Research on conservation of (zoo) populations at the AGCG

Thesis research of Animal Breeding and Genetics Students

Piter Bijma
Animal Breeding & Genomics Centre

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Education at the ABGC

- Historical
  - Agriculture & Livestock
  - Breeding value estimation, Genetic Improvement
  - Students from agricultural background
- Today
  - Students are interested in
    - Companion animals
    - Zoo animals & exotic species
    - Endangered domestic/natural populations
    - Livestock (cattle)

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Recent thesis subjects

- Genetic diversity in the European zoo population of Komodo dragons
  - Cooperation with Diergaarde Blijdorp
  - Data quality limiting

Diergaarde BLIJDORP rotterdam zoo

- Genetic diversity in the zoo populations of the Humboldt Pinguin
  - Noorder Dierenpark Emmen

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Recent thesis subjects

- Analyses of Genetic Diversity for the Baringo Giraffe studbook EEP
  - Cooperation with Burgers Dierenpark Arnhem
  - Large and good data sets
  - Large differences between (sub)species

BURGERS' ZOO

- Quantifying genetic diversity in the Gelderse Slenk pigeon
  - Thought to be extinct
  - Numerous hobby breeders have been found
  - DNA collection and molecular analyses to quantify diversity

Geldersch Landschap
Geldersche Kasteelen

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Recent thesis subjects

- Genetic diversity in the Veluwezoom population of Highland cattle (ongoing)
  - Alterra & Natuurmonumenten

Natuurmonumenten Beschermt natuur in Nederland

ALTERRA WAGENINGEN UR

- Demographic and Genetic analyses of the International Golden-Headed Lion Tamarin Breeding Program
  - Kristin Leus, Antwerpen Zoo

ZOO ANTWERPEN

Recent thesis subjects

- Genetic diversity in European cattle breeds
  - ABGC Lelystad and Utrecht University
    - Hans Lenstra & Jack Windig
    - European cattle diversity consortium

- Analysis of genetic diversity of Dutch adder populations with AFLP Markers
  - Jisca Huisman & Pedro Janssen
    - Werkgroep Adders Nederland (WAN)

Analysis of genetic diversity of Dutch adder populations with AFLP Markers

- Distribution of *Vipera berus* (common adder) in Europe and in The Netherlands

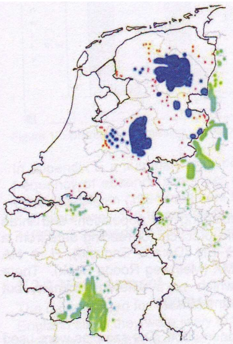
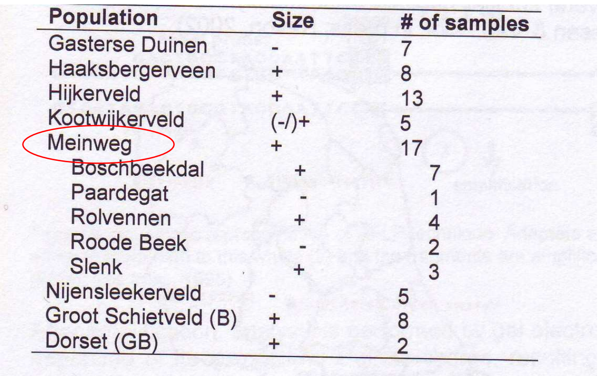


Fig 10: distribution of the Adder in the Netherlands (blue), Belgium and Germany (green) (incidental observations In red) (P. Janssen)

Fig 11: Location of the populations used in this study (P. Janssen)

Analysis of genetic diversity of Dutch adder populations with AFLP Markers

- Data
  - 93 AFLP Markers

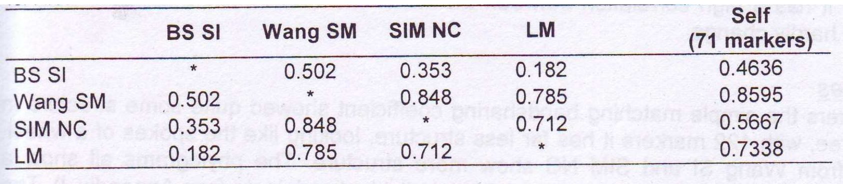


Population	Size	# of samples
Gasterse Duinen	-	7
Haaksbergerveen	+	8
Hijkerveld	+	13
Kootwijkerveld	(-/)+	5
Meinweg	+	17
Boschbeekdal	+	7
Paardegat	-	1
Rolvennen	+	4
Roode Beek	-	2
Slenk	+	3
Nijensleekerveld	-	5
Groot Schietveld (B)	+	8
Dorset (GB)	+	2

Analysis of genetic diversity of Dutch adder populations with AFLP Markers

- Results
  - Comparison of kinship estimators for **dominant** markers

Correlation between pair-wise kinship estimates from different methods



	BS SI	Wang SM	SIM NC	LM	Self (71 markers)
BS SI	*	0.502	0.353	0.182	0.4636
Wang SM	0.502	*	0.848	0.785	0.8595
SIM NC	0.353	0.848	*	0.712	0.5667
LM	0.182	0.785	0.712	*	0.7338

Which estimator to choose?

-Population genetic interpretation of results ?

-Suitability for structured populations ? **(Oliehoek et al., Genetics 2006)**

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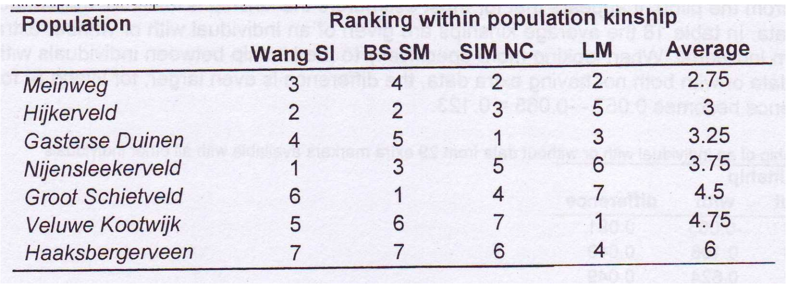
Analysis of genetic diversity of Dutch adder populations with AFLP Markers

- Results
  - Ranking of populations on diversity (lowest mean within kinship)



Population	Ranking within population kinship				
	Wang SI	BS SM	SIM NC	LM	Average
Meinweg	3	4	2	2	2.75
Hijkerveld	2	2	3	5	3
Gasterse Duinen	4	5	1	3	3.25
Nijensleekerveld	1	3	5	6	3.75
Groot Schietveld	6	1	4	7	4.5
Veluwe Kootwijk	5	6	7	1	4.75
Haaksbergerveen	7	7	6	4	6

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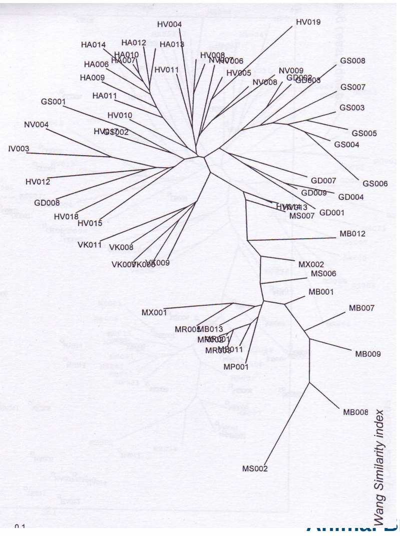
Analysis of genetic diversity of Dutch adder populations with AFLP Markers

- Results: Kinship tree



Our usual approach to manage *within species* diversity

- Key parameter: kinship (f, = coancestry)
- Background
  - Drift model → $Var(G_t) = (1-f_{avg})\ Var(G_0)$
  - Loss of additive genetic variance is proportional to f
  - Additive genetic variance → potential for genetic adaptation
- Maximizing diversity = minimizing mean pair-wise kinship
  - Including self-kinship

- Step 1
  - Estimate pair-wise and self kinship from pedigree and/or molecular data
- Step 2
  - Optimize management decisions to minimize kinship
    - GenCont (talk of Jack Windig)
- Step 3
  - Practical implementation

Issues

- Data
  - Combining molecular and incomplete pedigree data
  - Data quantity and quality
- Availability or development of molecular markers for exotic species
  - Labor and cost intensive
- Strongly fragmented population structures
  - Suitability of kinship estimators
  - Limited opportunities for diversity management
- Link between results and population genetic theory

Conclusions

- Current ABGC students are highly motivated to work on conservation genetics
- Short well-defined project offer good opportunity
  - Components of larger ongoing projects
  - Pilot studies prior to new projects

Thanks for your attention

- Acknowledgements
  - MSc-students of ABGC
  - Diergaarde Blijdorp
  - Noorder Dierenpark Emmen
  - Burgers Zoo
  - Geldersch Landschap
  - Natuurmonumenten
  - Werkgroep Adders Nederland
  - University of Utrecht
  - Alterra

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