
Photo: MTT

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Software tools for management of genetic variation

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EuReCa

Towards self-sustainable European Regional Cattle breeds

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Data from FABA Breeding / Anna Oksa & Jouni Laurila

Approach in two stages:

- **-describing the present state (and history)**
- **-maintenance of variation** **(Theo Meuwissen)**

Measures of diversity

- proportion of variable loci
- expected vs observed heterozygosity
- number of alleles per locus (long-term potential for selection)

Satisfactory genomic assessment still expensive

Genomic tools are powerful in detecting (long-term) changes

  - *admixtures*
  - *bottlenecks*
  - *population expansions*
  - *selection*
  - *etc*

Parameters based on ***pedigree*** give a cheap and holistic picture

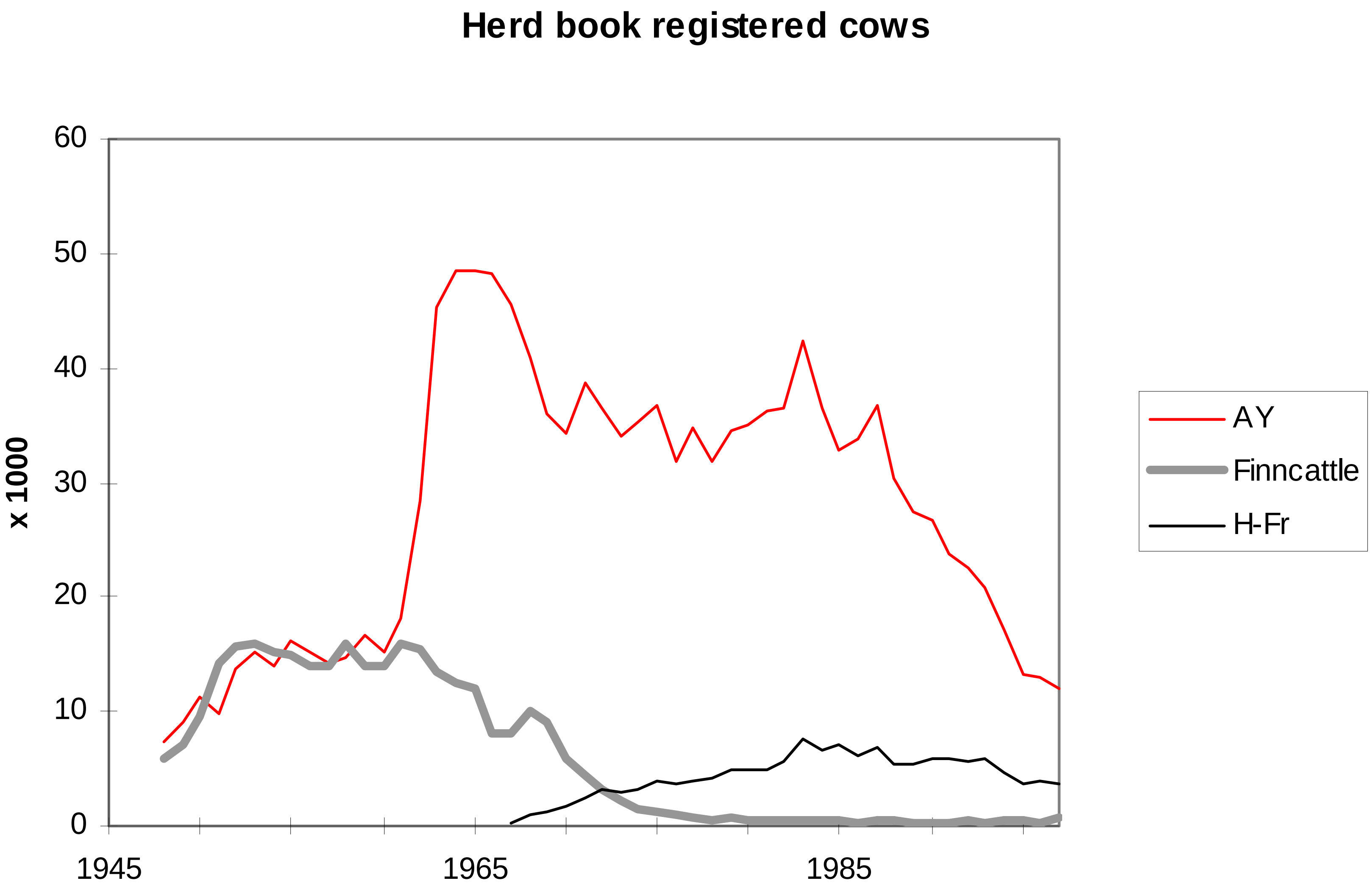
Inbreeding coefficient related to mean
Coancestry measures drift and changes in variance

Inbreeding is unavoidable.
- therefore the estimates depend on the depth of pedigree recording

Examples on Finncattle breeds

Eastern, Northern and Western Finncattle Societies formed around 1900

Ayrshire importation since 1850



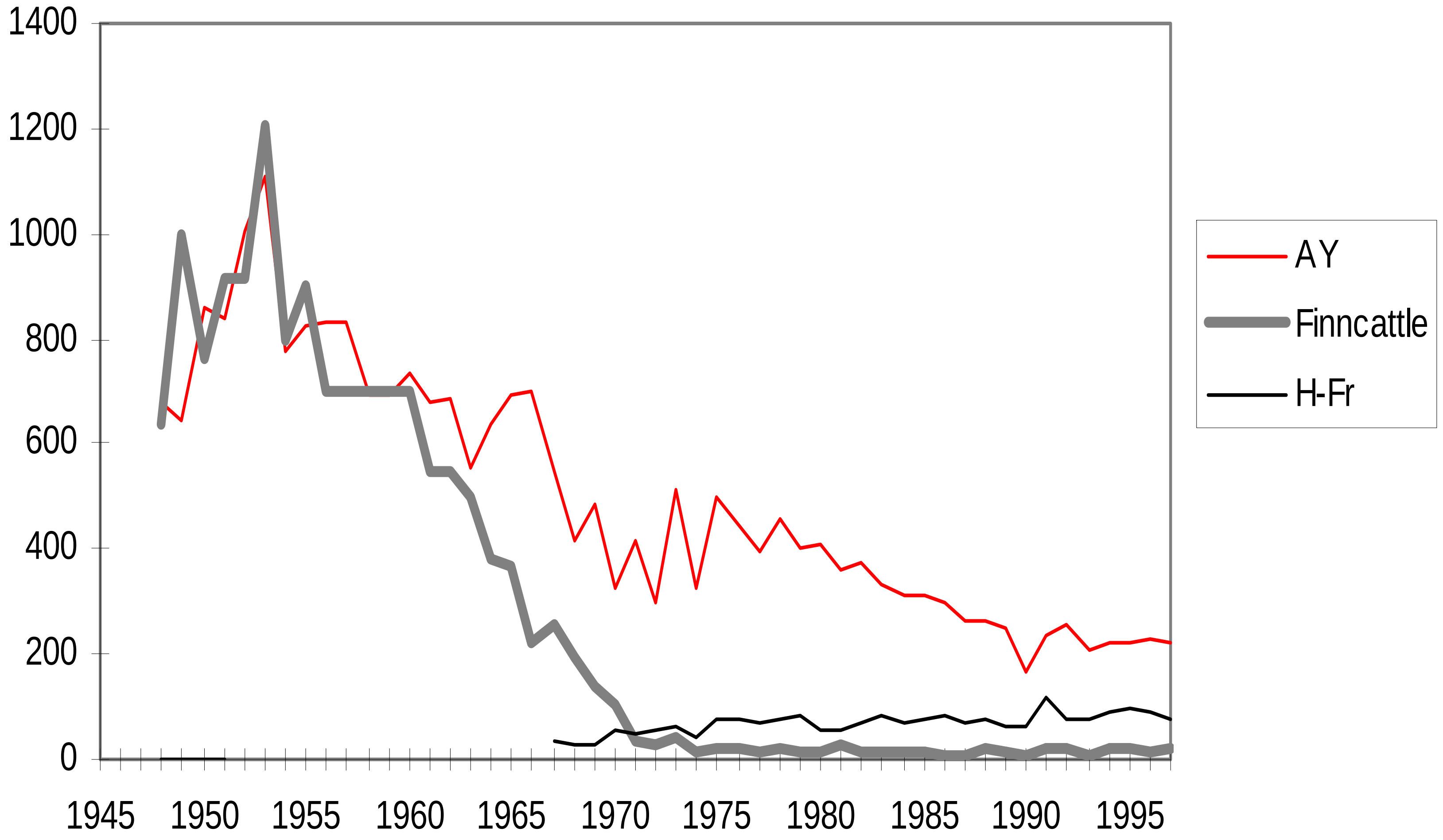
Finncattle breed societies fused together in 1947

Systematic policy to replace Finncattle with Holstein-Friesian since 1960

Revival of Finncattle breeds in the 1980's

Maijala 1998

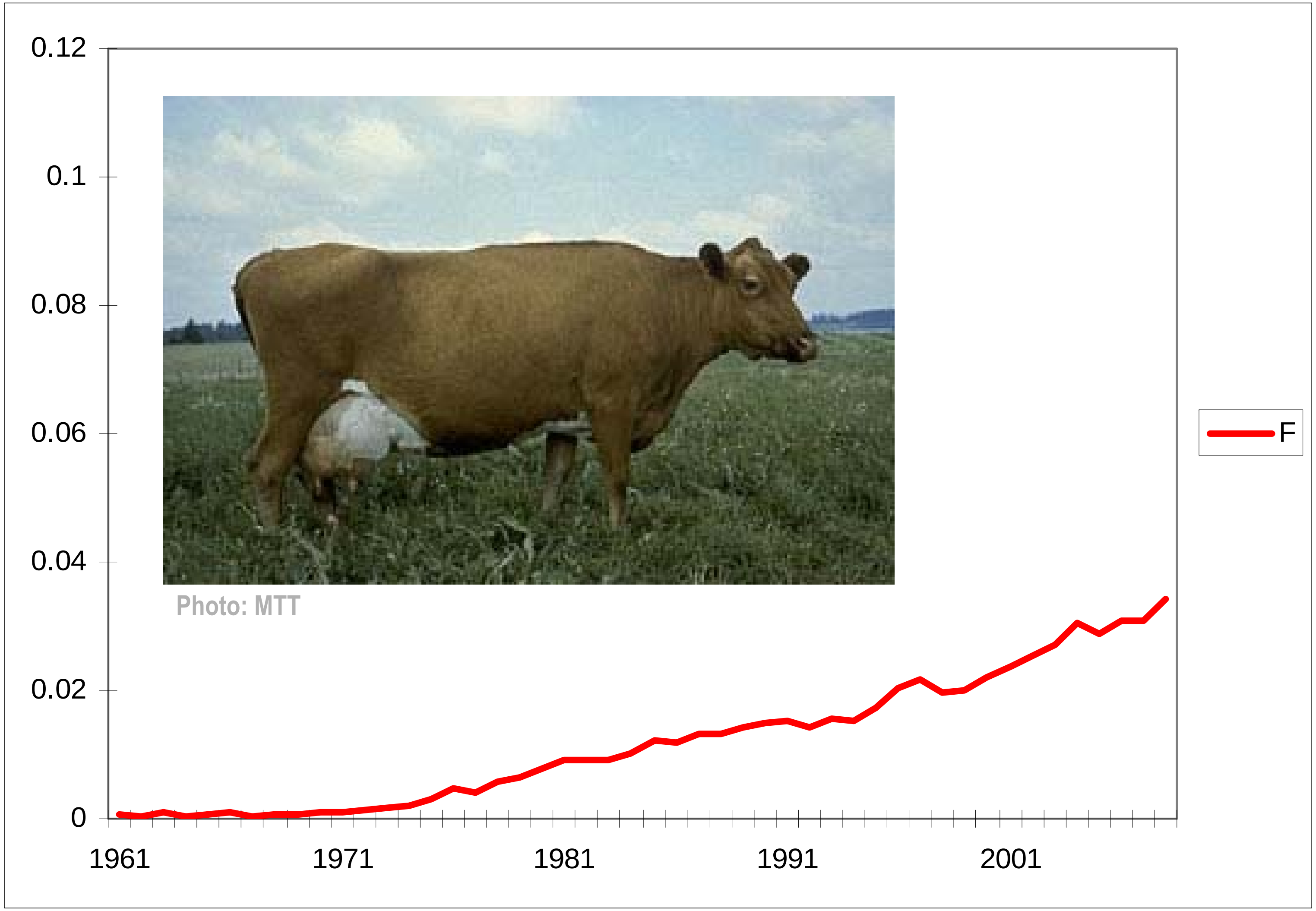
Herdbook registered bulls



AI started in mid-1940’s, use of frozen semen in mid-1960’s

Maijala 1998

Western Finncattle – level of inbreeding



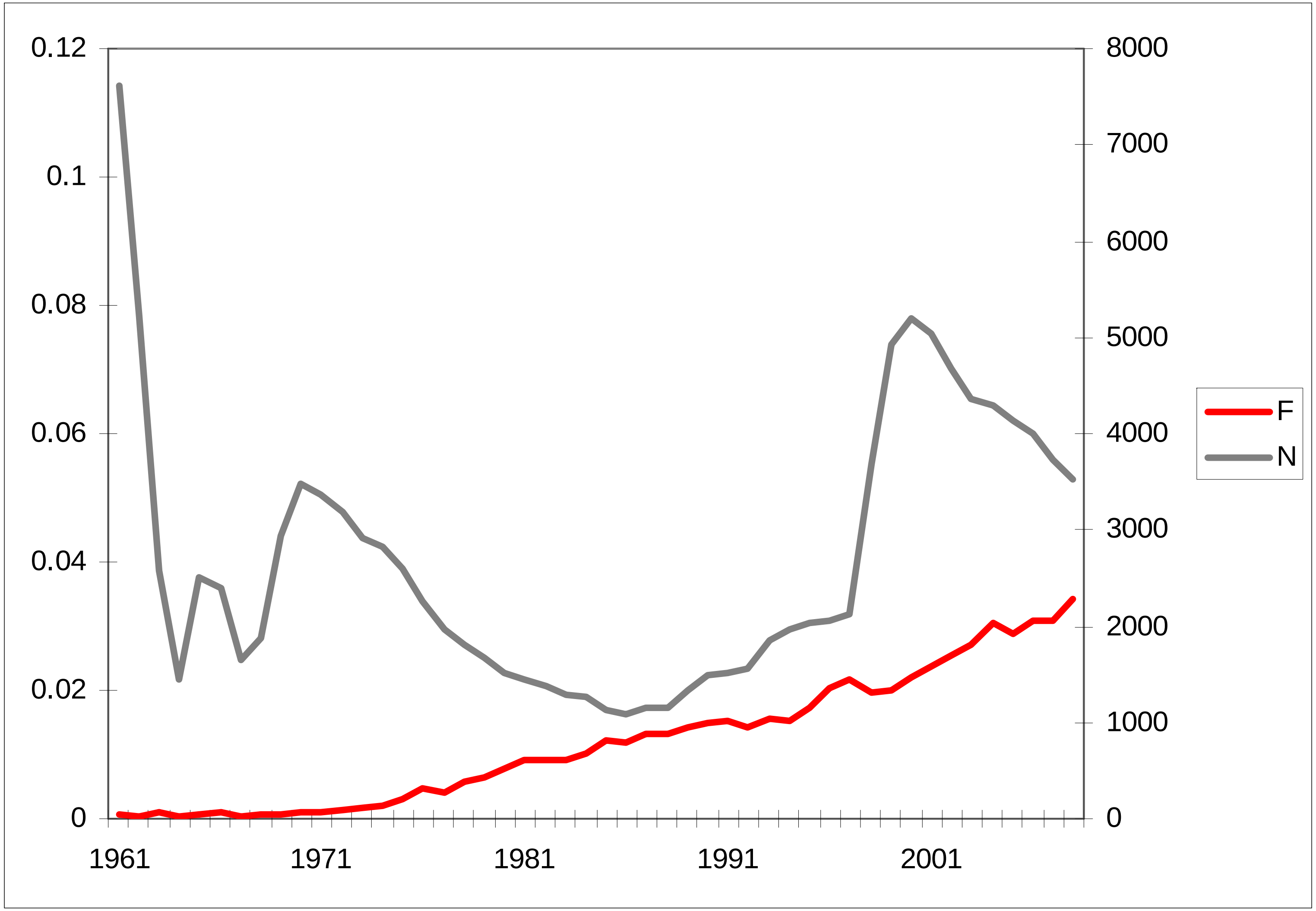
BETTER CONCEPT:

Proportional increment or ***rate of inbreeding*** ***($\Delta F = 1 / 2 N_e$)***
- stays constant over generations
- useful parameter for comparing populations (or phases in population history)

Effective population size N_e depends mainly on the number of parents used to produce the next generation

Existence of pedigree recording essential!

Western Finncattle – declining population



changes in popularity of herd book registration

Consider the demographic information

-number of male (N_m) and female (N_f) parents

$$N_e = \frac{4 N_m N_f}{N_m + N_f}$$

The small male number determines the effective size

- especially number of AI bulls

ENDOG program to compute Ne and respective parameters
http://www.ucm.es/info/prodanim/html/JP_Web_archivos/endog45.zip

Gutierrez & Goyache (2005) JABG 122: 172-176

Also resorted to **RelaX2**
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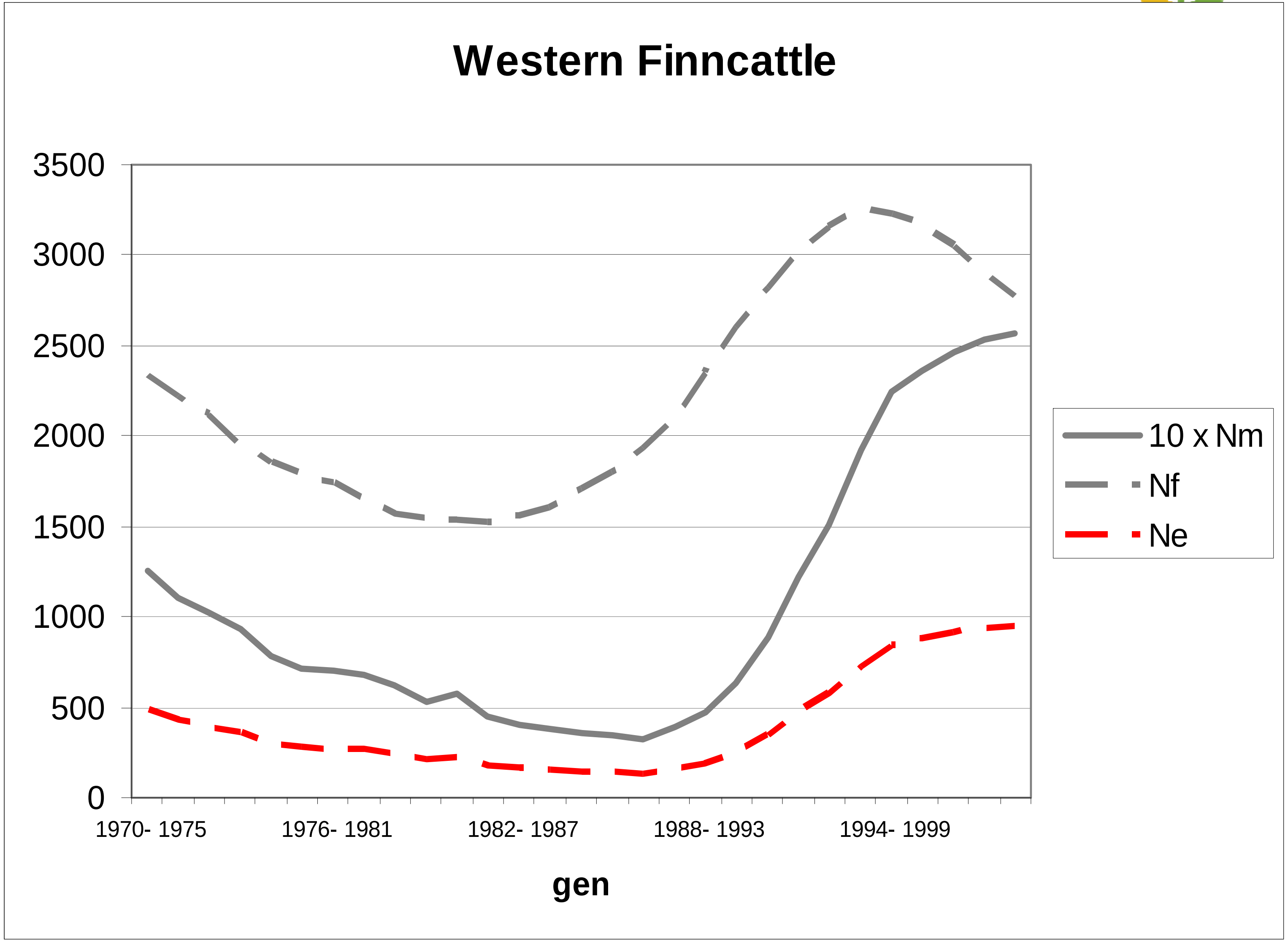
Strandén & Vuori (2006) 8th WCGALP

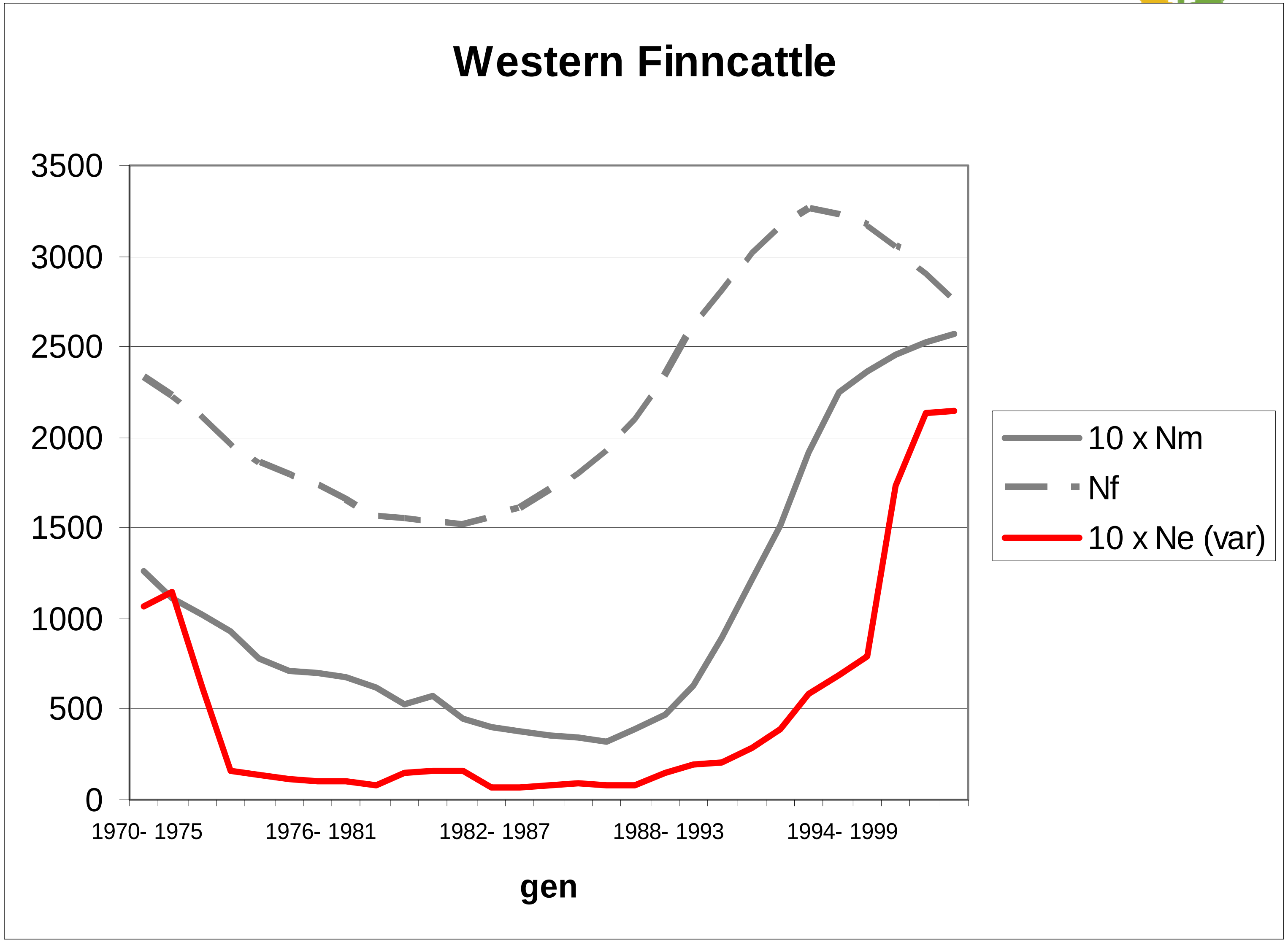


considering the population with 6 y windows

Some parents have more offspring than others because of

better performance (selection)
popular breed features
etc.

Essentially we have less parents and have to consider variation in progeny number


Western Finncattle
3500
3000
2500
2000
1500
1000
500
0
1970- 1975
1976- 1981
1982- 1987
1988- 1993
1994- 1999
gen
10 x Nm
Nf
10 x Ne (var)

Uneven representation (selection advantage) of families

inherited over generations

Estimation of proportional increment of inbreeding level F

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

or similarly we could compute the changes in coancestry (or ½ additive relationship)

(more stable and gives early signals about undesirable trends)

→ we need

separation of generations and the intervals between
inbreeding coefficients F (or pairwise coancestry of two individuals or relationship matrix A)

lots of methods to compute F

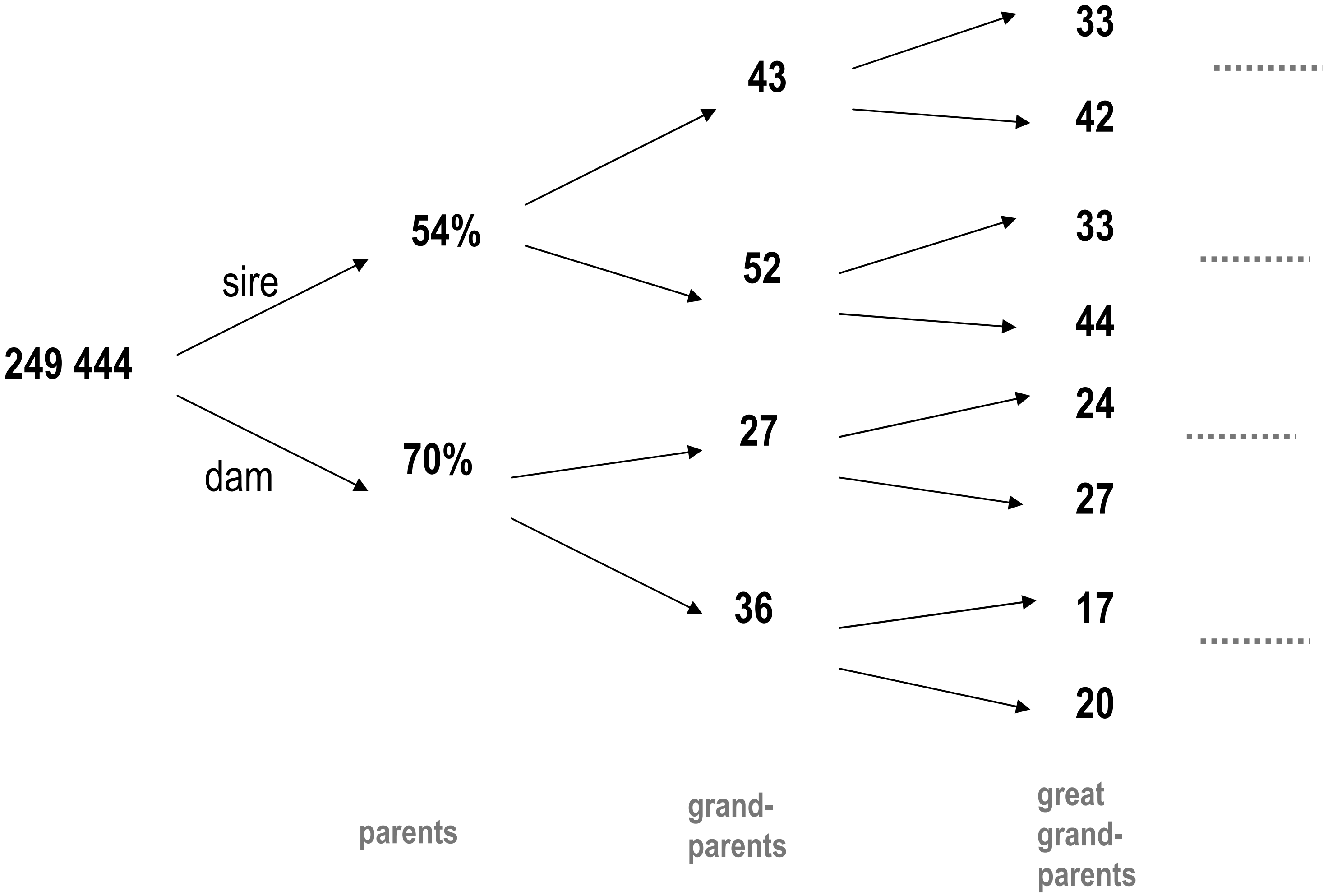
Wright's path method (Colleau, GENUP, PEDIGREEVIEWER)

tabular method (used in BLUP; e.g. Meuwissen; ***A*** given by EVA, ENDOG, PEDIG)

other methods: contribution, gene dropping

easy to compute → often the only parameter presented

Pedigree completeness in Western Finncattle



249 444

sire

dam

54%

70%

43

52

27

36

33

42

33

44

24

27

17

20

....

....

....

....

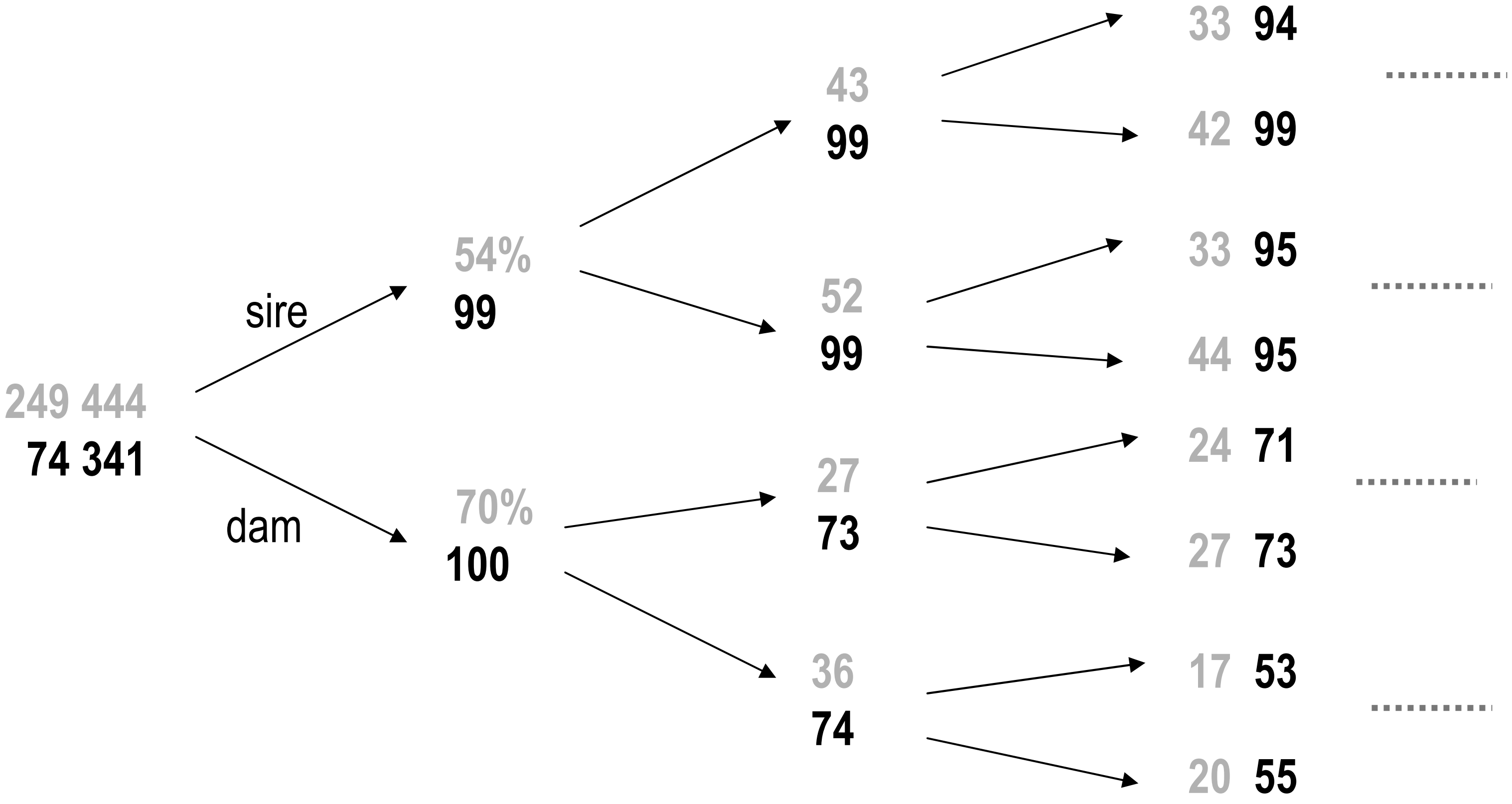
parents

grand-
parents

great
grand-
parents

Some animals have pedigree information over higher, some over lower number of generations

information from ≥ 3 equivalent generations



249 444
74 341

sire

dam

54%
99

70%
100

43
99

52
99

27
73

36
74

33 **94**

42 **99**

33 **95**

44 **95**

24 **71**

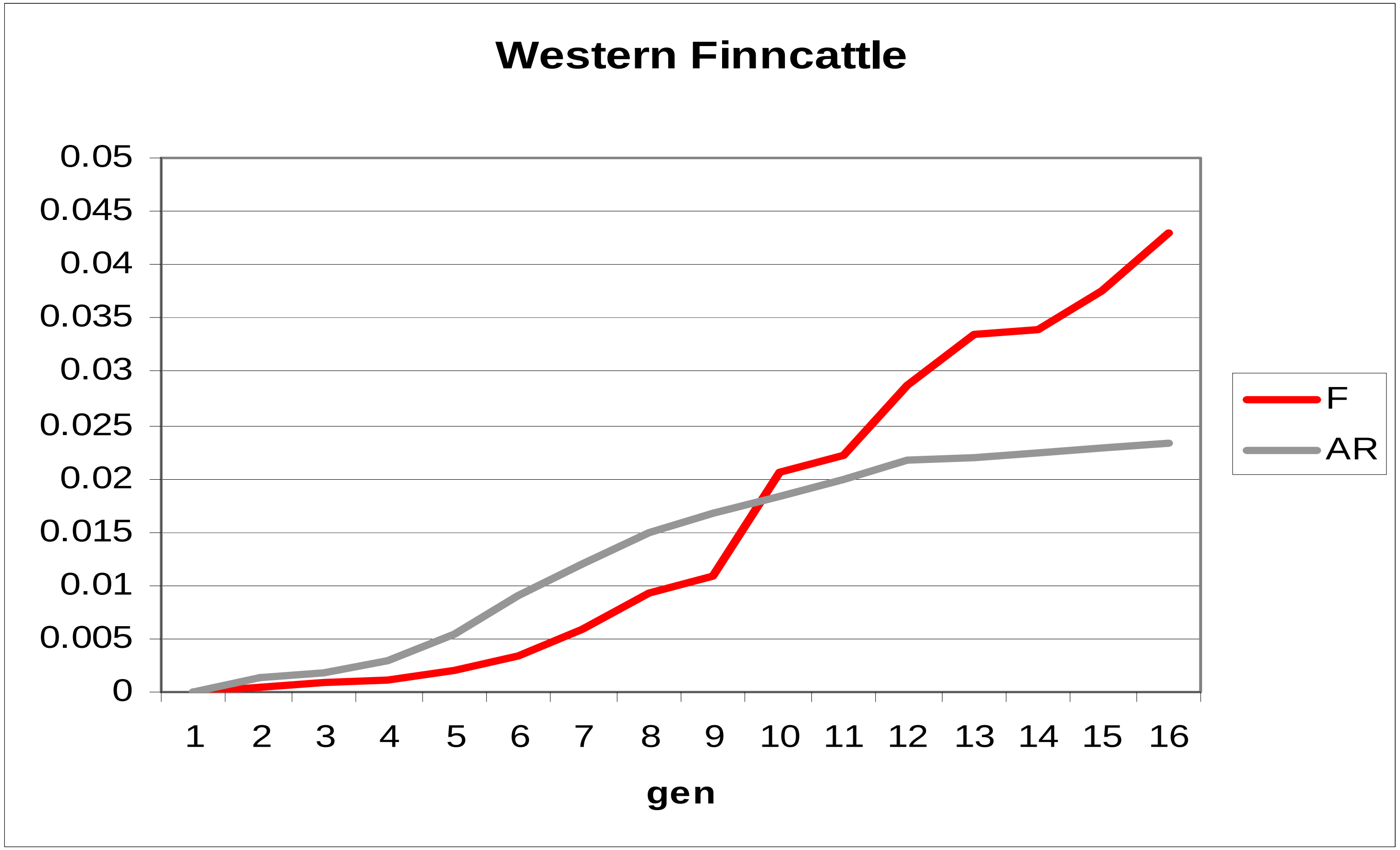
27 **73**

17 **53**

20 **55**

generation intervals in Western Finncattle

	all	≥ 3 gen	≥ 4 gen	≥ 5 gen
animals	249 444	74 341	51 682	34 528
sire → son	7.8	8.0	7.8	7.9
sire → daughter	7.2	7.0	7.1	7.2
dam → son	7.2	5.2	4.6	4.4
dam → daughter	4.8	4.3	4.1	3.9



information over ≥ 3 equivalent generations
average relatedness (pairwise coancestry & inbreeding)

N_e varies 50-1300 – harmonic mean over gen's 171

Overlapping generations and shallow pedigrees

Because at generation t the level of inbreeding is $F_t = 1 - (1 - \Delta F)^{t-1} = 1 - (1 - 1/2N_e)^{t-1}$

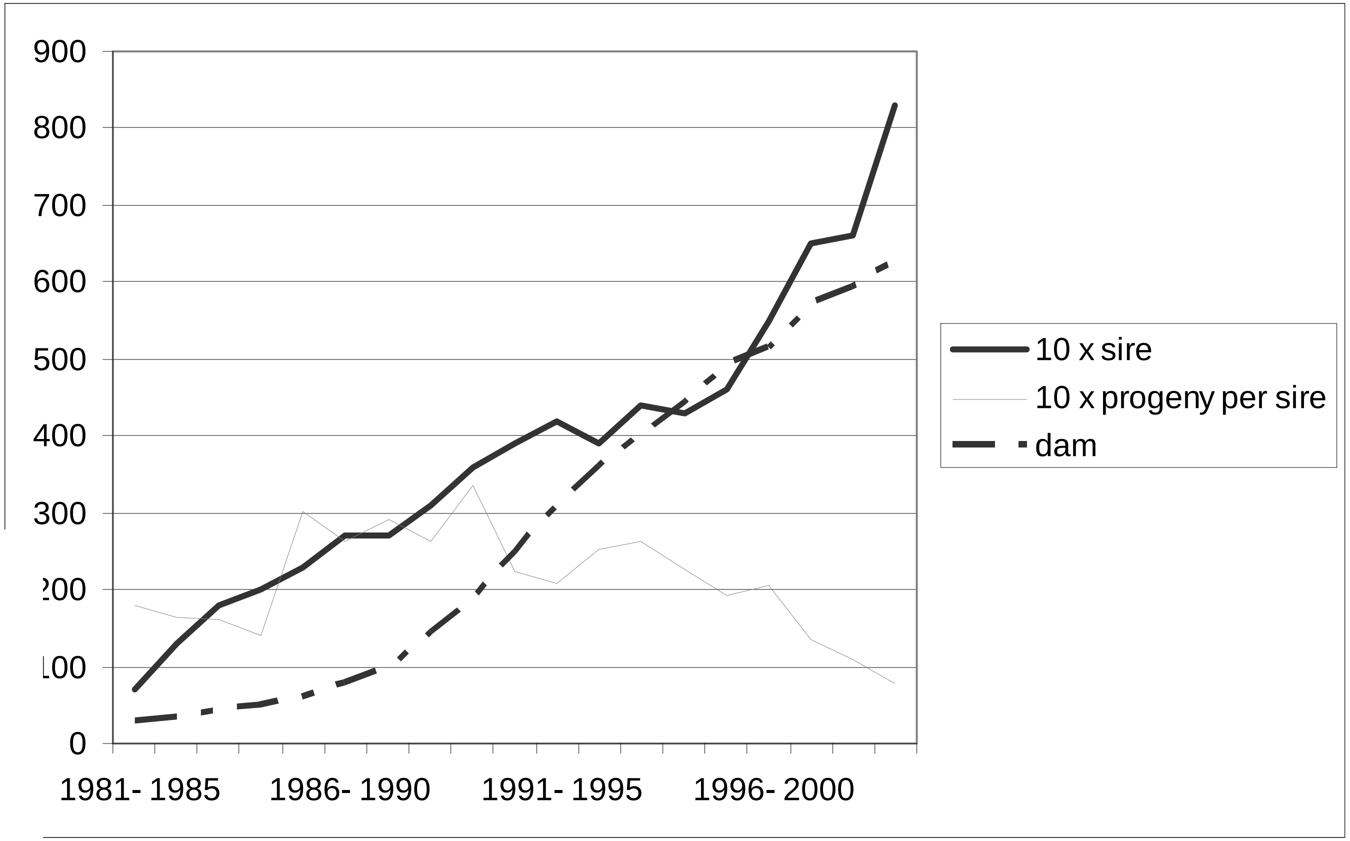
1) N_e is log regr of $(1 - F_t)$ on birth date / generation interval (Perez-Enciso 1995)

2) for individual i we have $\Delta F_i = 1 - \sqrt[t-1]{(1 - F_i)}$

and average N_e = 1 / 2 average ΔF (González-Recio et al 2007; Gutiérrez et al 2009))

For Western Finncattle 1) $N_e = 89$ and 2) $N_e = 109$

Northern Finncattle



15,408 animals in the pedigree

without requirements for the amount of information
estimates of N_e around 40-50

Conclusions

Pedigree recording, registers/databases and their utilisation produce very rewarding results

When pedigree information is missing, we can rely only on herd information

AI is an extremely powerful tool

- *Northern Finncattle*
  - *oldest bull from 1983*
  - *semen stored only from 4 bulls in '80's*

- *Western Finncattle*
  - *8 bulls from 1960's*
  - *35 bulls from 1970's*
  - *etc.*

…conclusions

ENDOG software

- **free – and very detailed and useful manual and support**

- **efficient pedigree checks**

-emphasis on useful concepts ΔF, N_e, pedigree completeness, depth, overlap…

- **several options for estimation** – *to get a desired answer*

- **requires computer skills (ACCESS)** *(no renumbering)*

- **possible improvements**
  - *addition of rows (and birth date) for parent individuals without pedigree*
  - *coancestry measure, var of family size*
  - *age distribution of progeny from AI bulls*
  - *pedigree completeness measure (MacCluer et al 1983)*