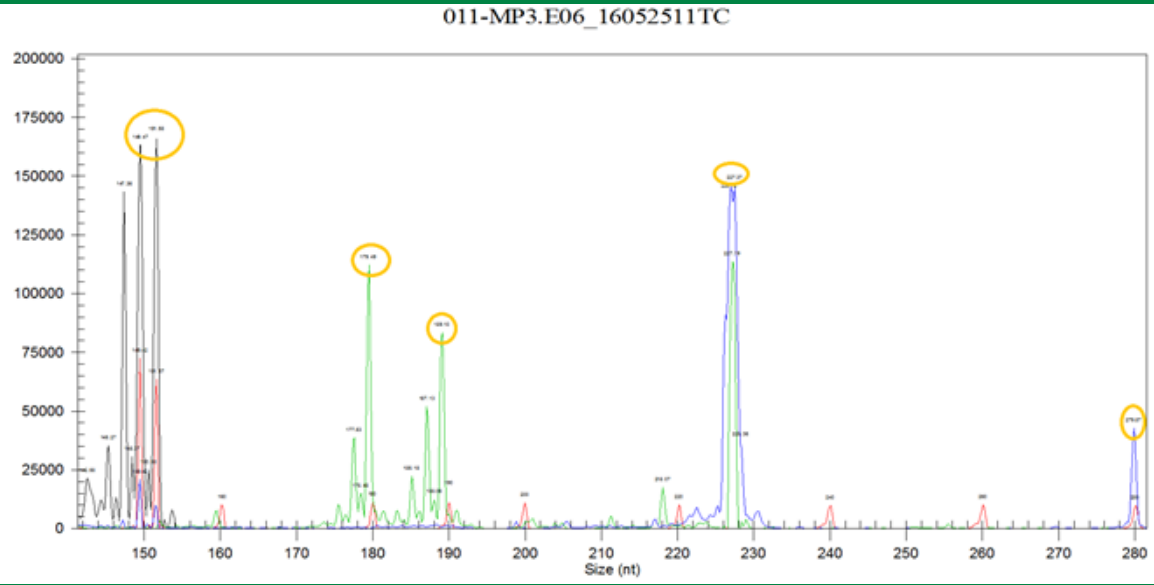
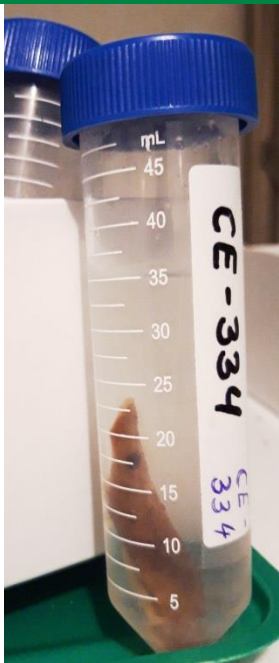


Genetic characterization of the red deer (*Cervus elaphus* L.) population structure in the Saxon Ore Mountains

Wildursprungsschein* (Nummer der Wildkarte) 0000000000
 Freistaat Sachsen
 zuständige Behörde
 Jagdbezirk / Erlegungsart: *Feldjagd / Rev. 02 / Art. 277*
 Jäger (Erleger):
 Erlegungsdatum am *9.1.16* um *2²⁴* Uhr
 Jagdort:
 Wildart: *Rothwild* Masse: *60* kg Altersklasse: *3/1*
 Geschlecht: männlich weiblich
 Feststellungen bei Abgabe an zugelassenen Wildbearbeitungsbetrieb:
 Vor dem Erlegen wurden keine Verhaltensstörungen des Tieres beobachtet.
 Es wurden von mir beim Untersuchen des Tieres keine auffälligen Merkmale beobachtet, die darauf schließen lassen, dass das Fleisch gesundheitlich bedenklich sein könnte.
 Es besteht kein Verdacht auf Umweltkontamination.
 Sonstiges / Güz des Schlüssels: *Ableit lassen*
 Datum, Unterschrift Jäger / Jagdausübungsberechtigter und der Kundigen Person:
 Amtliche Unterschrift (S. 8 Abs. 2 der Tierische Lebensmittel-ÜberwachungsVO)
 Zeitpunkt (Datum, Uhrzeit):
 Eingangsdatum:
 Untersuchungsergebnis oder Zeitpunkt, ab dem über das Wild verfügt werden darf:
 Wild: Fleisch Knochen Sehnen Milch Fett Blut Hirschhorn

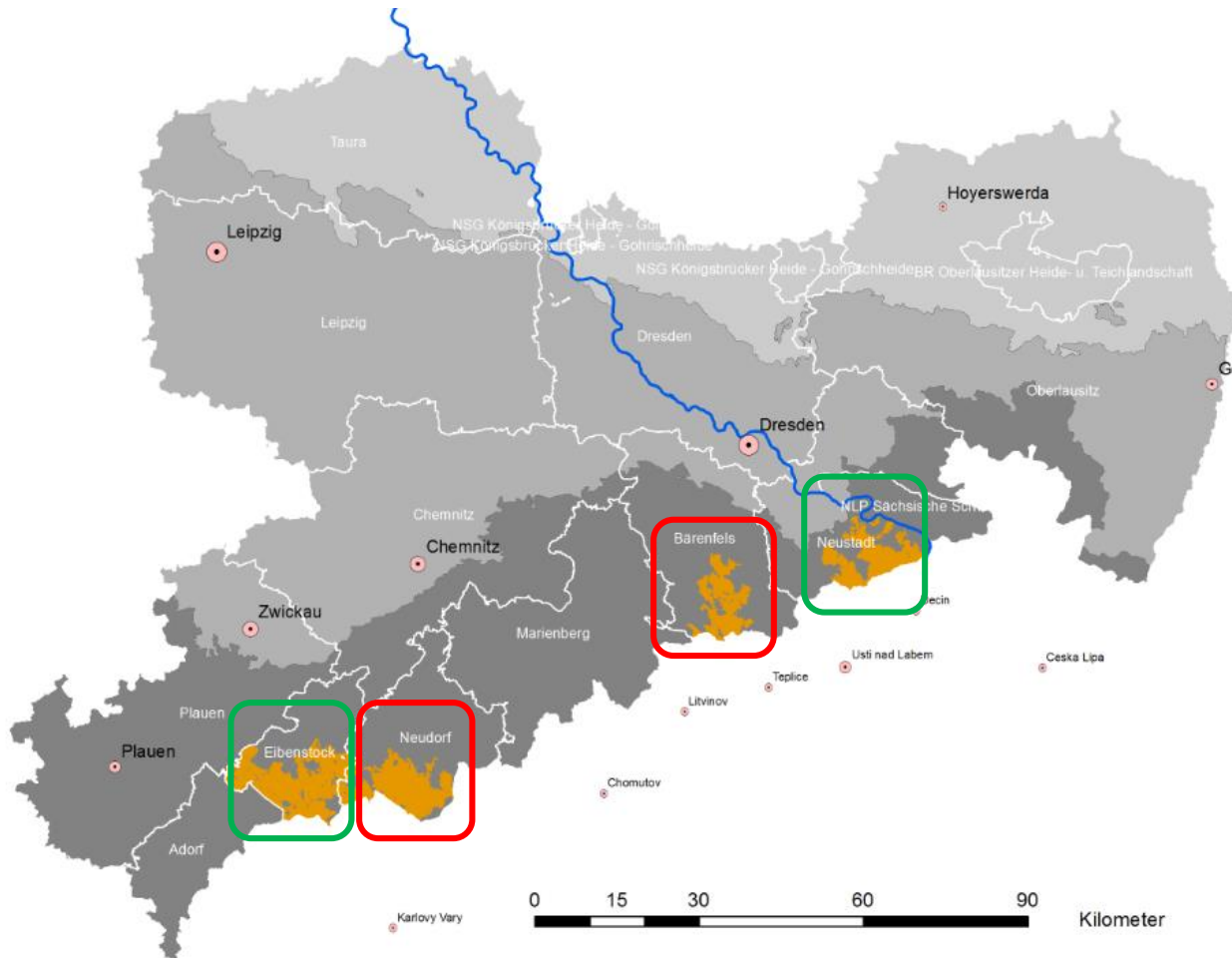


Red Deer and Forest Conversion in the Ore Mountains

Project Overview and first Results | Wernsdorf | November 5, 2019



Study areas



- Ore Mts. / Western Elbe Sandstone Mts., Σ 48.000 ha, State Forest
- Differences in cervid influence (browsing, bark stripping)
- Differences in landscape, forest structure and site characteristics
- Differences in forest conversion priority, efforts and outcomes
- **Field Work:** Jan. 2016 – Dec. 2018
- **Data Analysis:** 2019/2020

Project Structure

1:
Population ecology /
spatial behaviour

2:
Influence on forest
vegetation

3:
Red Deer habitat



4:
Synthesis
Development
of qualified
forest and
wildlife
management
strategies

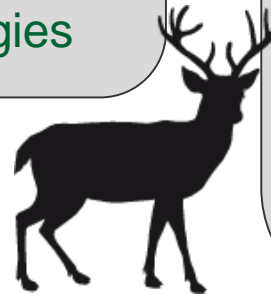


**Multifunctional, economical
and ecological sustainable
forests**

Successfull, economical,
responsible, large - scale **forest
conversion**

Tolerable **cervid browsing and bark
stripping influence**, depending on
forest structure, site conditions, and
forest conversion priority

Maintenance of a **vital red deer
population** as a part of the
transboundary Ore Mts. landscape



Part 5:
Knowledge transfer

Staatsbetrieb Sachsenforst



Sachsenforst

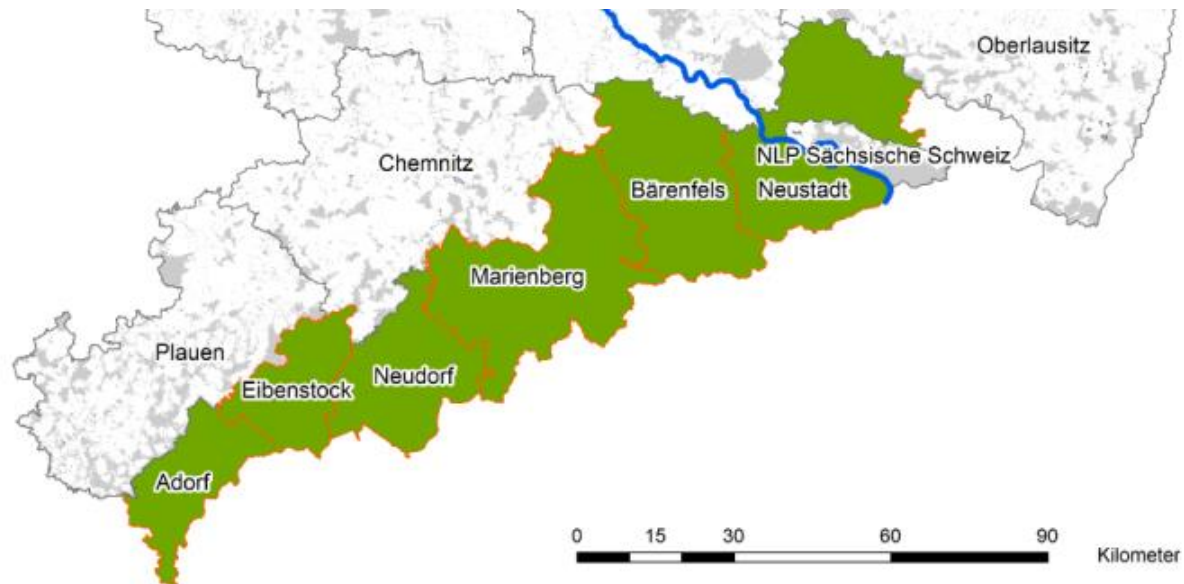
TU Dresden – Professur für Forstzoologie
AG Wildtierforschung



Aim of the present study

Genetic structure of the red deer population in the Ore mountains

- Is there a continuous population within the studied area?
- Does genetic differentiation between subpopulations indicate reduced gene flow or isolation?



Material

All in all	405 samples
From hunting year 2018/19 along the Ore m.	250
FoB Bärenfels 2015-2018	99
(NP 2015	11)
Hair samples of tagged animals	45

Objectives:

- Characterization of the genetic structure
- Delimitation of subpopulations?
- Statements about representation of the research design
(selection of tagged animals, studied areas, fecal collection)

Microsatellite markers used

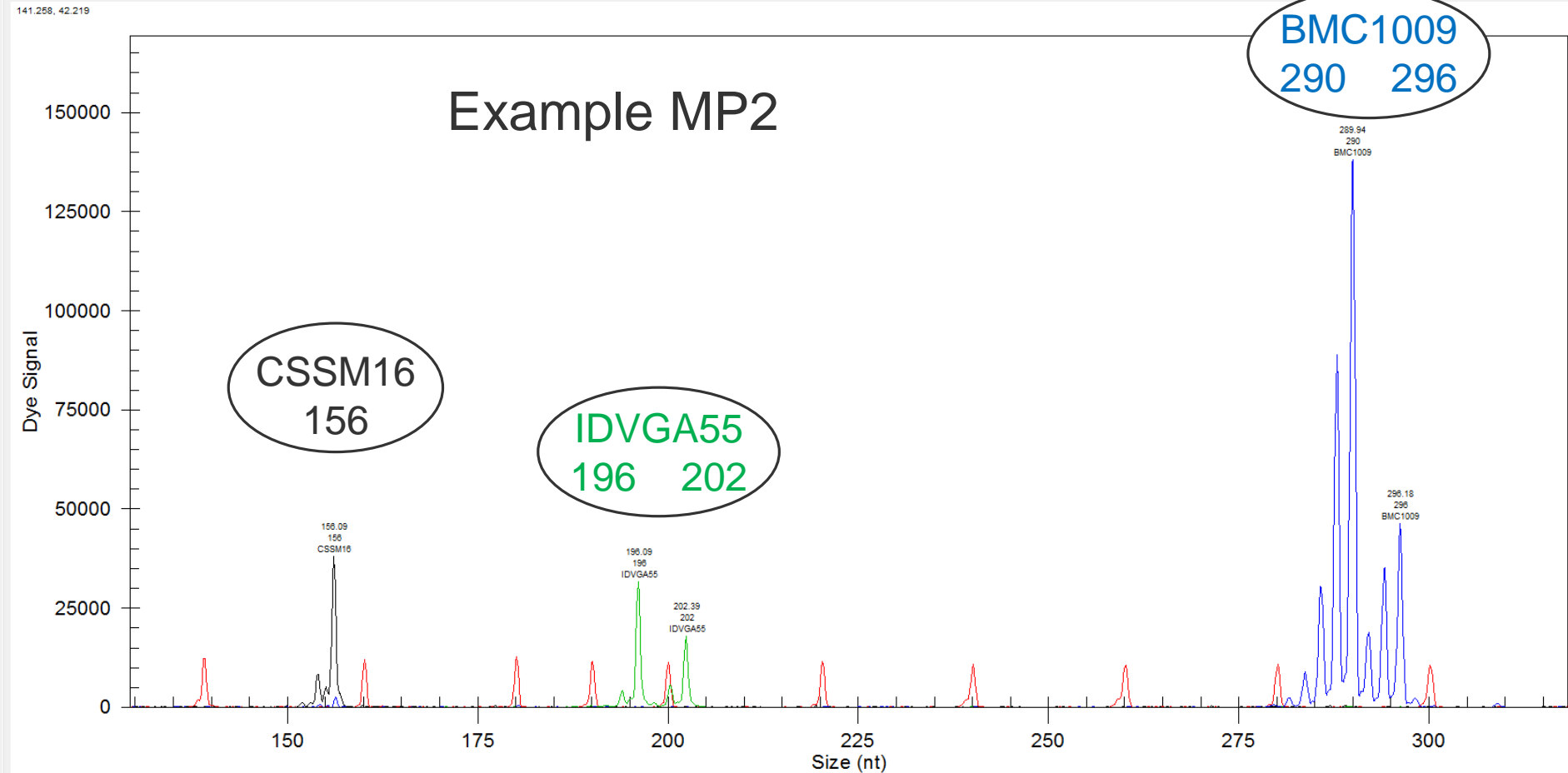
Marker	Label	Reference	Multiplex
Haut14	Cy5	Kuehn <i>et al.</i> 2003	MP1
TGLA53	DY-751	Valière <i>et al.</i> 2006	
BM203	BMN-6	Valière <i>et al.</i> 2006	
ILSTS06	Cy5	Kuehn <i>et al.</i> 2003	
CSSM16	DY-751	Kuehn <i>et al.</i> 2003	MP2
IDVGA55	BMN-6	Valière <i>et al.</i> 2006	
BCM1009	Cy5	Valière <i>et al.</i> 2006	
CSSM19	DY-751	Kuehn <i>et al.</i> 2003	MP3
CSSM66	BMN-6	Kuehn <i>et al.</i> 2003	
AMELXY	Cy5	Gurgul <i>et al.</i> 2010	
CSRM60	Cy5	Kuehn <i>et al.</i> 2003	Single PCR

Marker selection based on Ebert (2011)

Microsatellite markers used

Marker	Label	Reference	Multiplex
--------	-------	-----------	-----------

K667 MP2.D07_17032216TC
Fragment Data | Raw Data | Fragment List | Current | Inject Current | Voltage | Analysis Log | Run Log | Analysis Parameters | Quantitation | STR Locus Tags | SNP Locus Tags | Size Calibration | Dye Matrices | General/Notes | Property Set | Method/Consumables

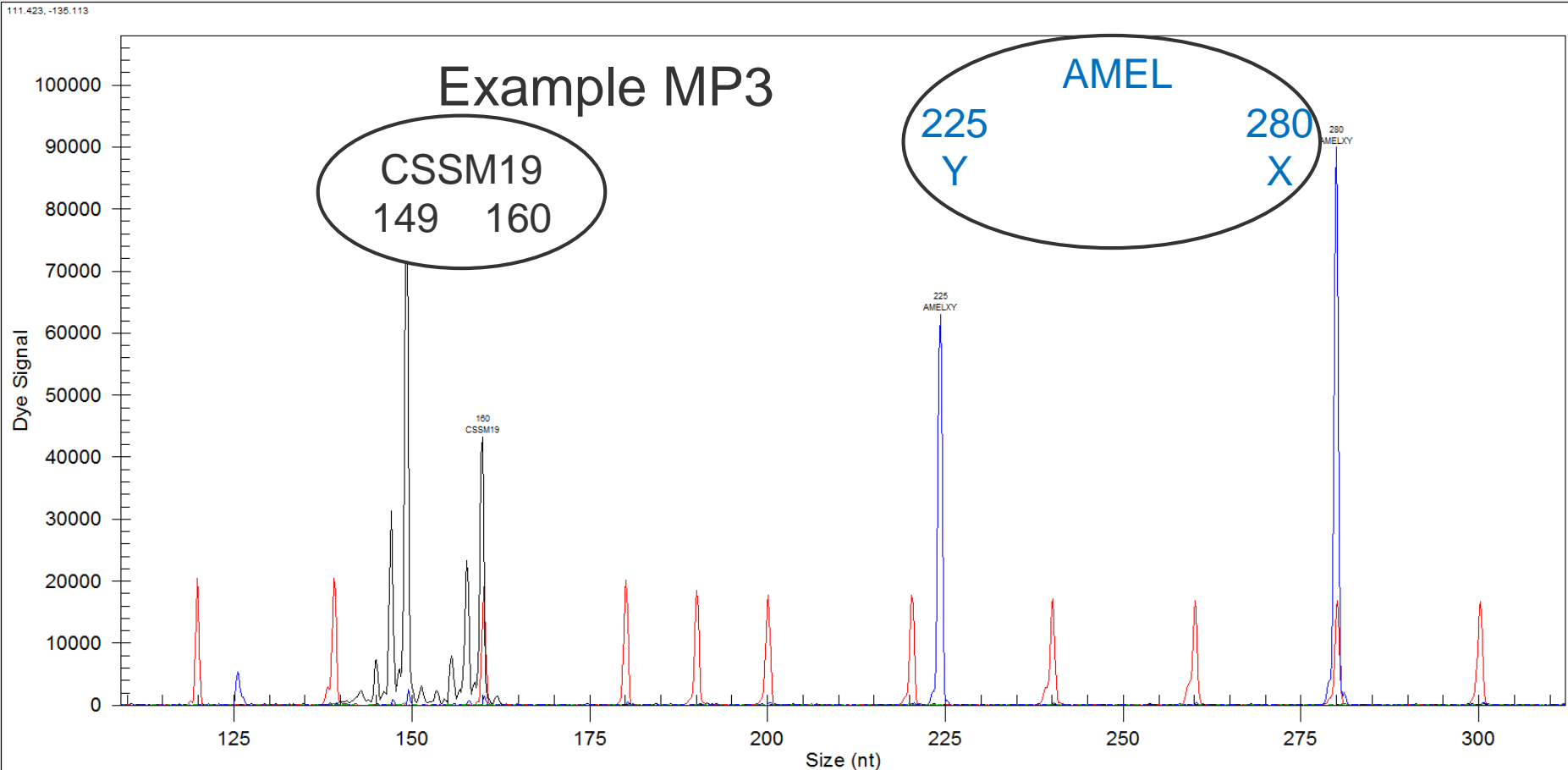


Microsatellite markers used

Marker	Label	Reference	Multiplex
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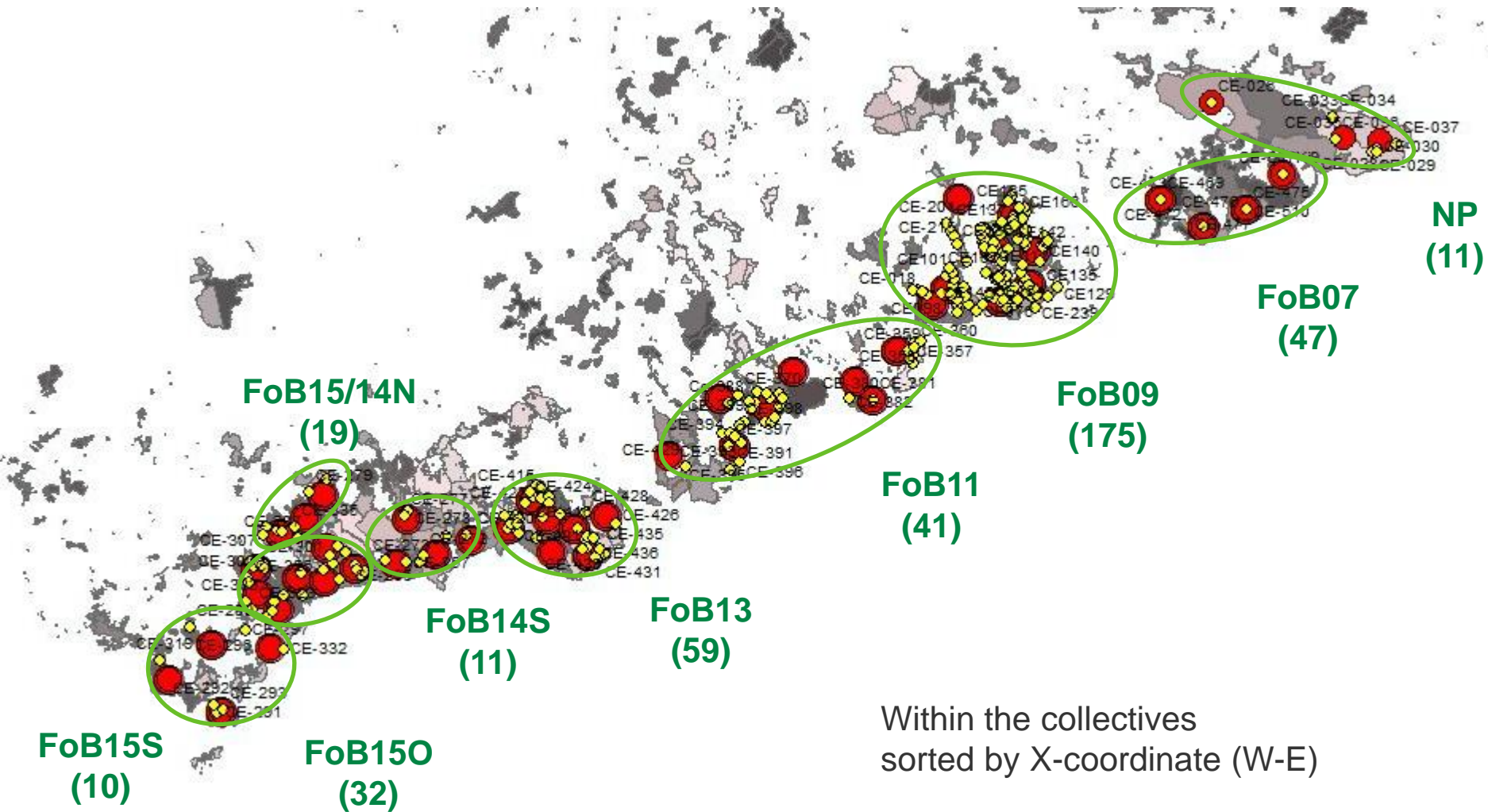
K667 MP2.D07_17032216TC
Fragment Data | Raw Data | Fragment List | Current | Inject Current | Voltage | Analysis Log | Run Log | Analysis Parameters | Quantitation | STR Locus Tags | SNP Locus Tags | Size Calibration | Dye Matrices | General/Notes | Property Set | Method/Consumables

K667 MP3.D07_170322160A
Fragment Data | Raw Data | Fragment List | Current | Inject Current | Voltage | Analysis Log | Run Log | Analysis Parameters | Quantitation | STR Locus Tags | SNP Locus Tags | Size Calibration | Dye Matrices | General/Notes | Property Set | Method/Consumables



Tissue analysis

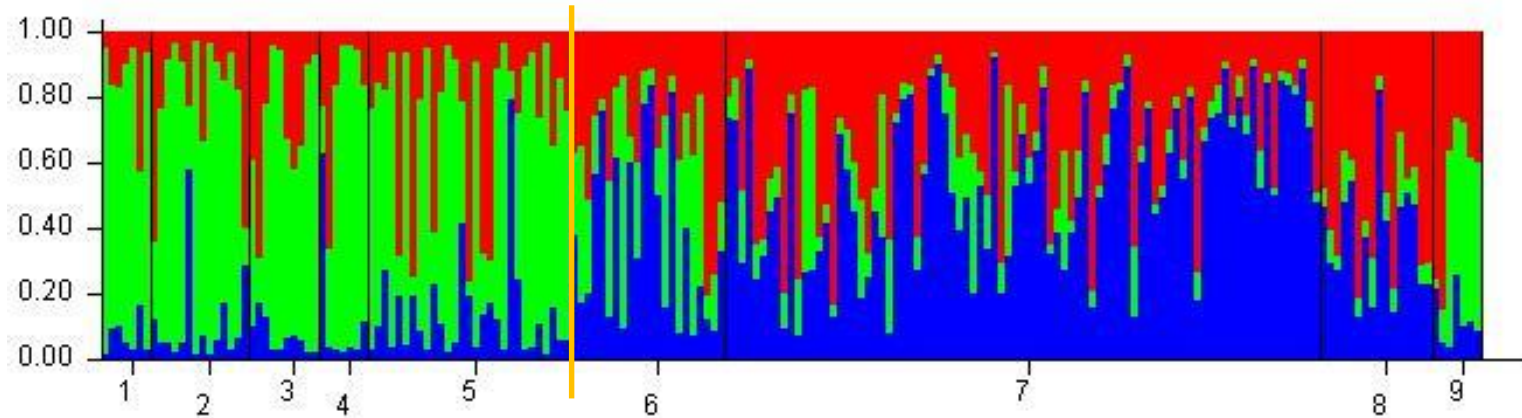
Search for geographically based subpopulations



Within the collectives
sorted by X-coordinate (W-E)

Results

Structure analysis of all female samples (N=197)



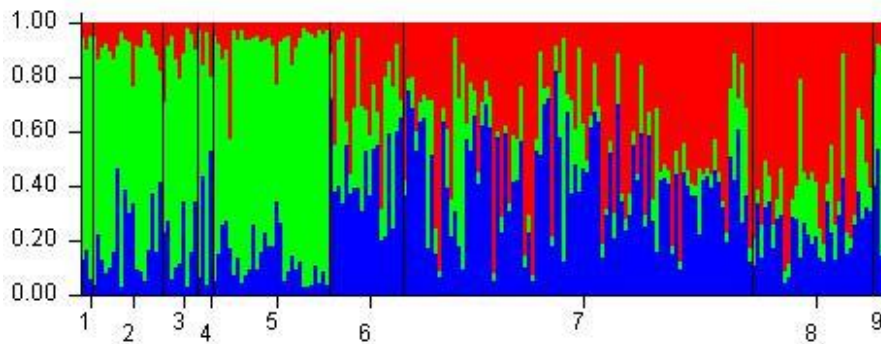
	1	2	3	4	5	6	7	8	9
	FoB15S	FoB15O	FoB1415N	FoB14S	FoB13	FoB11	FoB09	FoB07	NP
N	7	14	10	7	29	22	85	16	7

Proportion of membership of each pre-defined population in each of the 3 clusters

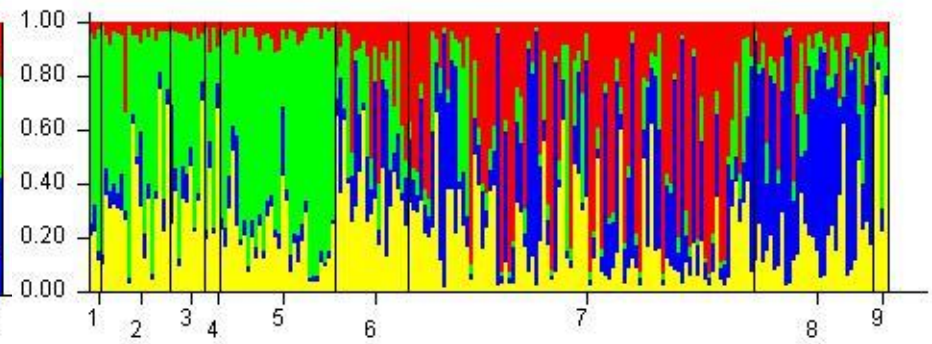
Given Pop	Inferred Cluster 1	Inferred Cluster 2	Inferred Cluster 3	Number of Individuals
1:	0.143	0.786	0.072	7
2:	0.197	0.686	0.117	14
3:	0.265	0.663	0.072	10
4:	0.191	0.678	0.130	7
5:	0.255	0.605	0.140	29
6:	0.336	0.288	0.376	22
7:	0.342	0.106	0.552	85
8:	0.536	0.085	0.379	16
9:	0.467	0.407	0.126	7

Results

Structure analysis of all male samples (N=208)



Proportion of membership of each pre-defined population in each of the **3** clusters



Proportion of membership of each pre-defined population in each of the **4** clusters

Given Pop	Inferred Cluster 1	Inferred Cluster 2	Inferred Cluster 3	Number of Individuals
-----------	--------------------	--------------------	--------------------	-----------------------

1:	0.068	0.812	0.121	3
2:	0.093	0.705	0.202	18
3:	0.113	0.701	0.186	9
4:	0.102	0.628	0.270	4
5:	0.076	0.791	0.133	30
6:	0.269	0.289	0.442	19
7:	0.441	0.143	0.416	90
8:	0.606	0.157	0.237	31
9:	0.136	0.485	0.379	4

Given Pop	Inferred Cluster 1	Inferred Cluster 2	Inferred Cluster 3	Inferred Cluster 4	Number of Individuals
-----------	--------------------	--------------------	--------------------	--------------------	-----------------------

1:	0.040	0.718	0.060	0.182	3
2:	0.057	0.538	0.073	0.332	18
3:	0.040	0.503	0.107	0.350	9
4:	0.059	0.491	0.061	0.390	4
5:	0.046	0.693	0.063	0.198	30
6:	0.209	0.208	0.206	0.377	19
7:	0.413	0.108	0.270	0.209	90
8:	0.154	0.107	0.546	0.193	31
9:	0.061	0.250	0.071	0.618	4

1	2	3	4	5	6	7	8	9
FoB15S	FoB15O	FoB1415N	FoB14S	FoB13	FoB11	FoB09	FoB07	NP

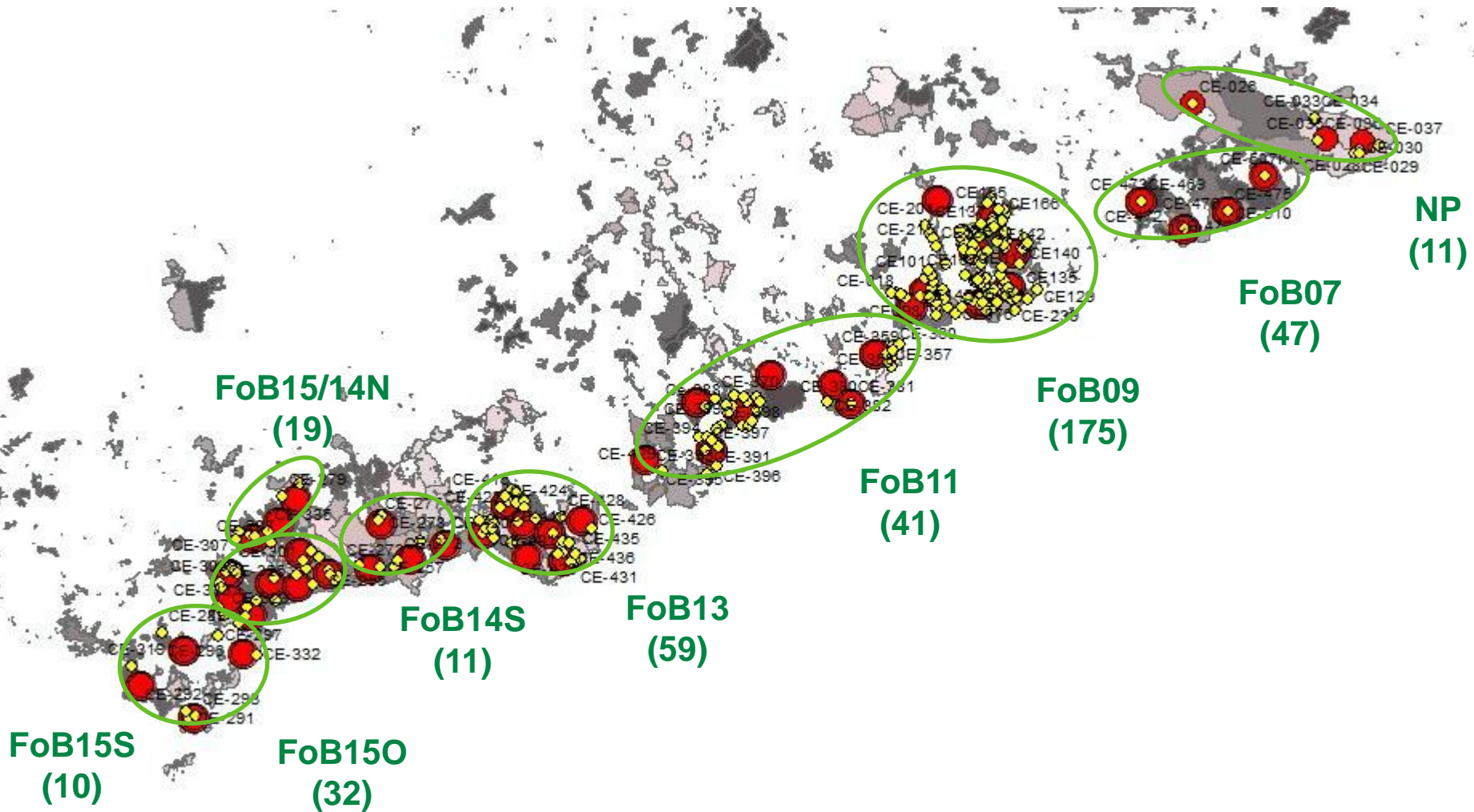
Results

Conclusions from STRUCTURE analysis:

- collectives 1 to 5 from region Vogtland/ western Ore mountains show very similar genetic structures; for further estimations they are pooled.
- collectives 6 to 8 differ clearly from this group.
- From middle Ore m. to the river Elbe, individual portions on the clusters change (clinal?)
- The sample size from NP eastern of the Elbe is too small to draw conclusions, they seem to differ from the other samples. They are not included in the further estimations.
- Sex specific sub-collectives look very similar.

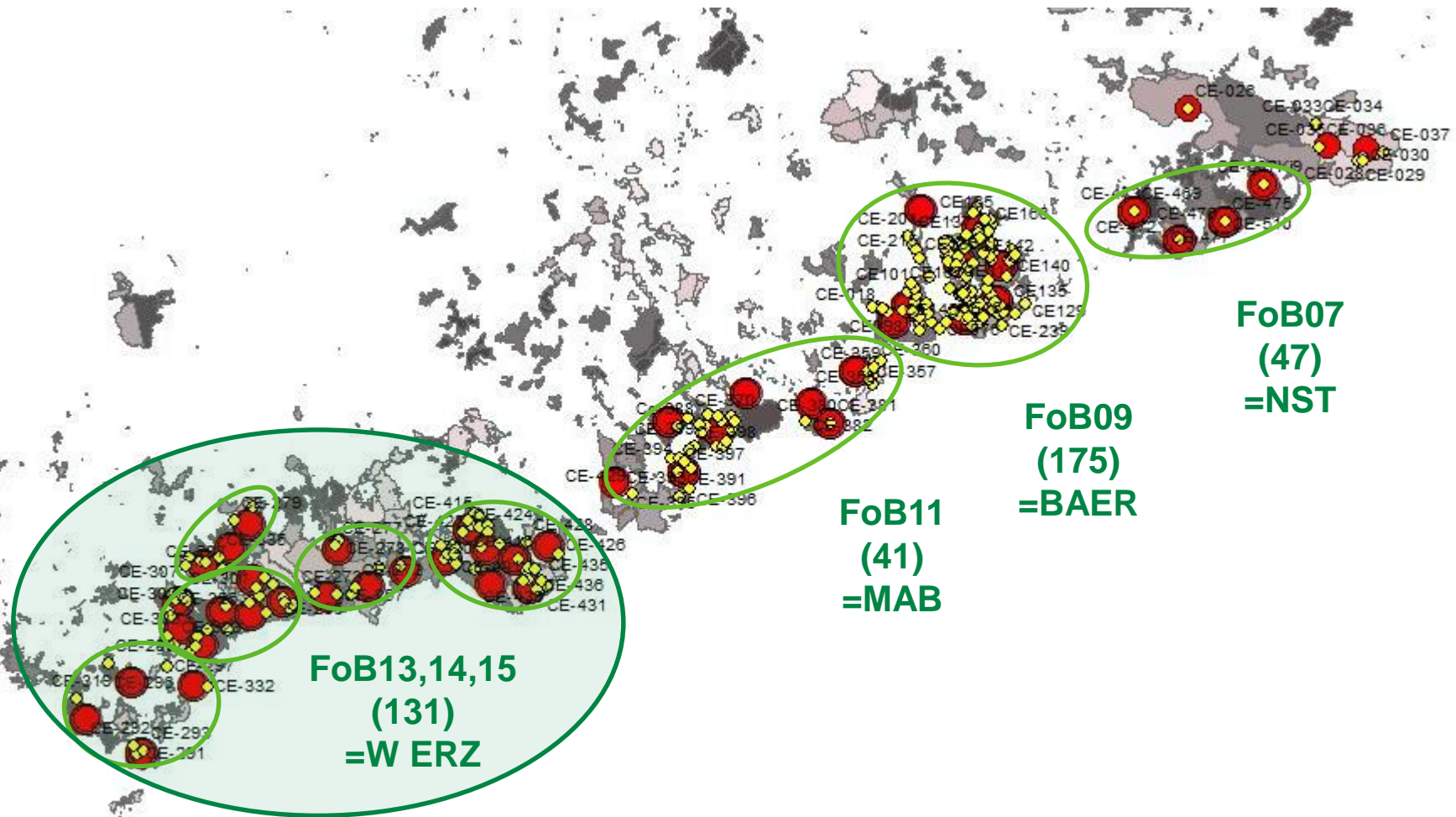
Results

preliminary geographically based collectives

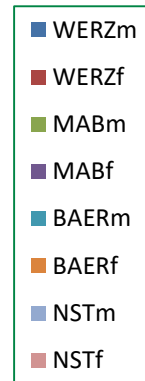
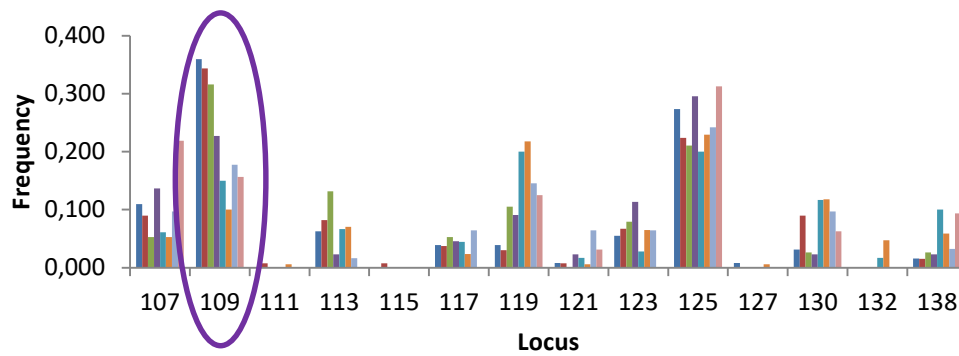


Results

4 geographically and genetically based subpopulations



Allele Frequency for HAUT14

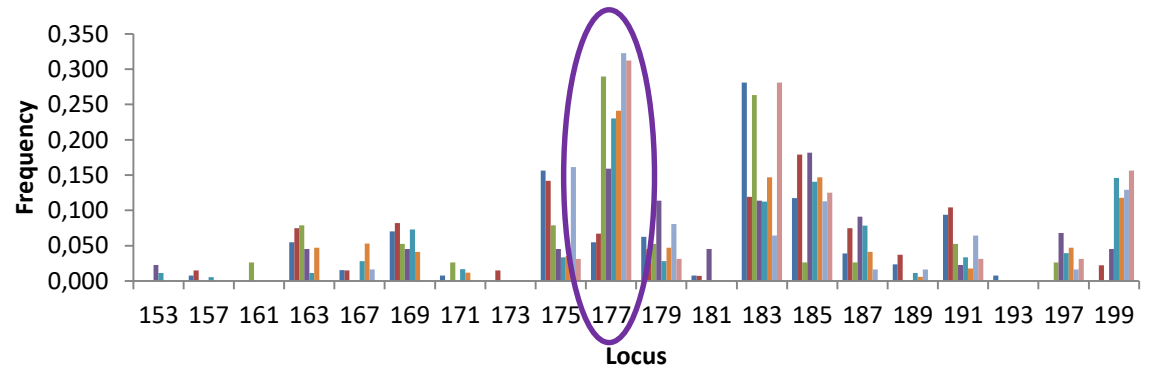


STAATSBETRIEB
SACHSENFORST

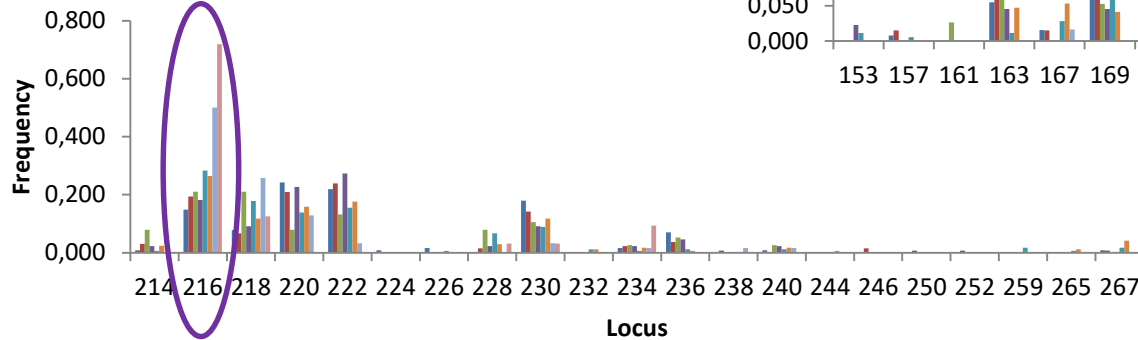


Freistaat
SACHSEN

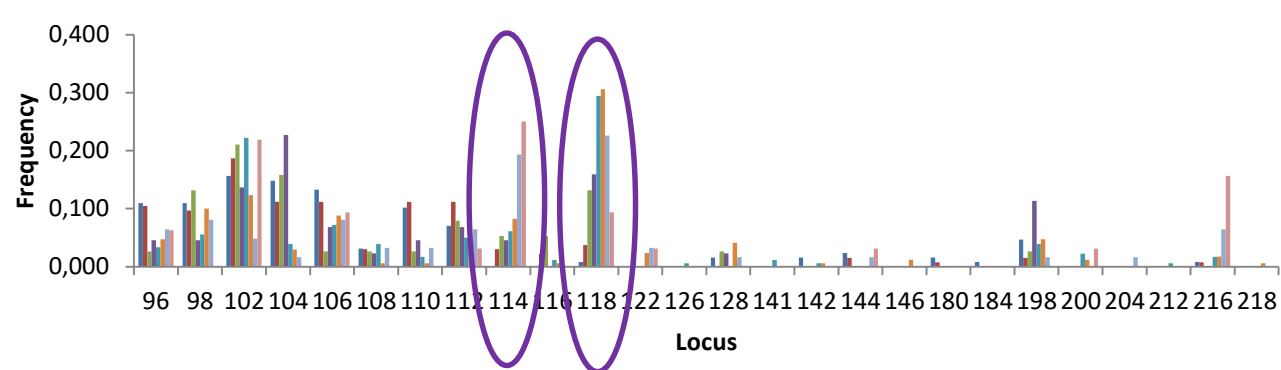
Allele Frequency for TGLA53




Allele Frequency for BM203



Allele Frequency for CSRM60



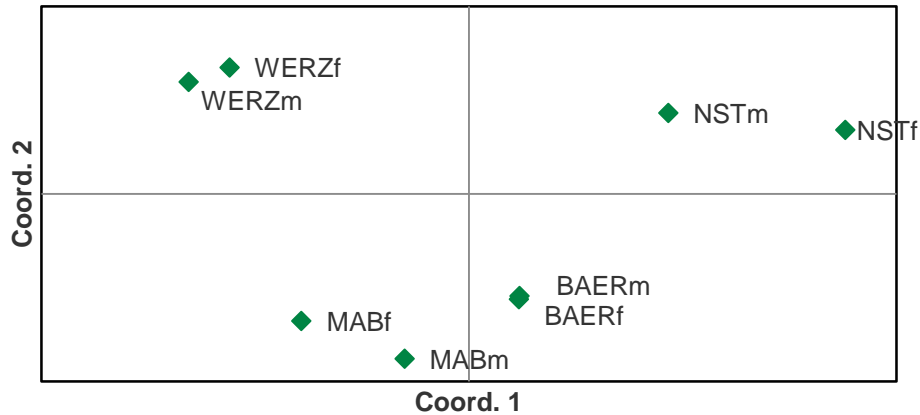
Relative allele frequencies according to region and sex (GenAIEx):

 Allels with clinal change of allele frequencies

Results

GenAIEx without NP (N = 394)

Principal Coordinates (PCoA)



PCoA via Distance matrix with data standardization

Percentage of variation explained by the first 3 axes

Axis	1	2	3
%	55.28	30.33	12.84
Cum %	55.28	85.61	98.45

Data basis: genetic distance (NEI)

Population	N	Na	Ne	Ho	He	F
Westerzgebirge	131	12.8	6.3	0.779	0.824	0.058
Marienber g	41	10.9	6.5	0.838	0.841	0.003
Bärenfels	175	13	6.4	0.804	0.839	0.041
Neustadt	47	10.1	5.6	0.766	0.793	0.033

Conclusions from GenAlEx analysis:

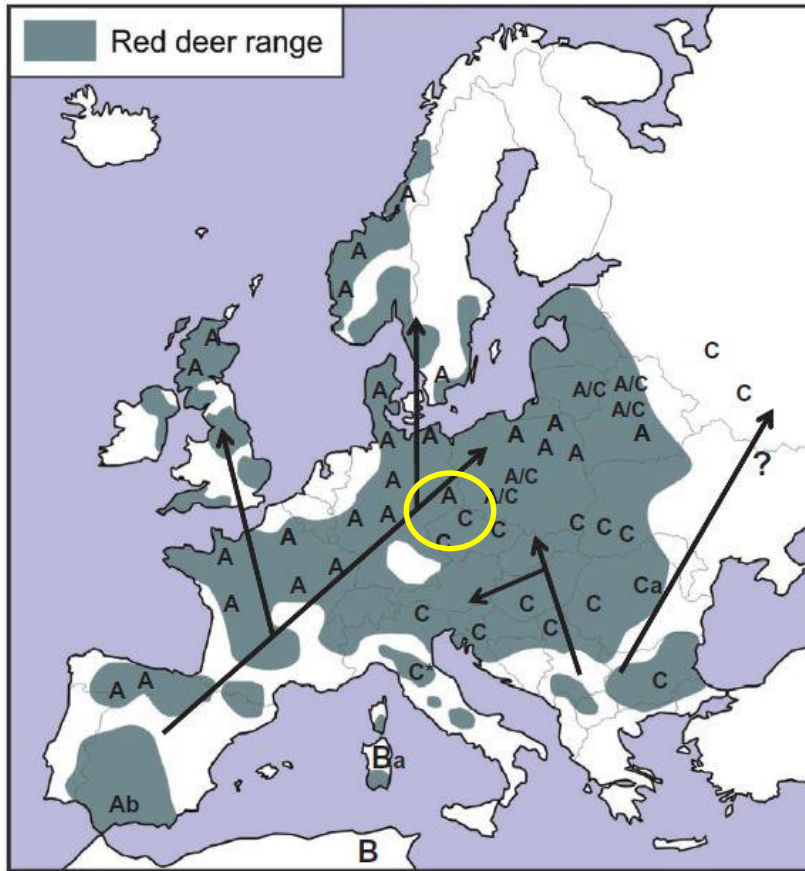
- The differences in the genetic structures are due to shifts in relative allele frequencies at several markers.
- If sample sizes are large enough, genetic differences between male and female subpopulation in the same region can be neglected.
- Subpopulation Marienberg represents the highest diversity and heterozygosity within the study, indicating more intensive genetic exchange
- In general, differences in parameters of genetic variation between regional subpopulations are very low.

Westekemper, K. 2022: Impacts of landscape fragmentation on red deer (*Cervus elaphus*) and European wildcat (*Felis silvestris silvestris*): a nation-wide landscape genetic analysis

Sample from middle part (MAB) of Saxon Ore mountains characterized by high allelic richness, low inbreeding and low isolation values in comparison with other German populations

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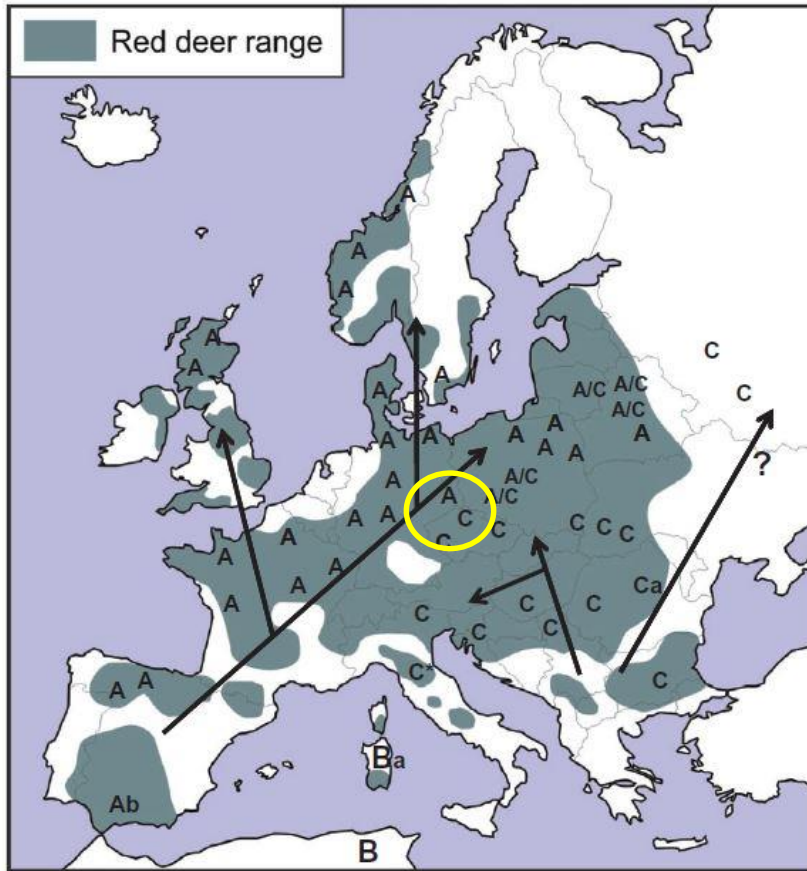


Zachos, F. E.; Hartl, G. B. (2011): Phylogeography, population genetics and conservation of the European red deer *Cervus elaphus*. In: *Mammal Review* 41 (2), S. 138–150.

Fig. 1. Distribution of the three mtDNA lineages A, B, and C in European red deer. Current distribution range is an approximation and does not include Russia. Lower-case letters (as in Ab) indicate phylogeographic outliers found by Skog et al. (2009), A/C refers to the occurrence of the two main lineages as revealed by Niedziałkowska et al. (2010), * = Mesola red deer, the lineage of which (A or C) is not fully resolved. Black arrows denote inferred postglacial recolonization routes. Map: courtesy of M. Niedziałkowska and B. Jędrzejewska.

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Krojerová-Prokešová, J. *et al.* (2015): Admixture of Eastern and Western European Red Deer Lineages as a Result of Postglacial Recolonization of the Czech Republic (Central Europe). In: *Journal of Heredity* 106 (4), S. 375–385. DOI: 10.1093/jhered/esv018.

found a population including both lineages (also on individual level) in the Czech Ore Mountains

Fig. 1. Distribution of the three mtDNA lineages A, B, and C in European red deer. Current distribution range is an approximation and does not include Russia. Lower-case letters (as in Ab) indicate phylogeographic outliers found by Skog *et al.* (2009), A/C refers to the occurrence of the two main lineages as revealed by Niedziałkowska *et al.* (2010), * = Mesola red deer, the lineage of which (A or C) is not fully resolved. Black arrows denote inferred postglacial recolonization routes. Map: courtesy of M. Niedziałkowska and B. Jędrzejewska.

Conclusions

- 4 subpopulations of red deer in the Saxon Ore Mountains, western part differing most clearly
- Relatively high genetic variation in general, highest in subpopulation Marienberg
- Genflow between subpopulations, low inbreeding
- Indication of an intact, adaptable population
- Higher reliability of results to be expected
 - Considering population on both sides of the border
 - Including mtDNA markers
 - Monitoring changes over time

Thanks are due to

STAATSBETRIEB
SACHSENFORST



- Colleagues and hunters for tissue sample collection
- our project partners for providing hair samples and movement data of the tagged animals
- Ursula Franke for managing the analyses

TU Dresden – Professur für Forstzoologie
AG Wildtierforschung



- Thank you for your attention