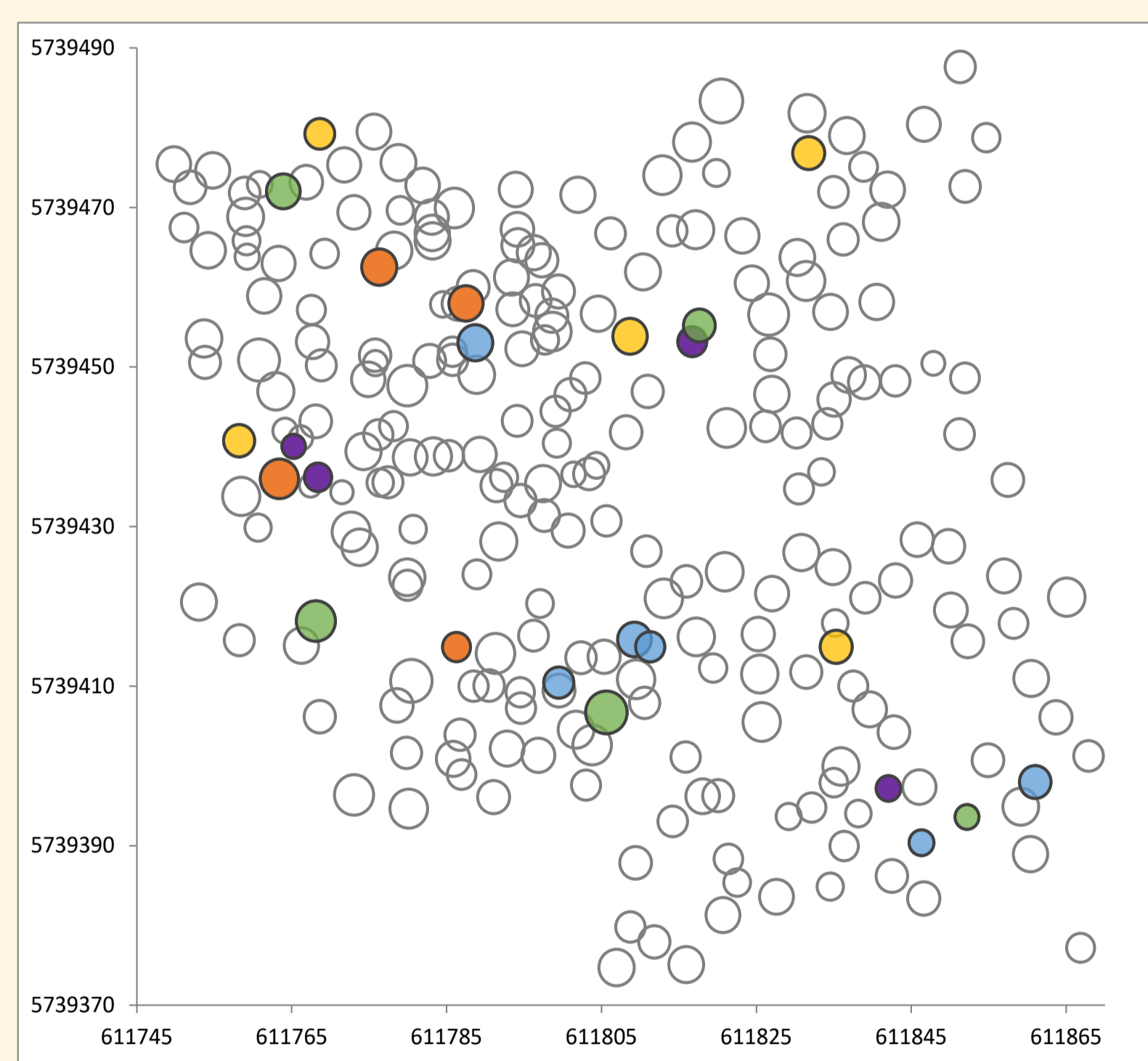


FIGURE 5: Reconstruction of the regeneration-phase of adult trees: the genetic results point to artificial regeneration due to the lack of spatial genetic structure. The members of the different families were distributed evenly on the whole plot. Meanwhile some natural regeneration has taken place, resulting in weak spatial genetic structure. The adult trees are forming 24 different families and consist of a mixture of forest reproductive material from different sources.

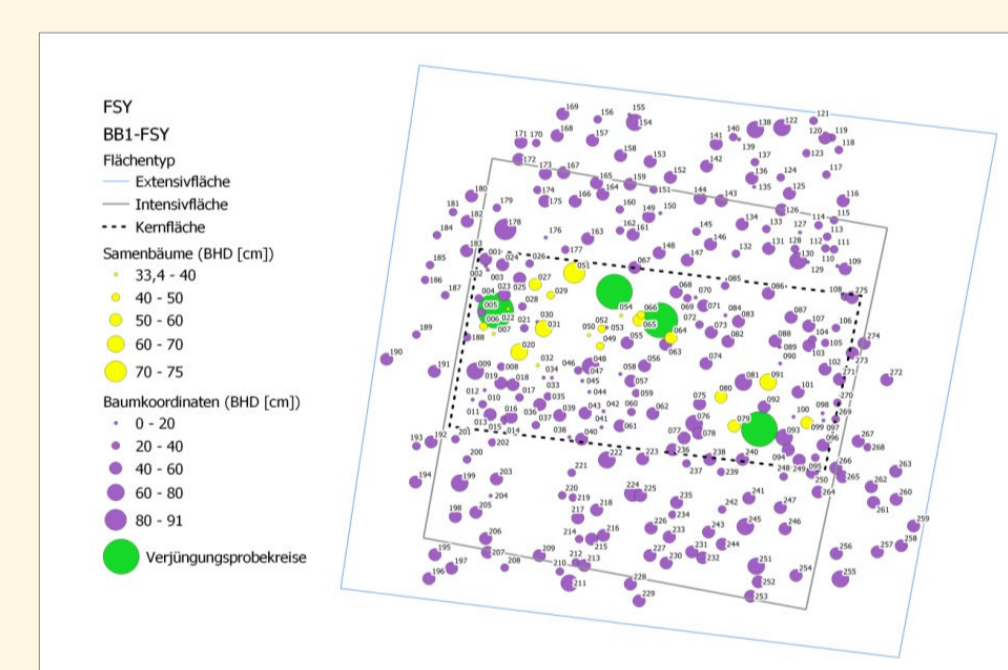


FIGURE 6: Beech stand in North-Eastern Germany „BB1-Rheinsberg“ (top: distribution and diameter of trees; below: Level II plot in the managed beech stand)

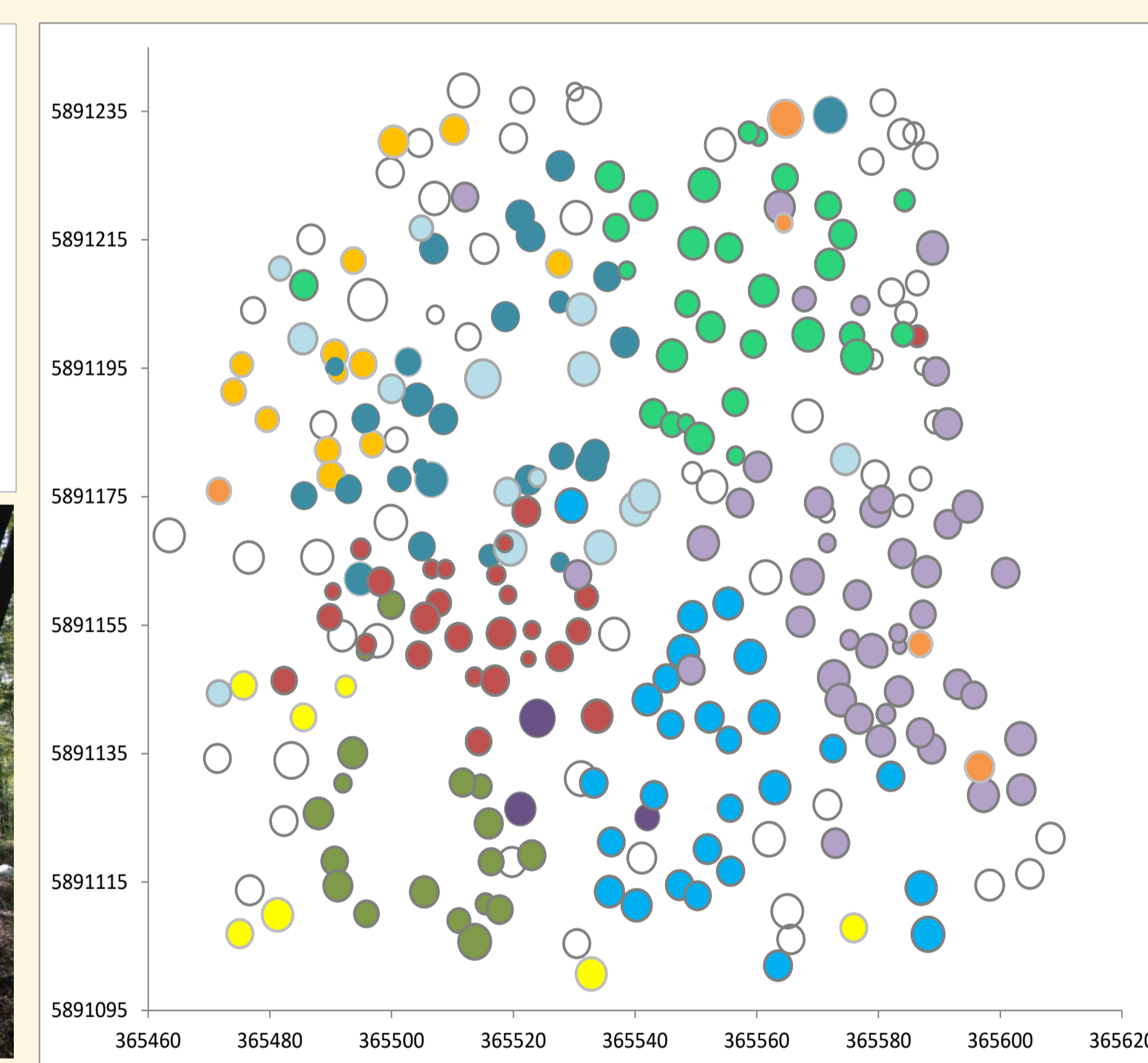


FIGURE 7: The reconstruction of the regeneration phase resulted in the most extreme picture of all plots. Family structures and spatial genetic structure point to a pronounced clustering of closely related individuals. Only few large families were found besides single trees and small families, which altogether refer to a once naturally established stand. The large families might be a result of a shelterwood cutting („Großschirmschlag“) with only a small number of seed trees remaining.

## CONCLUSIONS

- ✓ The first major step of plot establishment and assessment of baseline data for 24 FGM plots has been performed.
- ✓ In future, further analyses and data evaluation will allow the assessment of the intactness of the genetic mechanisms that ensure the conservation, production and transmission of genetic diversity to the next generation. This provides the basis for a monitoring system to estimate and evaluate the factors as well as the direction and intensity of their influence on adaptability of tree populations.
- ✓ Conclusions for management actions, minimum requirements and regulations for approved seed stands can be derived.
- ✓ Established plots are a valuable resource for further scientific studies (e.g. adaptation-relevant markers).

**REFERENCES**  
KONNERT, M., MAURER, W., DEGEN, B., KÄTZEL, R. (2011): Genetic monitoring in forests – early warning and controlling system for ecosystemic changes. iForest, 77 - 81;  
KÄTZEL, R., MAURER, W.D., KONNERT, M., SCHOLZ, F. (2005): Genetisches Monitoring in Wäldern. Forst und Holz 5, 179 - 183.

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