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Improving fertility and minimizing inbreeding within the endangered pig breed 'Bunte Bentheimer'

A.D.M. Biermann, E.C.G. Pimentel, M. Tietze, and S. König

Department of Animal Breeding, University of Kassel

Witzenhausen, Germany

The Breed Bunte Bentheimer

Typical characteristics

- Middle-sized breed
- Floppy ears
- Black/white spotted
- Robust and therefore suitable for extensive production systems

- High fertility
- Good mothering ability
  - High fat content in the carcass
  - High backfat thickness
  - Marketable in high-prized segments

Historical Background

- Origin in North-Western Germany (amongst others Bad Bentheim)
- In 1900 black and white spotted pigs resulted from the crossbreed of different boars (e.g. Berkshire, Cornwall) with local Landrace sows
- 1950 official registration of the Bunte Bentheimer pig in the herd book

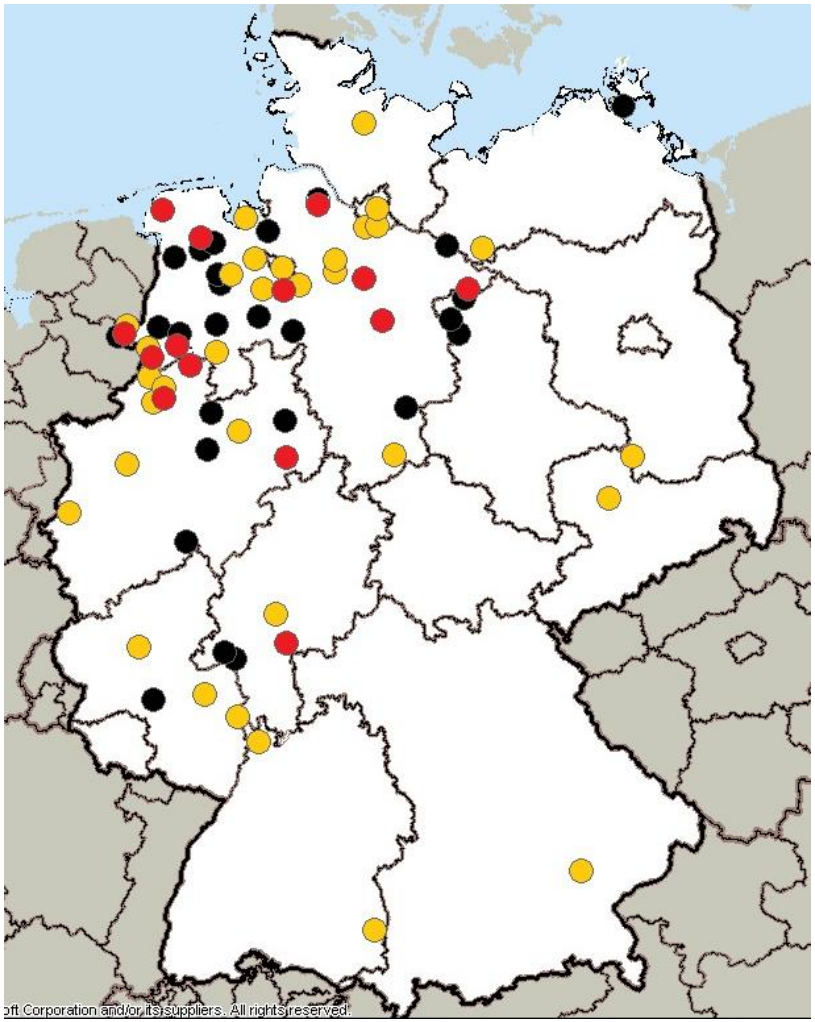
- Middle of the 20th century changes of market requirements and the breeding goal
  - → high lean meat percentage
  - → less backfat thickness

- Breeding goal did not exactly fit market requirements
- 1964: end of herd book registration
- Substantial decrease of the population size

Historical Background

- 1964 – 1987 one breeder was left (with at last 22 sows and 2 boars)
- but genetic originality could be preserved (Glodek, 1987)

→ since 1988 registration in the herd book



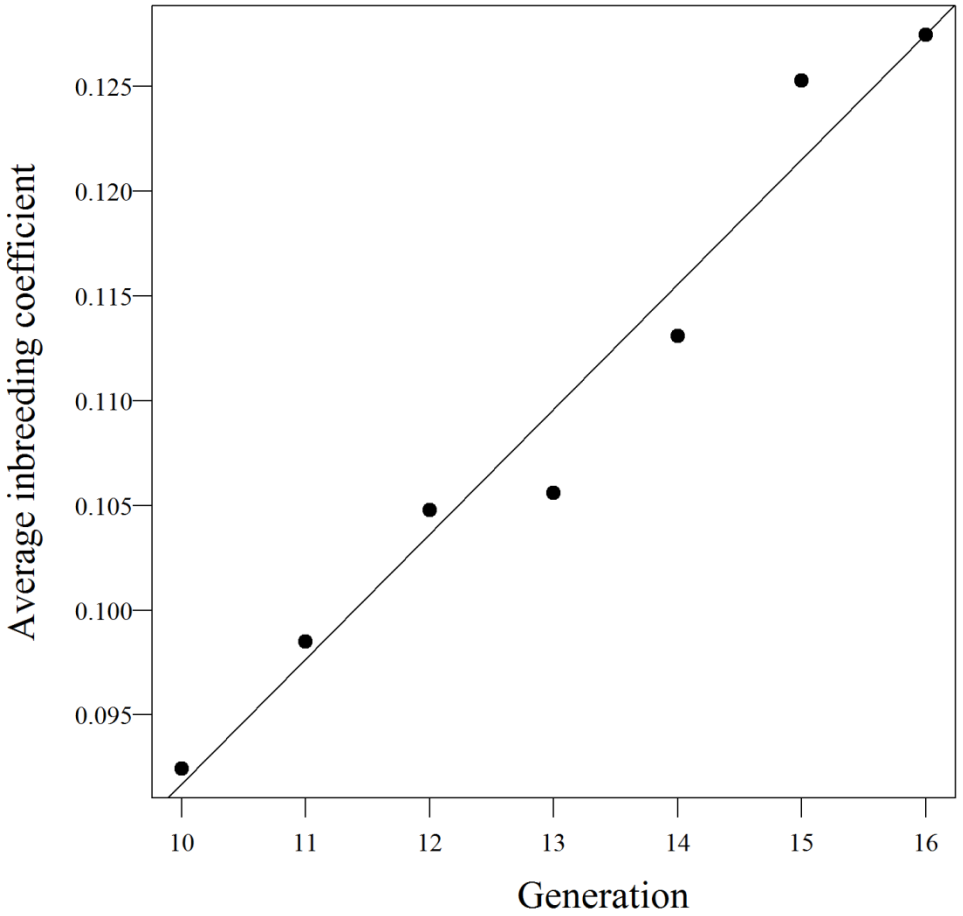
Distribution of herds and No. of sires
Herds without sire ●
Herds with 1 sire ●
Herds with 2 sires ●

Population Structure today

- Analysis of the pedigree (1540 individuals)
- The active population (07.04.2012) contains 333 in the herd book registered animals

Inbred animals (%)	98.5
F (%)	11.30
Average relationships	25.53

Population Structure



- ΔF (%) = 0.58 %
- $N_e = \frac{1}{2\Delta F} = 86$

→Status of an endangered breed

Motivation

- Currently no genetic evaluation is practiced!
- Selection based on phenotypes of
  - number of piglets born alive (NBA)
  - number of piglets weaned (NW)
- No other records!

<u>Conception of a ‘first’ breeding goal</u>

- Considering relationships and female fertility

Objectives of this study

Control of inbreeding and simultaneously maximize genetic gain in fertility

- Optimum genetic contribution theory (OGC)

→ implemented in GENCONT (*Meuwissen, 2002*)

→ selection of sires and dams with their optimal mating frequencies

- Specific mating designs using the simulated annealing algorithm based on the GENCONT output
  - MATE (*Sonesson and Meuwissen,2000)*
    - → artificial insemination is assumed
    - → mating within the whole country
  - ns-MATE (*own modified simulated annealing algorithm*)
    - → natural service is assumed
    - → mating within federal states

Genetic parameters and breeding values

1. Estimation of genetic parameters and breeding values

- DMU (*Madsen and Jensen, 2000*)
- 3008 records of NBA and NW (1985-2012)
- Pedigree
- Using a bivariate animal model and AI-REML

- EBV were standardized to a mean of 100 and standard deviation of 20

Model equation

$$y_{ijklm} = \mu + p_i + h_j + g_k + a_l + s_m + pe_l + \beta a_{li} + e_{ijklm}$$

y_{ijklm} = observation of the trait
μ = overall mean
p_i = fixed effect of parity i
h_j = fixed effect of herd j
g_k = fixed effect of year k
a_l = random additive genetic effect of sow l
s_m = random genetic effect of piglet sire m
pe_l = random permanent environment effect of sow l
βa_{li} = regression on the age of sow l at parity i
e_{ijklm} = random residual term

Results - Genetic parameters

	Number born alive	Number weaned
Number born alive	0.12	0.96
Number weaned		0.12
σ_a^2	0.61 (0.22)	0.56 (0.20)
σ_s^2	0.13 (0.07)	0.16 (0.08)
σ_p^2	0.25 (0.15)	0.08 (0.13)
σ_e^2	4.08 (0.14)	4.00 (0.13)

→ Heritabilities as expected
→ High genetic correlation between NBA and NW
→ Moderate genetic variances allow selection strategies

Optimum genetic contribution

2. Selection of sires and dams to breed the next generation

GENECONT - Input

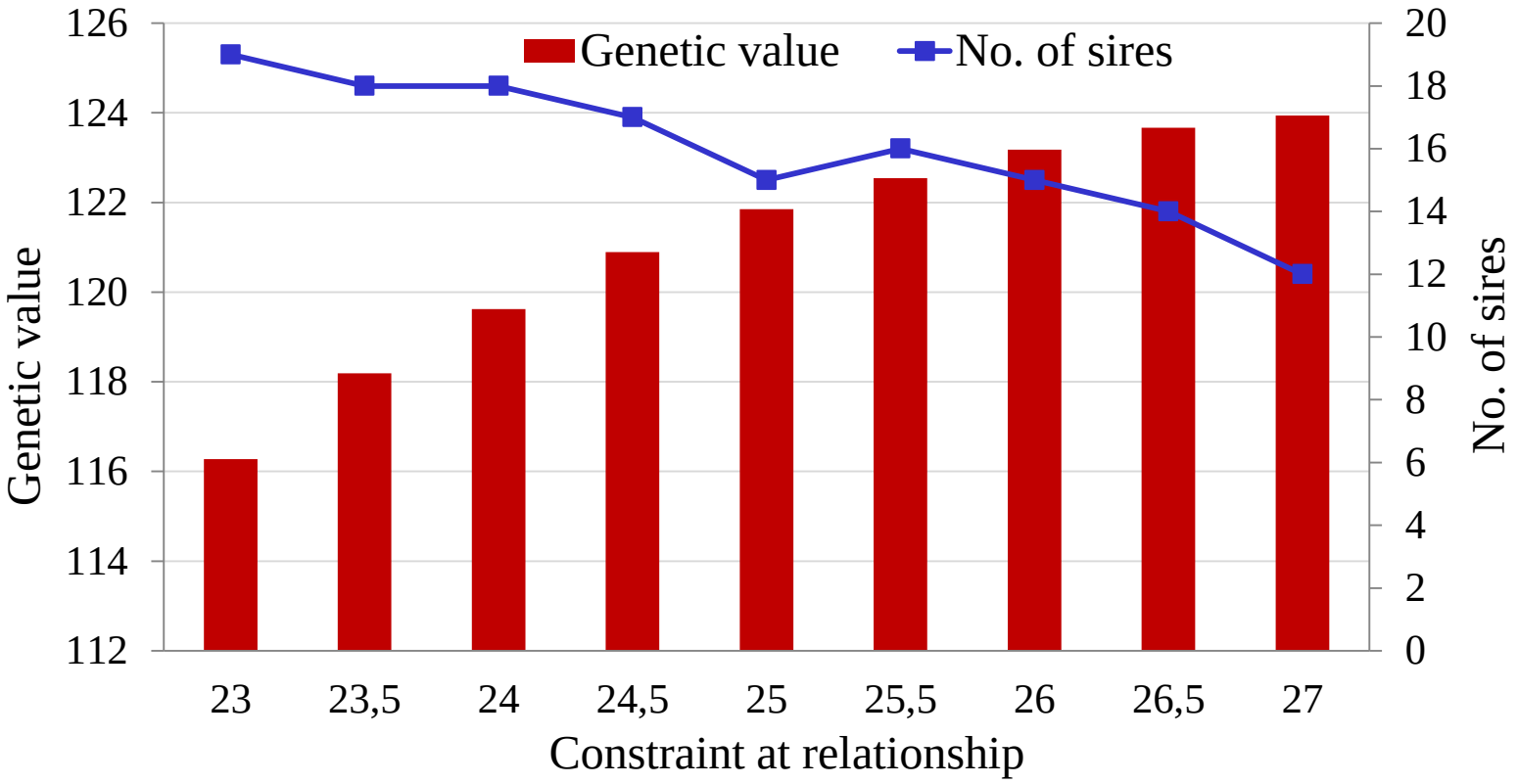
- Pedigree
- Potential selection candidates = active population (63 sires, 270 dams)
- EBV for NBA

- Selection of 30 sows with equal contributions
- Max. contribution of a sire (10%)
- Constrained relationships (scenarios 23-27%)

GENECONT - Output

- 30 sows with equal contributions (3.33%)
- Number of sires with their optimal mating frequencies

Results - Optimum genetic contribution for NBA



→ Less constrained relationship → genetic value↑ and number of sires↓
→ Genetic progress increases marginally for higher relationships
→ A compromise should be met

Mating design

3. Application of specific mating designs to reduce inbreeding in the next generation

MATE / ns-MATE - Input

- GENCONT output
- relationship of every possible mate

→ test of every possible combination until the optimum is achieved
→ criterion of the optimum = average relationship among the progeny

Results - Mating designs

Additive genetic relationship for matings											
	No. of		Mean			Minimum			Maximum		
Scenario	sires	matings NS-Mate	All	NS-Mate	Mate	All	NS-Mate	Mate	All	NS-Mate	Mate
0.23	19	23	0.208	0.151	0.159	0.000	0.000	0.000	0.636	0.227	0.215
0.24	18	10	0.215	0.179	0.167	0.000	0.058	0.000	0.665	0.229	0.227
0.25	15	23	0.220	0.175	0.178	0.000	0.000	0.000	0.665	0.228	0.233
0.26	15	25	0.227	0.180	0.188	0.000	0.000	0.000	0.665	0.228	0.233
0.27	12	25	0.232	0.191	0.197	0.000	0.000	0.000	0.665	0.293	0.247

→ ns-MATE could not fulfill criteria of the GENCONT output due to the limited number of sires in some regions

Conclusions

- Genetic parameters for NBA and NW in the small endangered population reflect estimates in conventional populations

- Using OGC and specific mating designs:
  a ‘valuable tool’ for constraining relationships without loosing genetic gain

- Artificial insemination is required to transfer theoretical GENCONT - suggestions into practice

- The mating concept will be extended for an overall breeding goal, that additionally includes behavior and meat quality

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