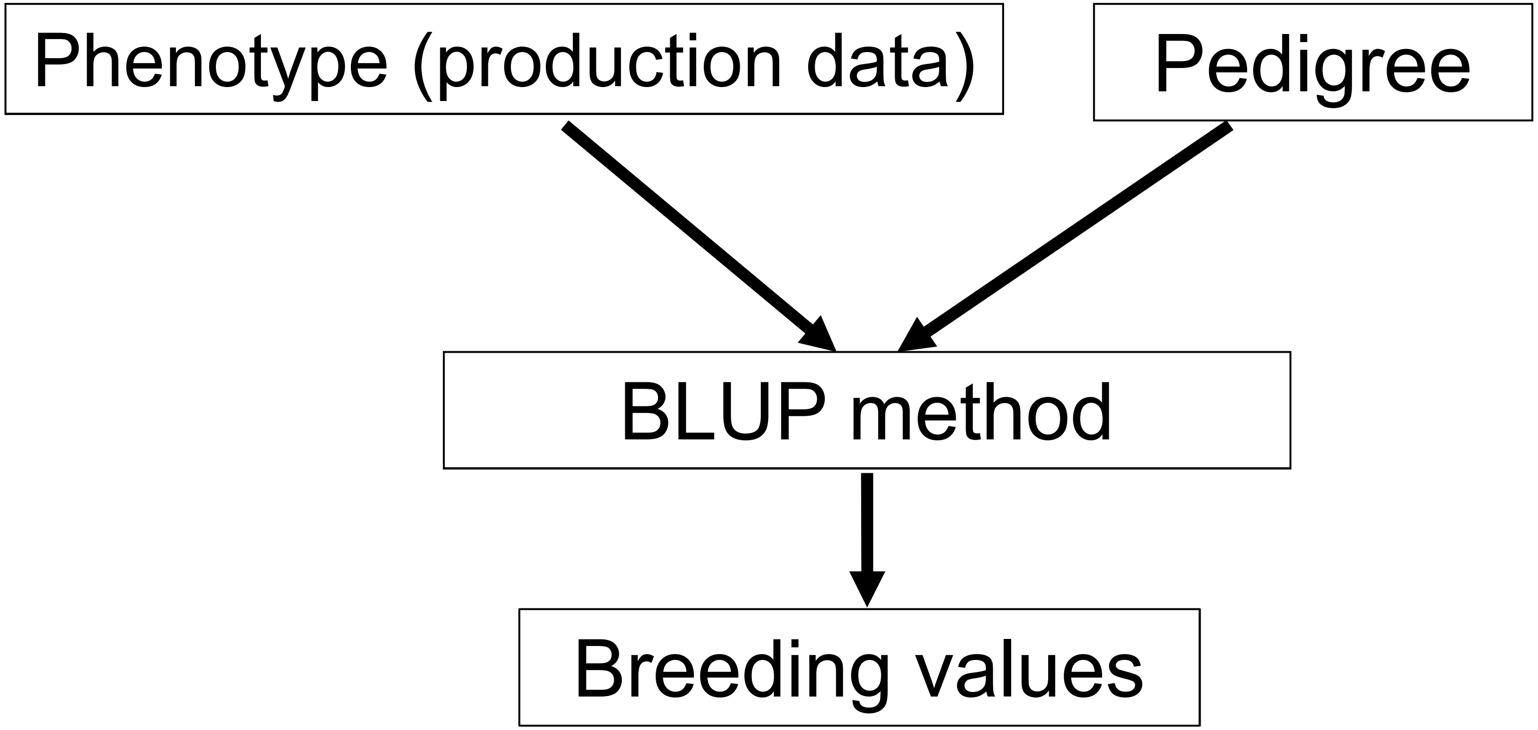
Partition of genetic trends by origin in Croatian dairy cattle

Špehar M.[1], Ivkić Z. [1], Bulić V. [1], Barać Z.[1] , Gorjanc G.[2]

[1]Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia
[2]University of Ljubljana, Biotechnical Fac., Animal Science Dep., Groblje 3, 1260 Domžale, Slovenia

Introduction



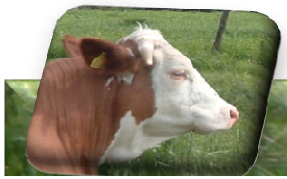
Genetic trend

average breeding value per birth year of individuals

Genetic improvement

- Domestic selection
- Import (animals or semen)

- **Aim**: partition the genetic trend in Croatian Simmental cattle according to the origin of selection



Material

- Breeding values from routine genetic evaluation
  - Lactation protein yield (2003 to 2011)
  - Net daily gain (2006 to 2011)
- Pedigree information
- Central database of Croatian Agricultural Agency

Origin / Trait	Number of animals	
	Phenotype data	Pedigree data
Protein yield (kg)	101,475	170,610
AUT	1,88	6,13
CRO	96,80	89,49
CZE	0,58	0,31
DEU	0,74	3,96
UCN (USA, Canada, The Netherlands)	/	0,08
Other	/	0,03
Net daily gain (g/day)	121,029	303,348
AUT	/	1,72
CRO	100,0	96,9
CZE	/	/
DEU	/	1,19
UCN (USA, Canada, The Netherlands)	/	0,06
Other	/	0,13

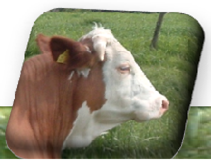
Method

- Prior model for $\boldsymbol{a}$ in animal model
  - known parents $a_i = 1/2\left(a_{f(i)} + a_{m(i)}\right) + w_i$
  - unknown parents $a_i = w_i$

$$\boldsymbol{a} = \boldsymbol{T}\boldsymbol{w}, \boldsymbol{w} = \boldsymbol{T}^{-1}\boldsymbol{a}$$

- García-Cortés et al. (2008)
- Define $\boldsymbol{k}$ partitions (countries) $\boldsymbol{P}_1 + \boldsymbol{P}_2 + \cdots + \boldsymbol{P}_k = \boldsymbol{I}$

$$\begin{aligned}\boldsymbol{a} &= \boldsymbol{T}\boldsymbol{w} = \boldsymbol{T}\boldsymbol{T}^{-1}\boldsymbol{a} \\ &= \boldsymbol{T}(\boldsymbol{P}_1 + \boldsymbol{P}_2 + \cdots + \boldsymbol{P}_k)\boldsymbol{T}^{-1}\boldsymbol{a} \\ &= \boldsymbol{T}\boldsymbol{P}_1\boldsymbol{T}^{-1}\boldsymbol{a} + \boldsymbol{T}\boldsymbol{P}_2\boldsymbol{T}^{-1}\boldsymbol{a} + \cdots + \boldsymbol{T}\boldsymbol{P}_k\boldsymbol{T}^{-1}\boldsymbol{a} \\ &= \boldsymbol{a}_1 + \boldsymbol{a}_2 + \ldots + \boldsymbol{a}_k\end{aligned}$$



Method (2)

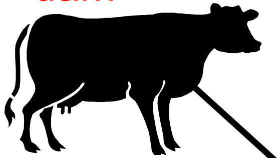
$$\hat{\boldsymbol{a}} = \boldsymbol{T}\boldsymbol{P}_1\boldsymbol{T}^{-1}\hat{\boldsymbol{a}} + \boldsymbol{T}\boldsymbol{P}_2\boldsymbol{T}^{-1}\hat{\boldsymbol{a}} + \cdots + \boldsymbol{T}\boldsymbol{P}_k\boldsymbol{T}^{-1}\hat{\boldsymbol{a}}$$

the flow of genes through pedigree

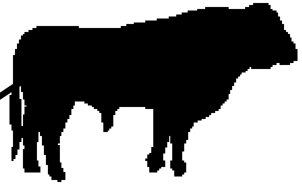
the “path” matrix for the i-th origin

Example (1)

EBV_{dam} = 90



EBV_{sire} = 110



Foreign

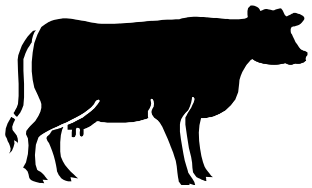
Parent average = ½ EBV_{dam} + ½ EBV_{sire}

= ½ [(90) +(110)]= 100

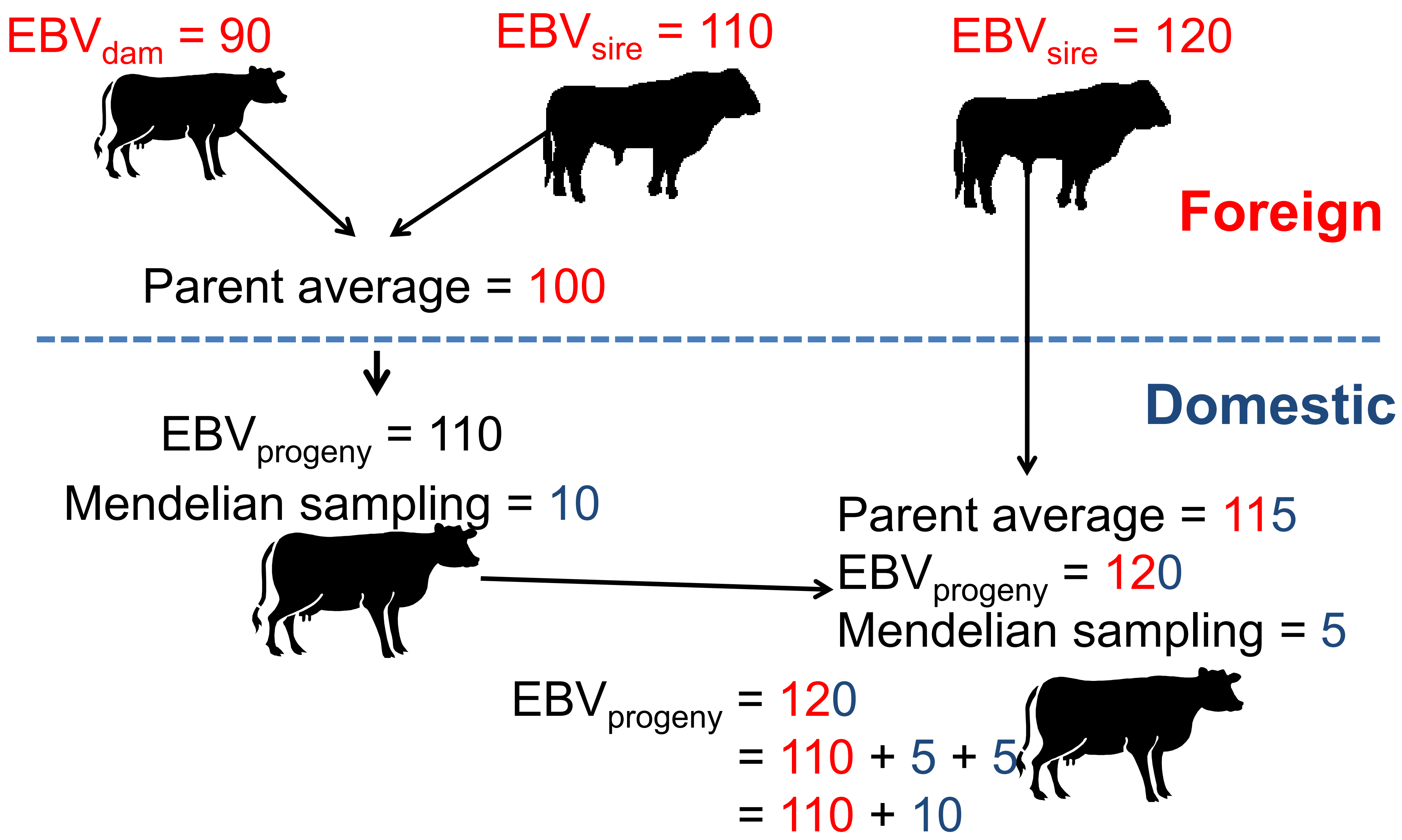
Domestic

$EBV_{progeny}$ = 110

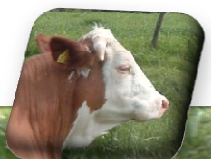
Mendelian sampling = 110 – 100 = 10



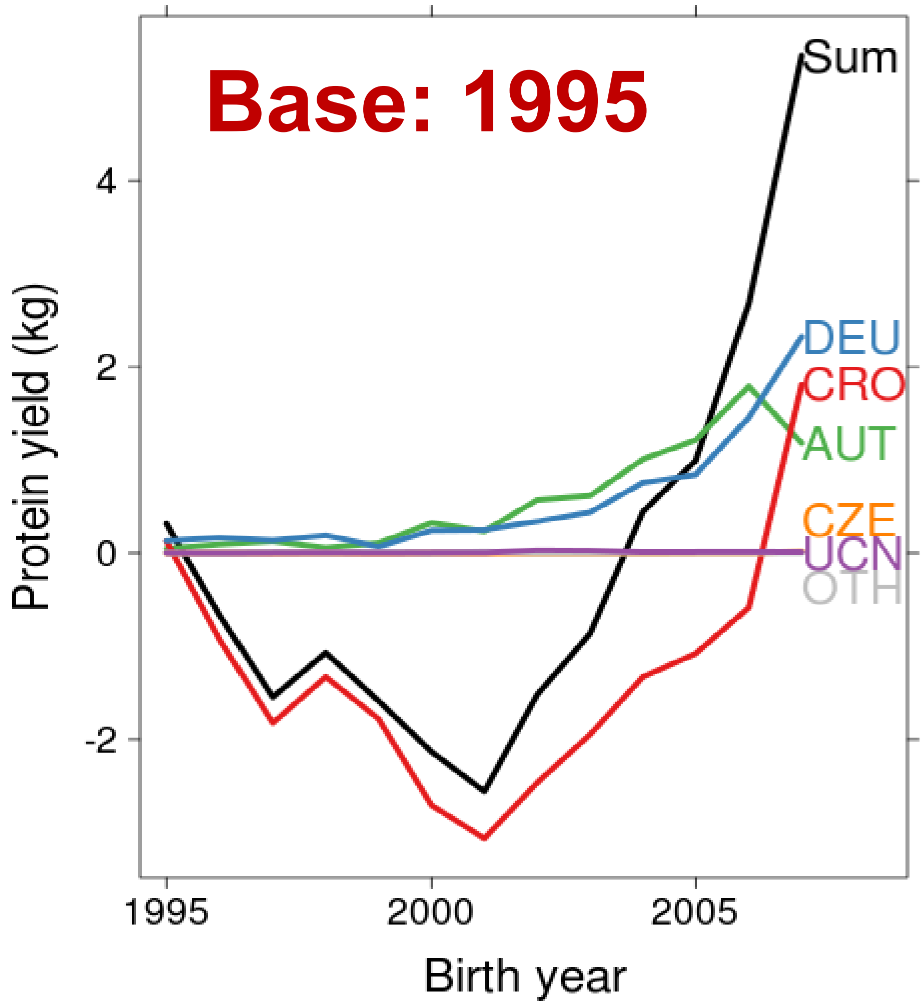
Example (2)

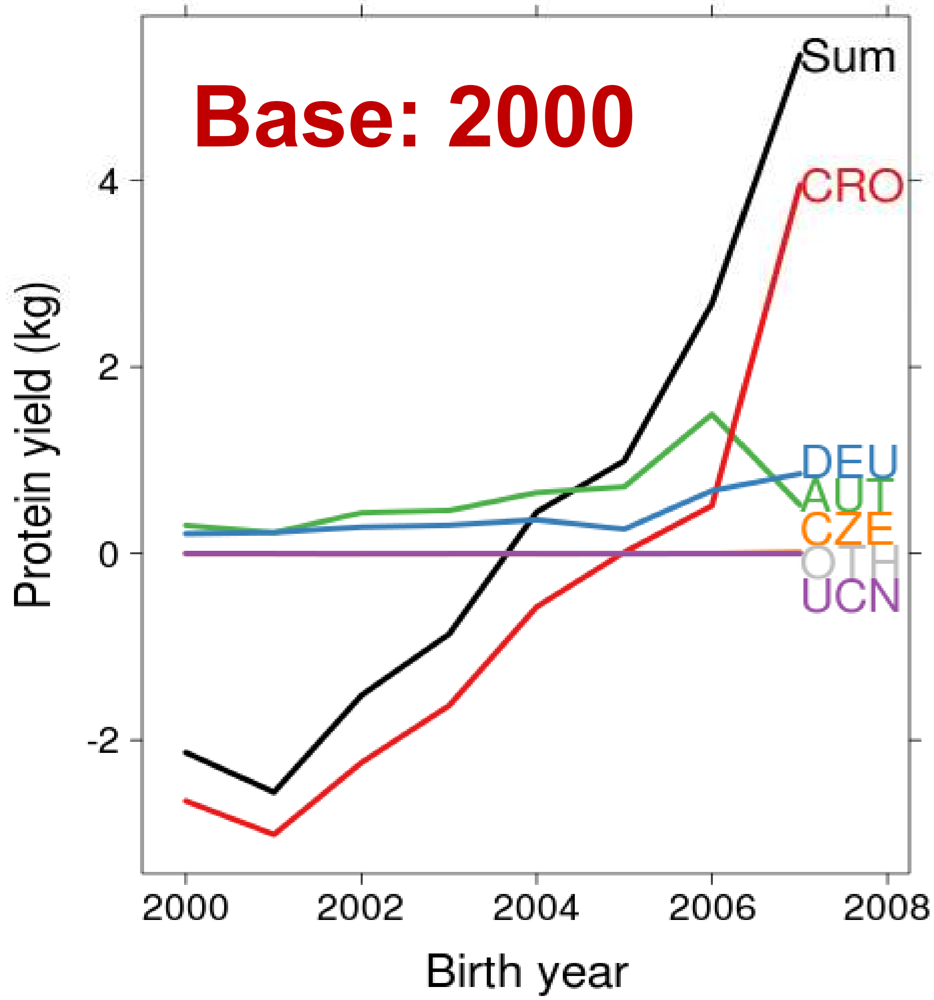

EBV_{dam} = 90
EBV_{sire} = 110
EBV_{sire} = 120
Foreign
Parent average = 100
Domestic
$EBV_{progeny}$ = 110
Mendelian sampling = 10
Parent average = 115
$EBV_{progeny}$ = 120
Mendelian sampling = 5
$EBV_{progeny}$ = 120
= 110 + 5 + 5
= 110 + 10

Results

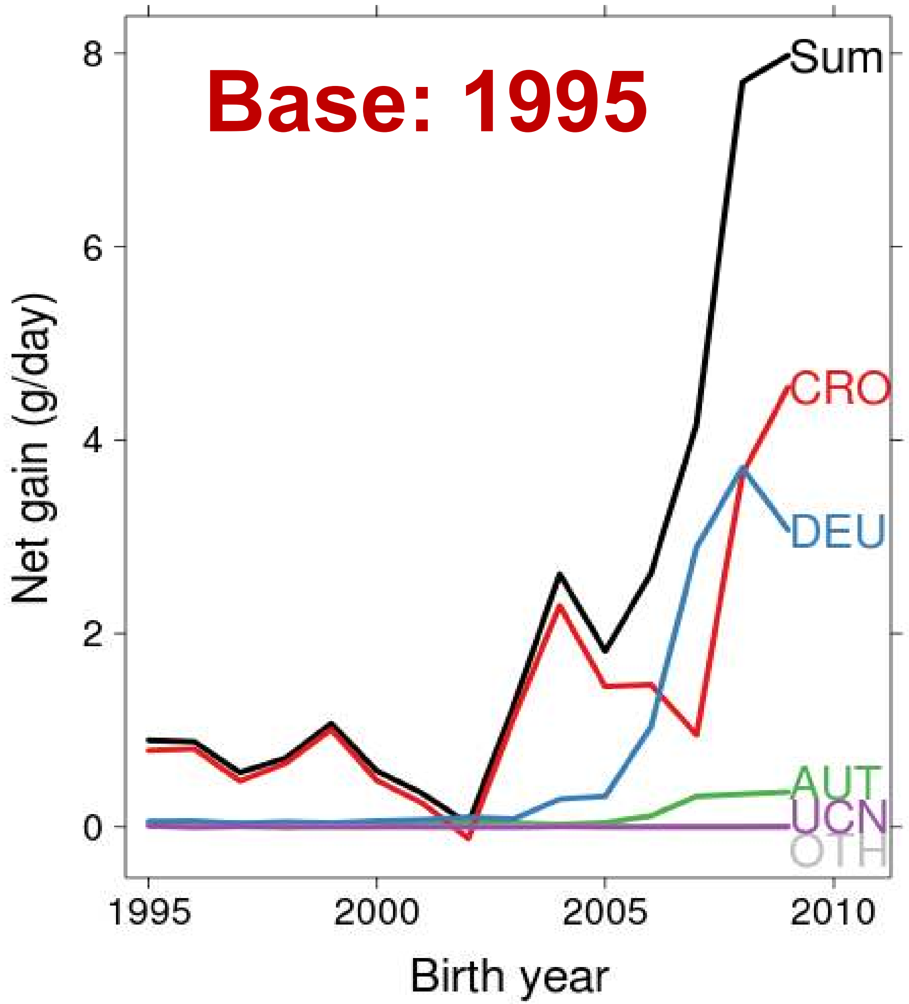


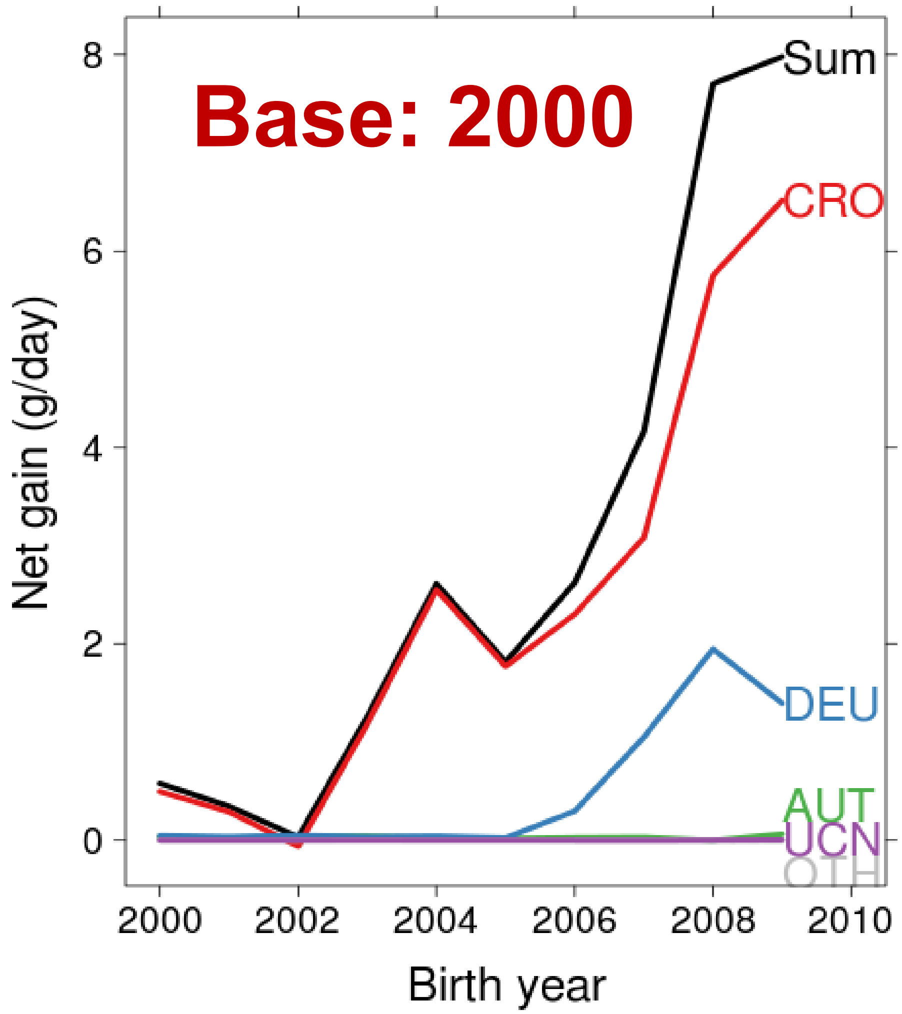
Protein yield - base population effect





Net gain – base population effect





Conclusions

- Positive genetic trend
- Large influence of DEU and AUT origin
- National work → 34% for protein yield and 57% for net daily gain
- Countries can achieve some additional genetic progress even when there is an abundant import of live animals and semen