Genetic variability indicators on the Web

Providing tools to preserve genetic diversity in pig breeding programmes

Canadian Centre for Swine Improvement Inc

Background

✓ Why do we care about genetic variability ?

- Avoid increase in inbreeding
    - Inbreeding depression
    - Recessive abnormalities
- Preserve diversity and flexibility
- Preserve long-term progress

✓ Intense, short-term selection very efficient
✓ But risk of bottlenecks
✓ Selecton of related animals facilitated with BLUP

Context

✓ Breeders on the Canadian Swine Improvement Program have access to basic tools on CCSI website

- inbreeding coefficients
- family trees
- mating plans

✓ Need for more tools to optimise selection strategies while managing genetic variability

✓ Specific emphasis on the impact of the extensive use of some boars in selection

Cletus icon in PigsOnTheWeb

EBVs For SOGM 8501R (YO)

Tattoo: SOGM 8501R
CLRC Registration: 1605165
Name: SOGEPORC M 8501R

Sex: F
Breed: YOYOYOYO (R)
Birth: Oct-20-2005
IC: 0.153

Sire: SOGE 5591P (YO)
Dam: SOGM 8228P (YO)
Herd: SogeporcMarees (PQ 304)

Boar B (Duroc)

Boar B
Duroc

162
purebred litters

34
herds

128
daughters in selection herds

48
sons in AI studs

1047
total progeny

Boar B (Duroc)

Sireline	EBV	
Age to 100 kg (mm)	-5.6	☺ ☺ ☺
Backfat at 100 kg (mm)	-0.77	☺
Loin depth (mm)	+4.97	☺ ☺ ☺
Loin eye area (cm^2)	+4.73	☺ ☺ ☺
Feed conv. ratio (kg/kg)	-0.096	☺ ☺ ☺
Lean Yield (%)	+1.01	☺ ☺
Total born (piglets/litter)	-0.47	☹
Sire line Index (pts)	152	☺ ☺ ☺ ☺
Dam Line Index (pts)	120	☺

Extensive use of some boars : what is the problem ?

✓ Bottlenecks in pedigrees

✓ Reduced choices in mating plans at the next generation

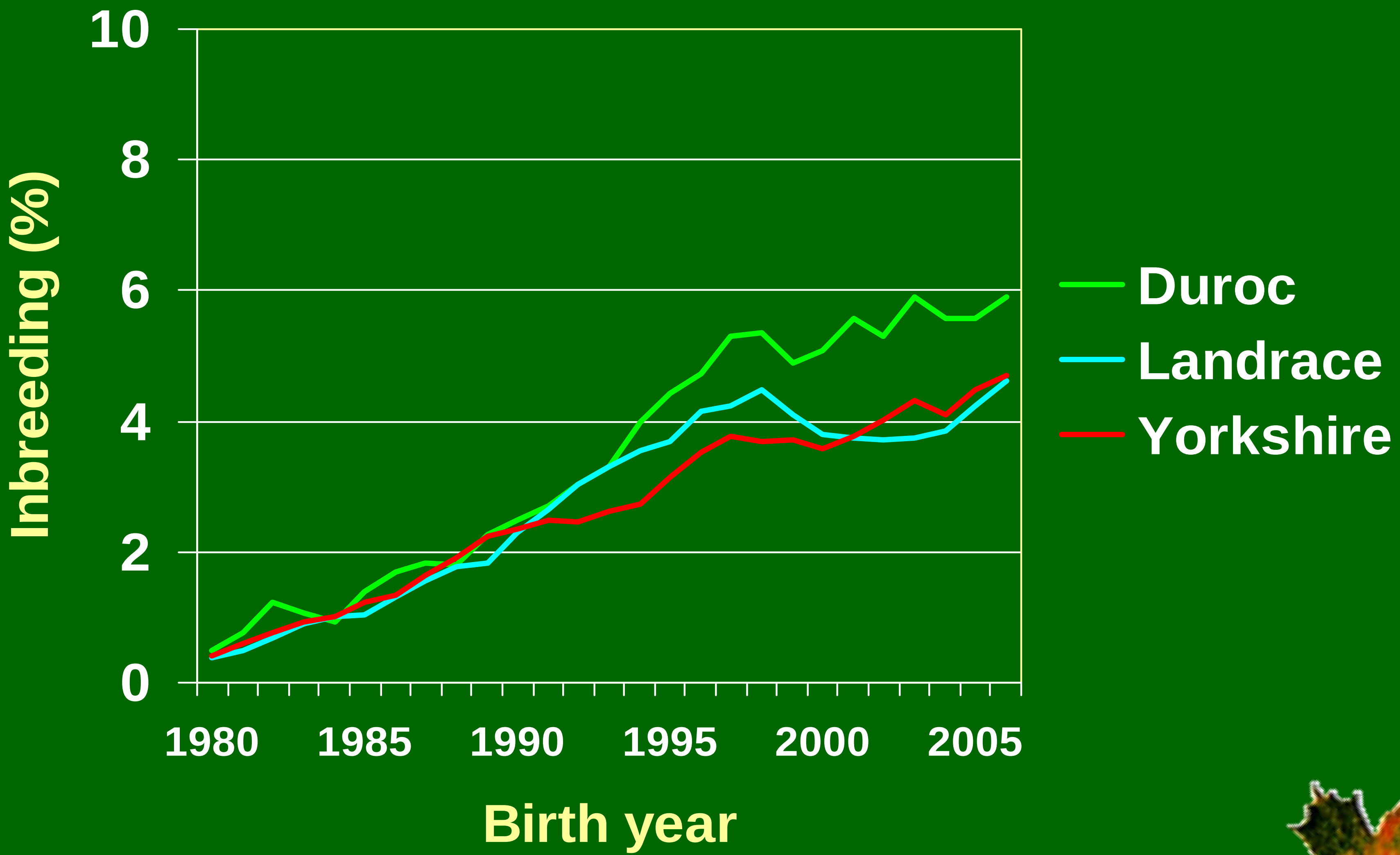
✓ Long-term reduction of genetic variability

✓ Increased inbreeding

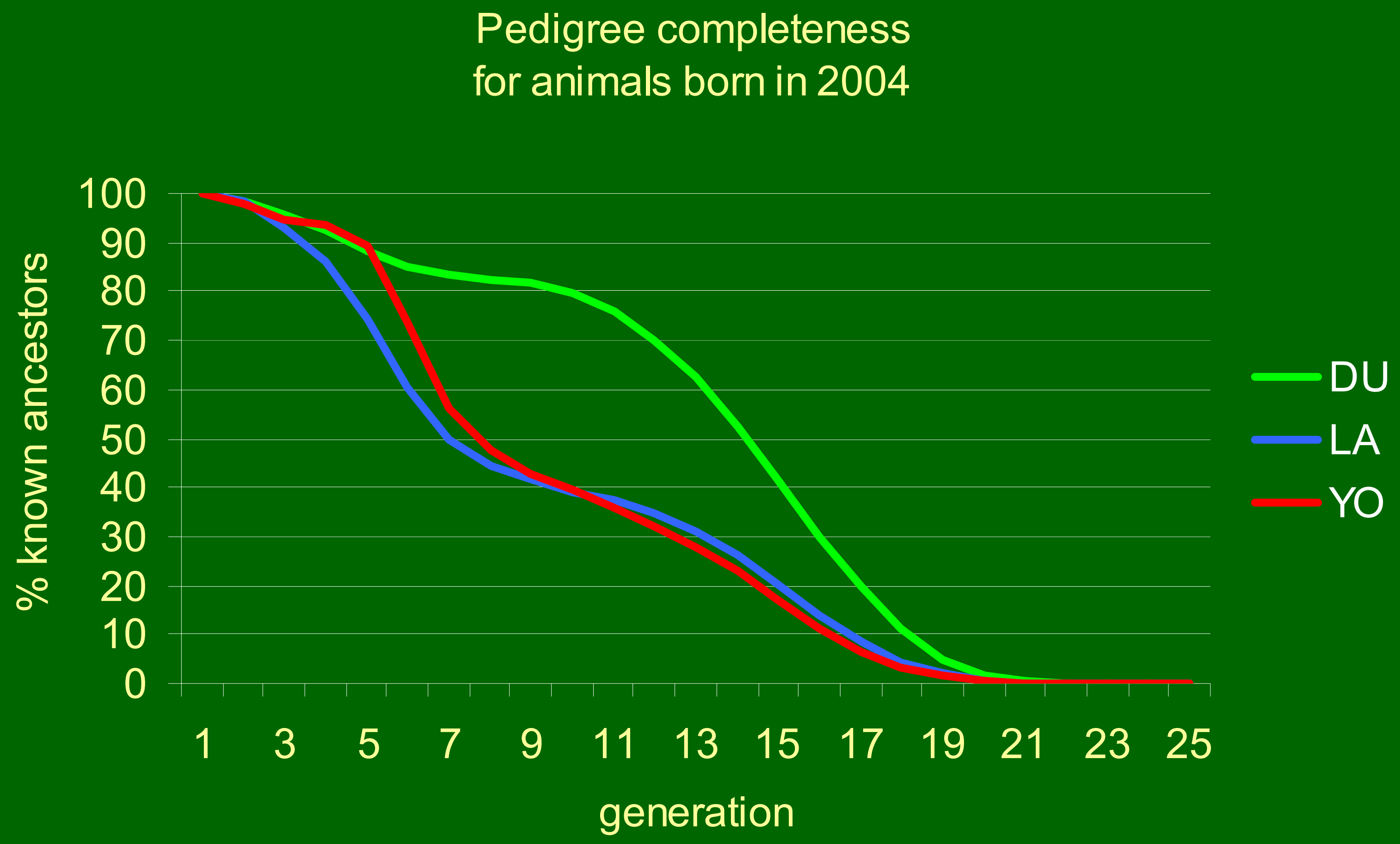
✓ Risk of transmission of undesirable genes

« Short-term gain = Long-term pain »

Inbreeding trends in Canadian swine populations



Available pedigree information



Probablilities of gene origin : definitions

F

Number of founders

=

Number of ancestors with unknown parents

(usually ‘informatic’ founders)

Probablilities of gene origin : definitions

Fe

Effective number of founders

=

number of equally contributing founders that would be expected to produce the same variability as in the population under study

Computed using contributions of each founder to a reference population : $Fe = 1/\Sigma q_k^2$

$$Fe \leq F$$

Probablilities of gene origin : definitions

Fa

Effective number of ancestors

=

Minimum number of ancestors (founders or not) necessary to explain the complete genetic diversity of the population under study

Computed using the marginal contribution of each ancestor

$$Fa \leq Fe \leq F$$

Probablilities of gene origin : definitions

Ng

Effectve number of remaining founder genomes

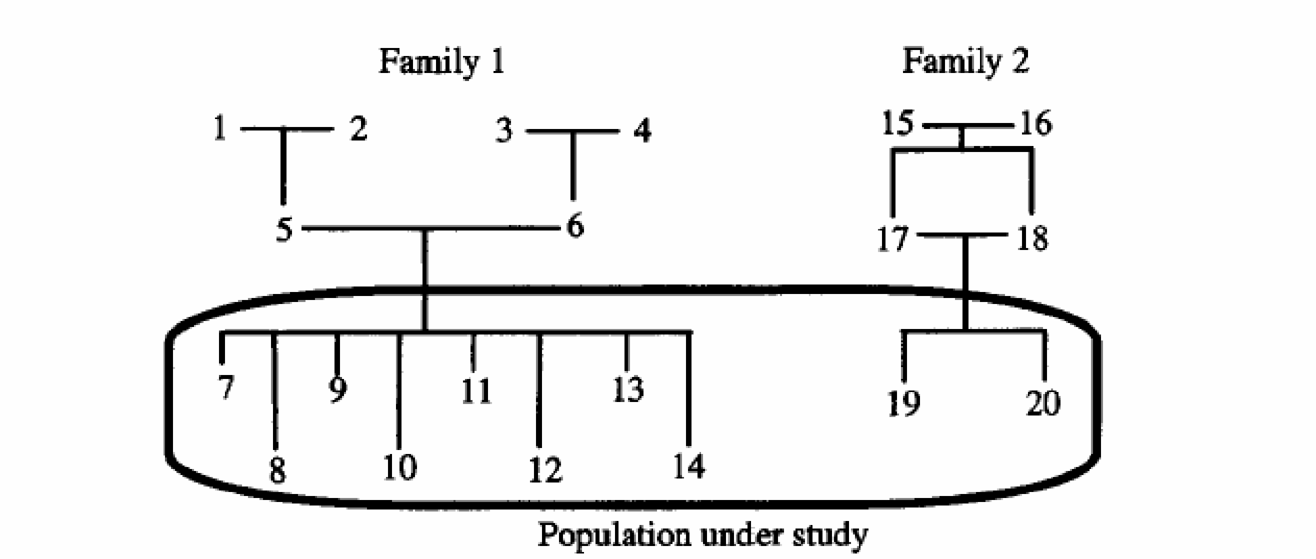
=

based on the probability that a given gene present in the founders (‘founder gene’) is still present in the population under study

Computed by simulation of allele transmission through the real pedigree, using Monte Carlo simulation (>=500 replications)

$$Ng \leq Fa \leq Fe \leq F$$

Example



Population	F	F_e	F_a	N_g
Total	6	5.6	2.9	2.5
Family 1	4	4	2	1.8
Family 2	2	2	2	1.1

Why several criteria ?

What's taken into account :

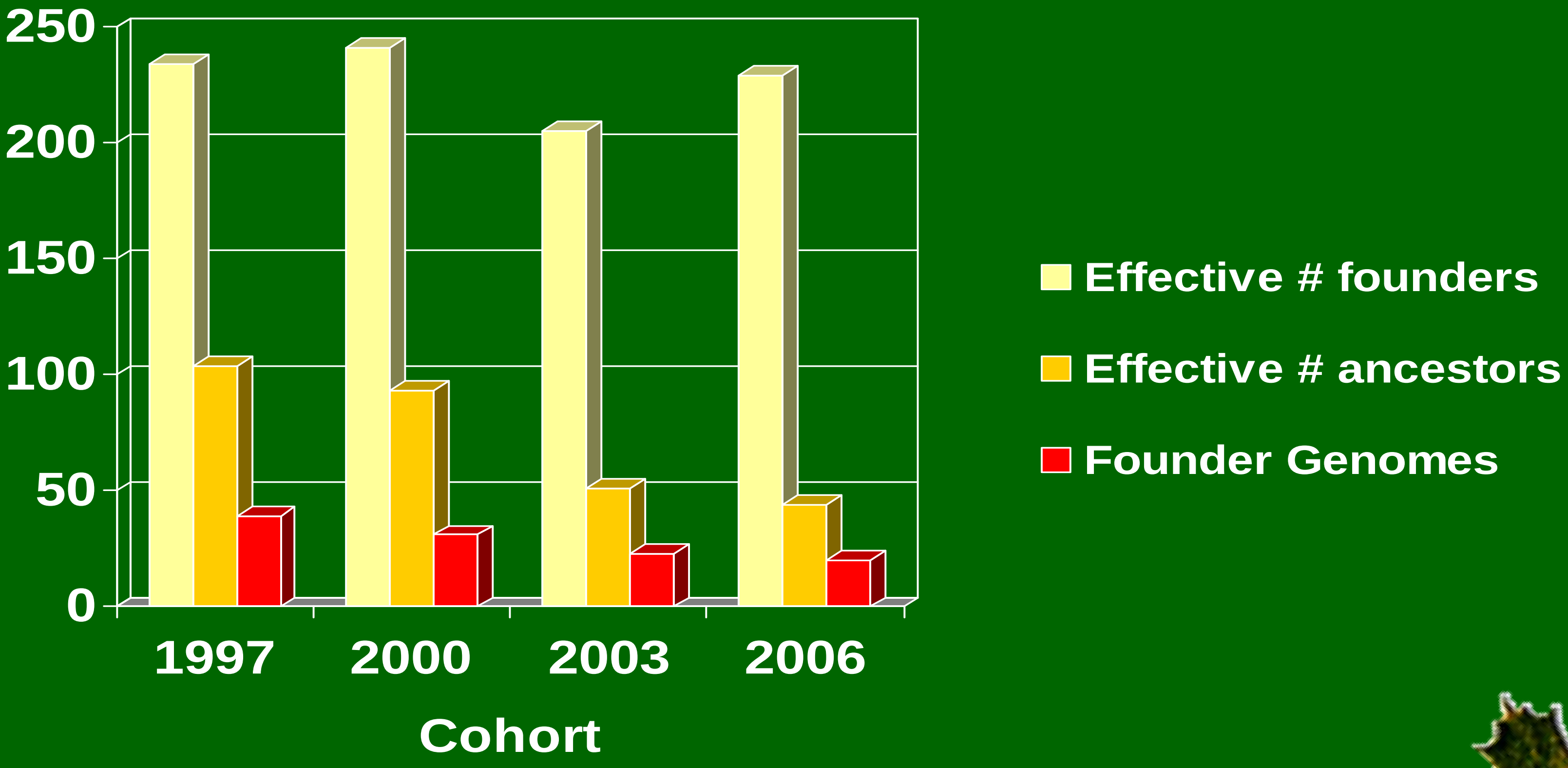
- ✓*Fe* : contributions of founders
- ✓*Fa* : contributions of founders + bottlenecks
- ✓*Ng* : contributions of founders + bottlenecks + genetic drift

$$Ng \leq Fa \leq Fe \leq F$$

What’s the situation in Canadian swine populations ?

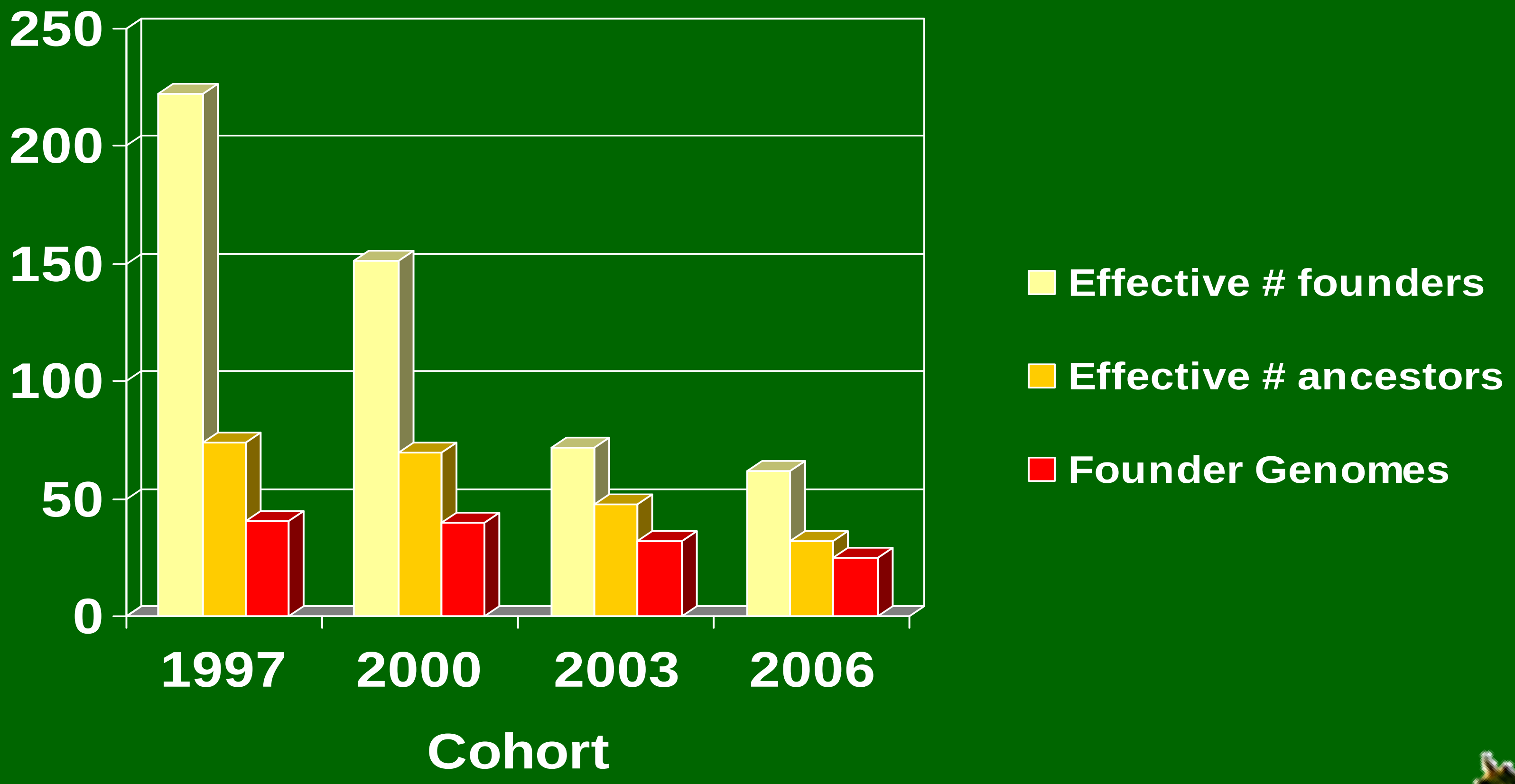
Duroc breed

~ 21,000 pigs born/year



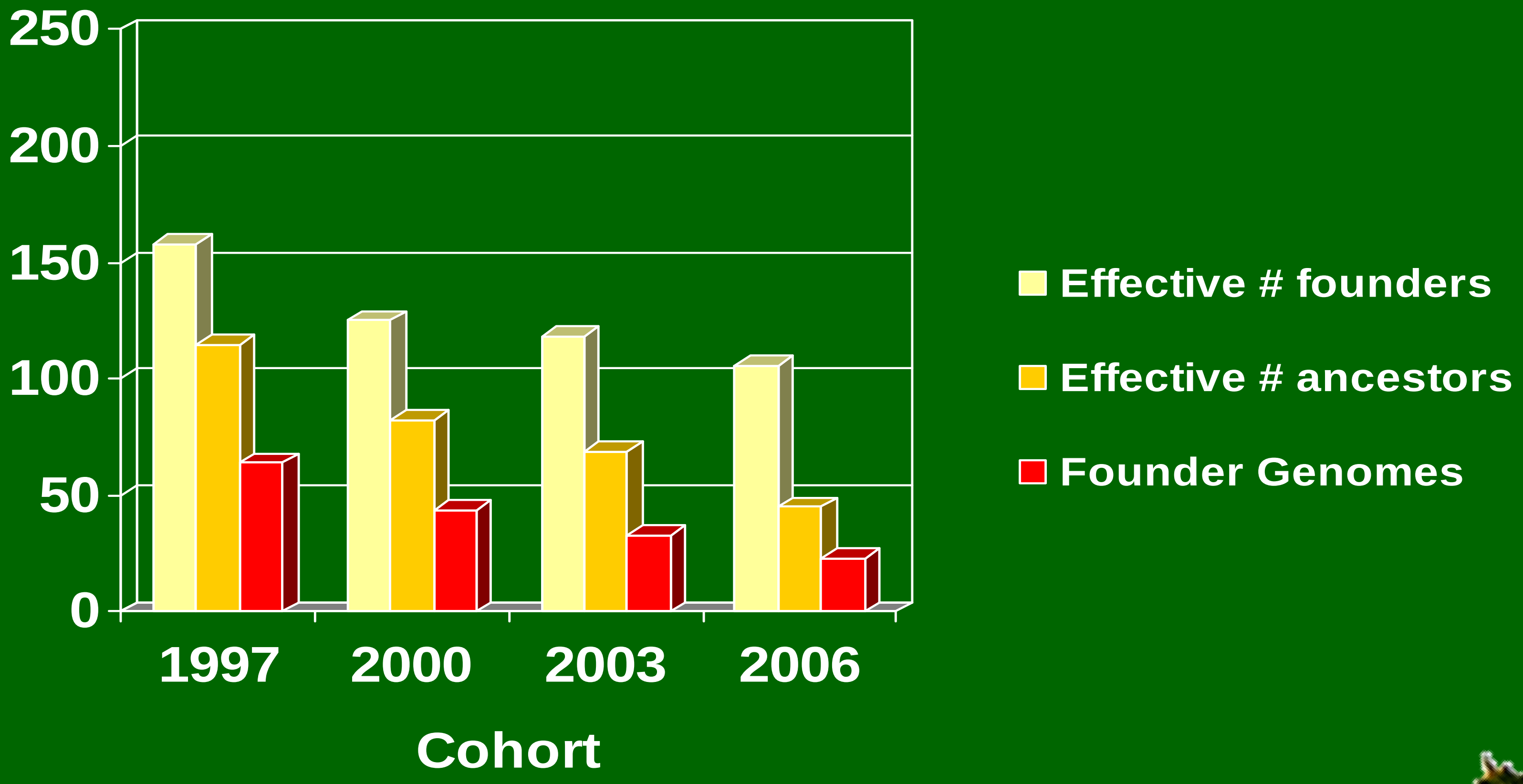
Landrace breed

~ 35,000 pigs born/year



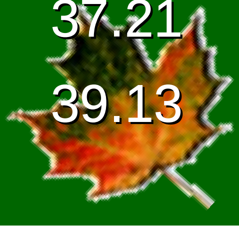
Yorkshire breed

~ 53,000 pigs born/year

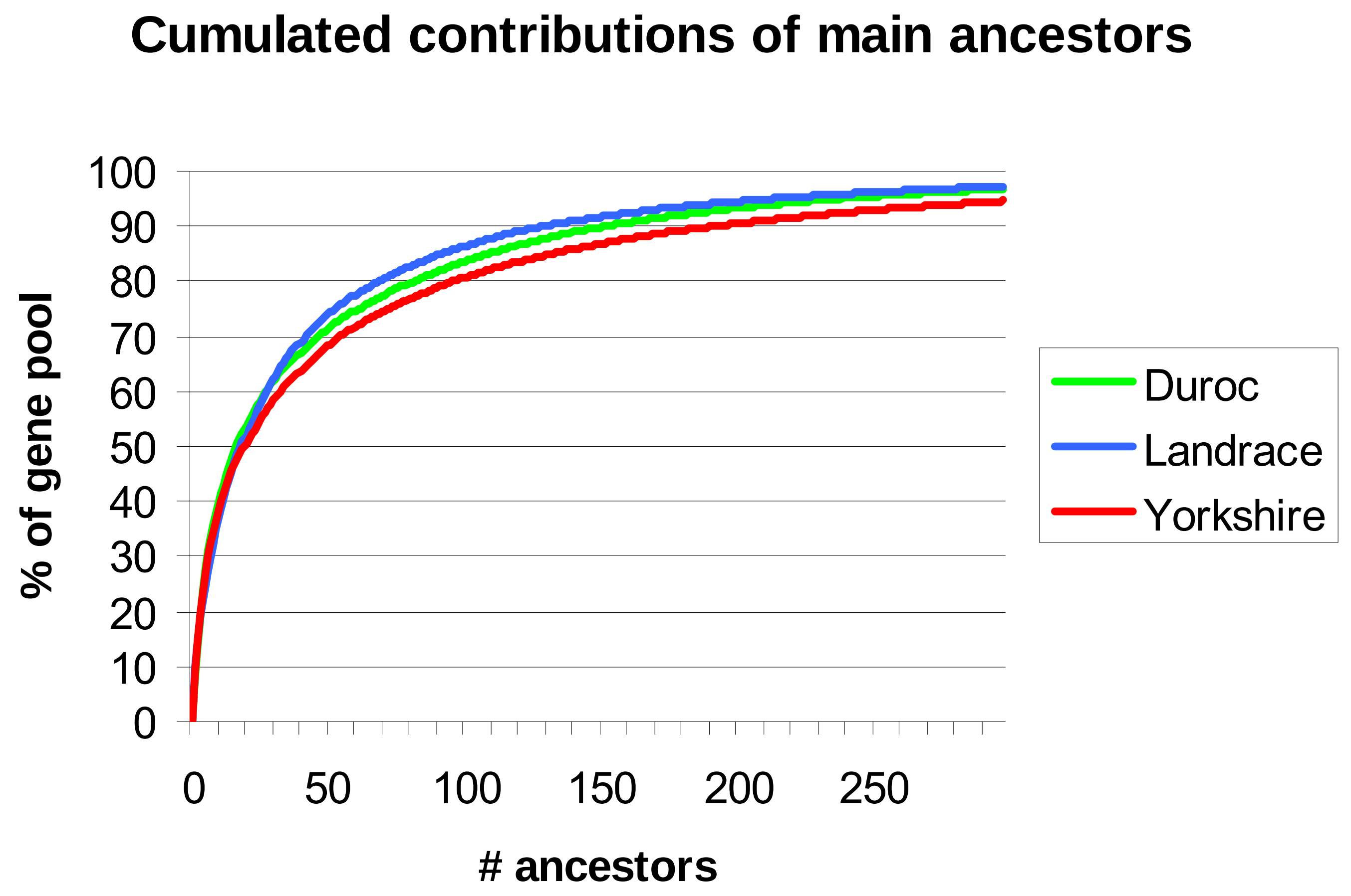


Most influential ancestors to gene pool - Duroc 2004-2006

	Tattoo	sex	Birth year	#direct Progeny	Marginal contribution	Cumulated contribution
1	DLDA53H	M	1998	398	5.82	5.82
2	USA86H	M	1998	958	5.43	11.26
3	MALU1297G	M	1997	945	5.25	16.50
4	USA321M	M	2002	1431	5.23	21.73
5	ASGE812E	M	1995	1001	5.07	26.80
6	DLDA93L	M	2001	1083	3.15	29.96
7	SOGE2348F	M	1996	250	2.85	32.81
8	JML131Y	M	1989	327	2.48	35.29
9	LEF785C	M	1993	348	1.92	37.21
10	ASZG1194E	M	1995	415	1.92	39.13



Most influential ancestors to gene pool



Summary

- ✓ Inbreeding trends not very accurate due to pedigree incompleteness
- ✓ Inbreeding usually well controlled with accurate mating plan tools
- ✓ Effective numbers of ancestors (F_a) and number of remaining founder genomes (N_g) more meaningful

Implications

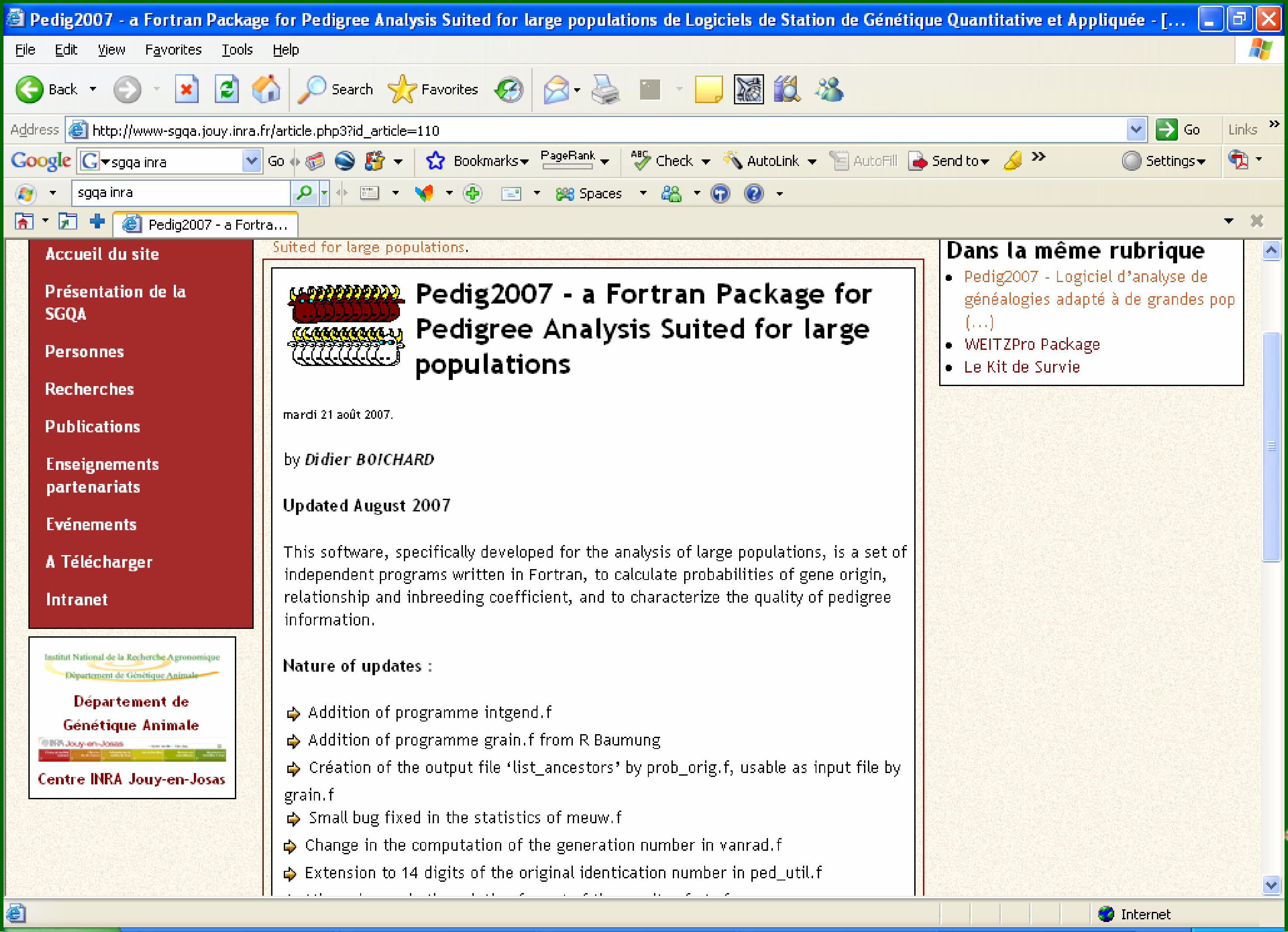
✓ These criteria are retrospective, but useful to make breeders aware of the situation

✓ In spite of imports, there is evidence of a loss of genetic variability in all breeds

✓ This is a consequence of bottlenecks in pedigrees (widely used boars, Hal eradication programs, etc) but also of BLUP-based selection which facilitates the selection of related candidates.

Programs for pedigree analysis available at

http://www-sgqa.jouy.inra.fr/



Suited for large populations.

- Accueil du site
- Présentation de la SGQA
- Personnes
- Recherches
- Publications
- Enseignements partenariats
- Evénements
- A Télécharger
- Intranet

Institut National de la Recherche Agronomique
Département de Génétique Animale
Département de Génétique Animale
INRA Jouy-en-Josas
Centre INRA Jouy-en-Josas

Pedig2007 - a Fortran Package for Pedigree Analysis Suited for large populations

mardi 21 août 2007.

by *Didier BOICHARD*

Updated August 2007

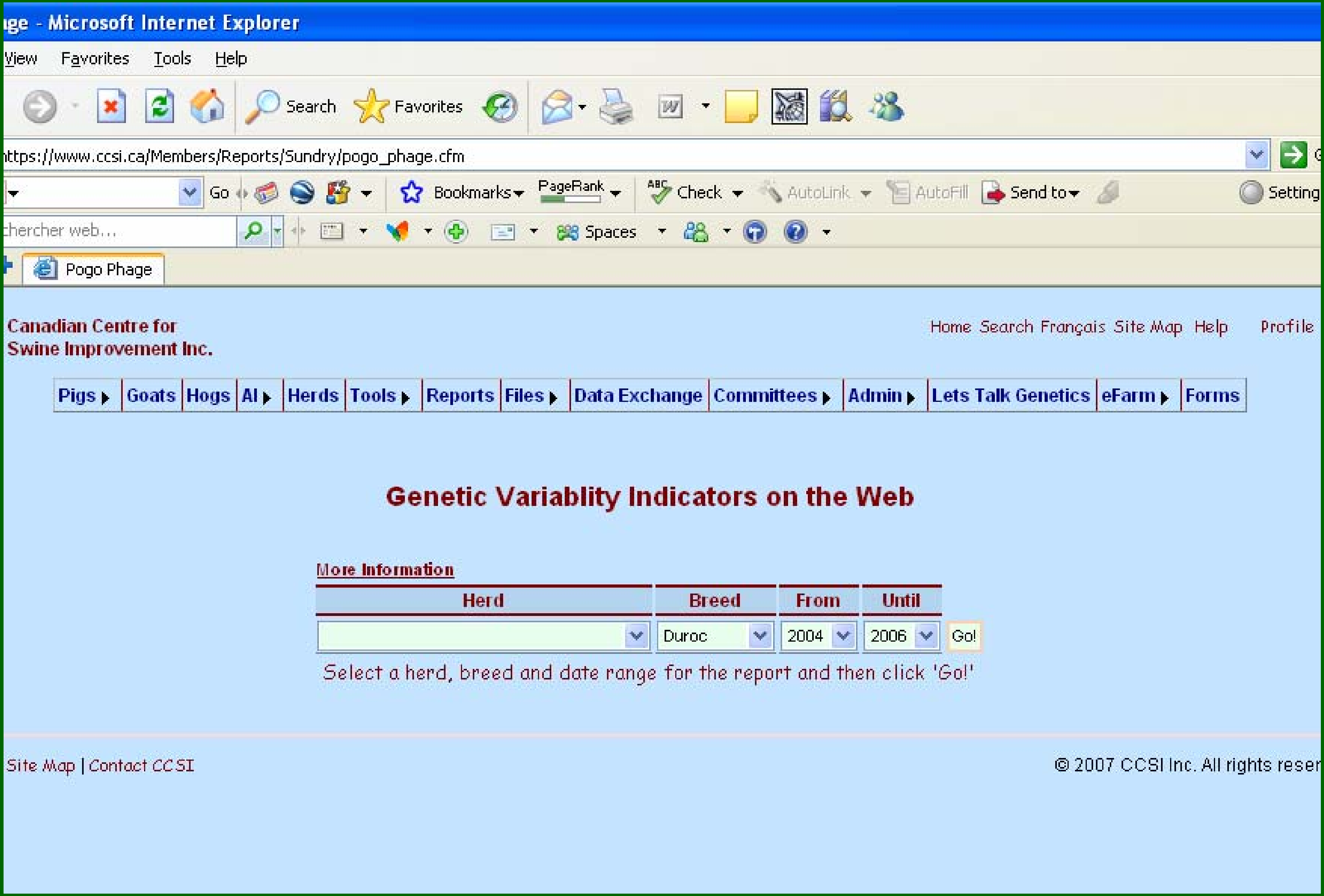
This software, specifically developed for the analysis of large populations, is a set of independent programs written in Fortran, to calculate probabilities of gene origin, relationship and inbreeding coefficient, and to characterize the quality of pedigree information.

Nature of updates :

- Addition of programme intgend.f
- Addition of programme grain.f from R Baumung
- Création of the output file 'list_ancestors' by prob_orig.f, usable as input file by grain.f
- Small bug fixed in the statistics of meuw.f
- Change in the computation of the generation number in vanrad.f
- Extension to 14 digits of the original identication number in ped_util.f

Dans la même rubrique

- Pedig2007 - Logiciel d'analyse de généalogies adapté à de grandes pop (...)
- WEITZPro Package
- Le Kit de Survie



Canadian Centre for
Swine Improvement Inc.

Genetic Variablity Indicators on the Web

More Information

Herd	Breed	From	Until
	Duroc	2004	2006

Select a herd, breed and date range for the report and then click 'Go!'

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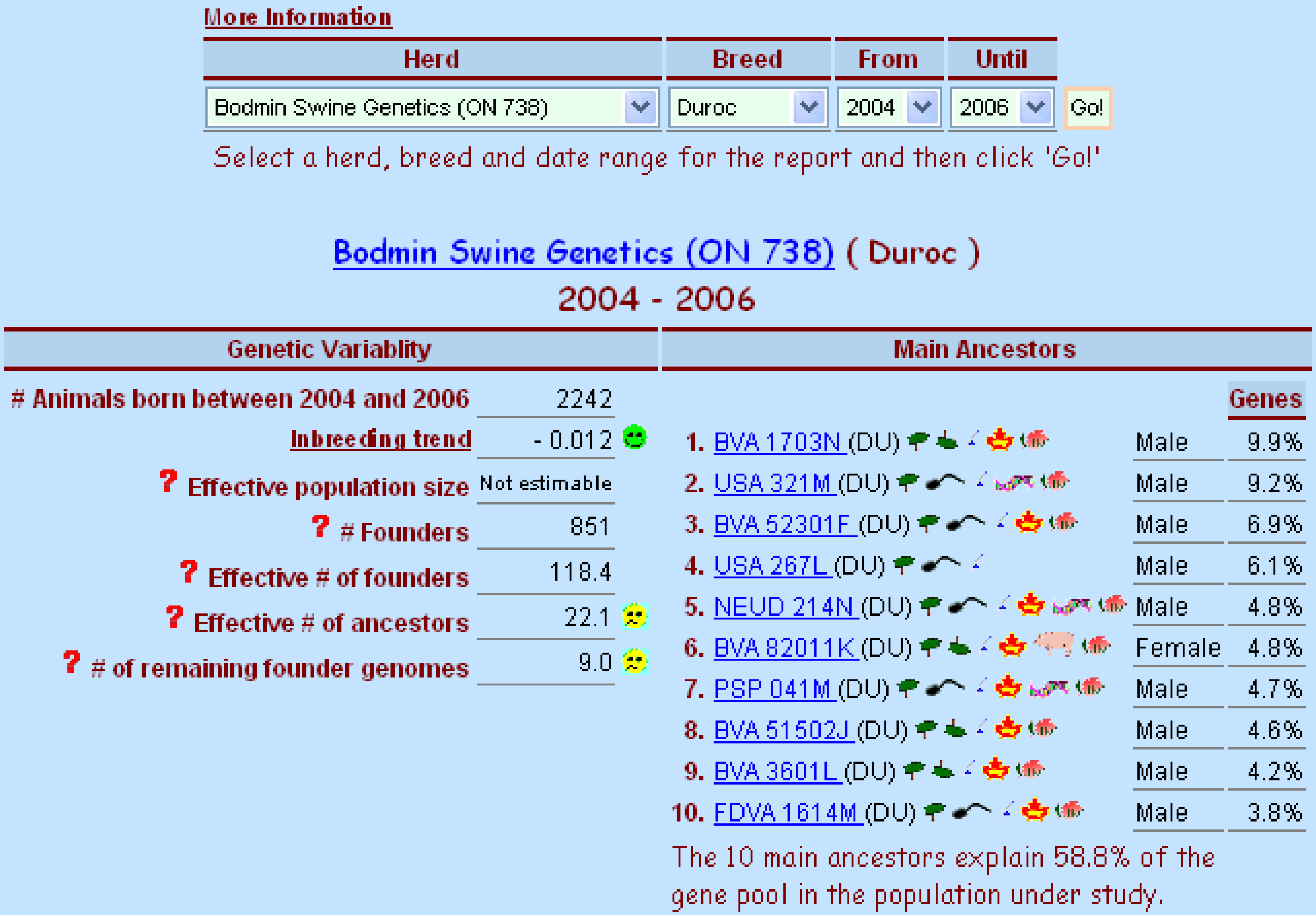


More Information

Herd	Breed	From	Until	
Bodmin Swine Genetics (ON 738)	Duroc	2004	2006	Go!

Select a herd, breed and date range for the report and then click 'Go!'

Bodmin Swine Genetics (ON 738) (Duroc)

2004 - 2006

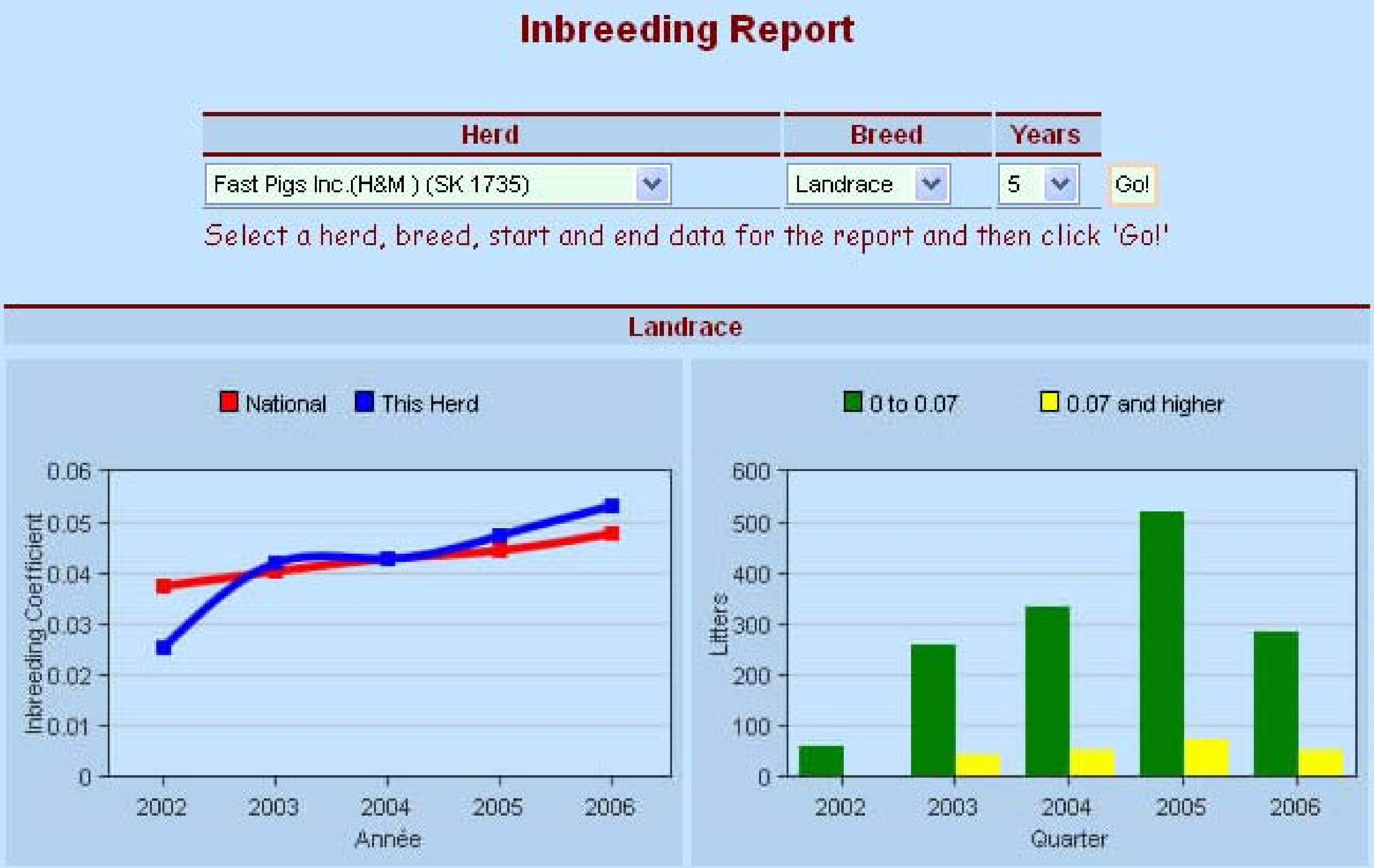
Genetic Variablity

# Animals born between 2004 and 2006	2242
Inbreeding trend	- 0.012 ☺
? Effective population size	Not estimable
? # Founders	851
? Effective # of founders	118.4
? Effective # of ancestors	22.1 ☹
? # of remaining founder genomes	9.0 ☹

Main Ancestors

			Genes
1.	BVA 1703N (DU)	Male	9.9%
2.	USA 321M (DU)	Male	9.2%
3.	BVA 52301F (DU)	Male	6.9%
4.	USA 267L (DU)	Male	6.1%
5.	NEUD 214N (DU)	Male	4.8%
6.	BVA 82011K (DU)	Female	4.8%
7.	PSP 041M (DU)	Male	4.7%
8.	BVA 51502J (DU)	Male	4.6%
9.	BVA 3601L (DU)	Male	4.2%
10.	FDVA 1614M (DU)	Male	3.8%

The 10 main ancestors explain 58.8% of the gene pool in the population under study.



Inbreeding Report

Herd	Breed	Years	
Fast Pigs Inc.(H&M) (SK 1735)	Landrace	5	Go!

Select a herd, breed, start and end data for the report and then click 'Go!'

Landrace

Work in progress (1)

- More monitoring → warnings
- Provide more indicators
  - Coancestry index for each pig (NIG)
  - Inclusion in selection indices ?
- Use of molecular information to approach and manage 'real' genetic variability (CAGR – Centre for Animal Genetic ressources in Saskatoon)

Work in progress (2)

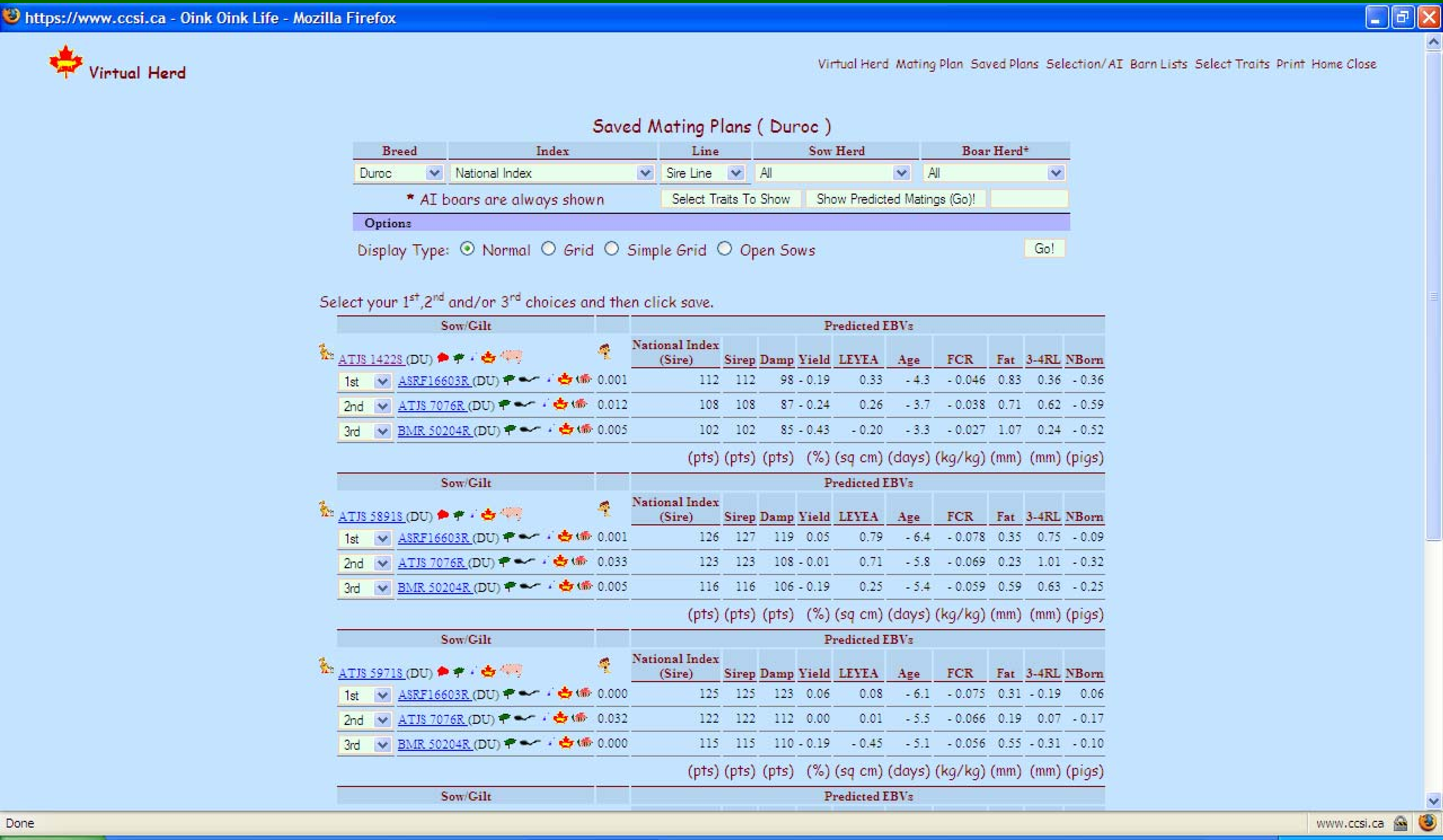
- ✓ So far we have looked at genetic improvement and genetic diversity separately → need for optimizing genetic progress and genetic diversity jointly

- ✓ Optimize steps in the breeding scheme which have a major impact on genetic variablity:
  - Mating plans
  - Selection of replacements

- ✓ Need for on-line tools, working within herds, alliances, overall

- ✓ Central database very useful in this context, but need for very up to date information (culling, service, new candidates, etc)

Suggested matings



Saved Mating Plans (Duroc)

Breed	Index	Line	Sow Herd	Boar Herd*
Duroc	National Index	Sire Line	All	All

* AI boars are always shown

Options

Display Type: ● Normal ○ Grid ○ Simple Grid ○ Open Sows

Select your 1st,2nd and/or 3rd choices and then click save.

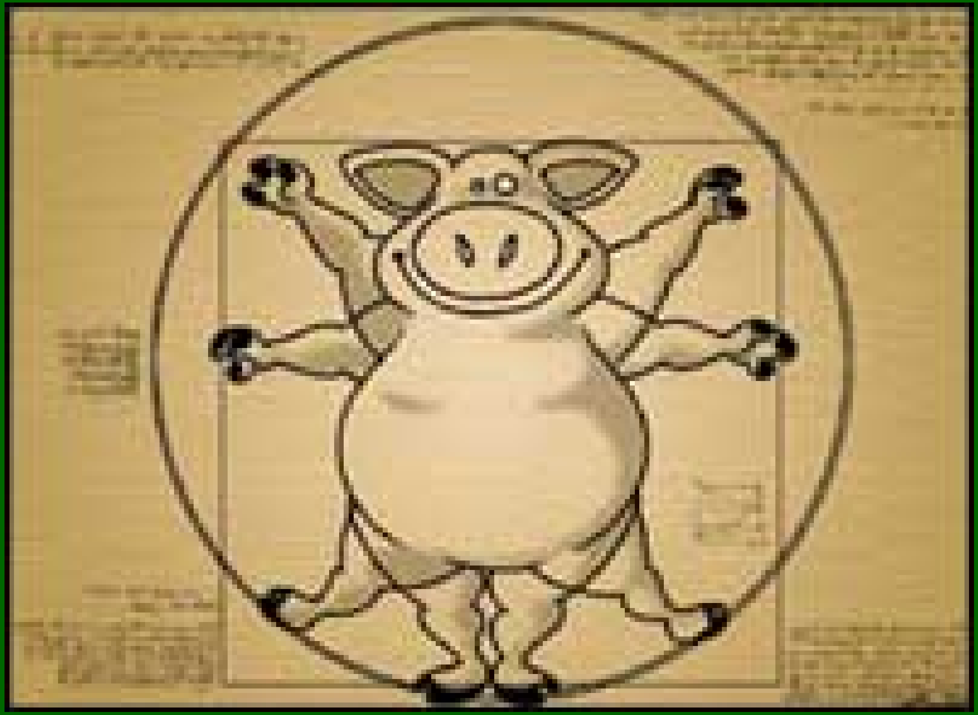
Sow/Gilt			Predicted EBVs									
	ATJS 14228 (DU)		National Index (Sire)	Sirep	Damp	Yield	LEYEA	Age	FCR	Fat	3-4RL	NBorn
1st	ASRF16603R (DU)	0.001	112	112	98	- 0.19	0.33	- 4.3	- 0.046	0.83	0.36	- 0.36
2nd	ATJS 7076R (DU)	0.012	108	108	87	- 0.24	0.26	- 3.7	- 0.038	0.71	0.62	- 0.59
3rd	BMR 50204R (DU)	0.005	102	102	85	- 0.43	- 0.20	- 3.3	- 0.027	1.07	0.24	- 0.52
			(pts)	(pts)	(pts)	(%)	(sq cm)	(days)	(kg/kg)	(mm)	(mm)	(pigs)

Sow/Gilt			Predicted EBVs									
	ATJS 58918 (DU)		National Index (Sire)	Sirep	Damp	Yield	LEYEA	Age	FCR	Fat	3-4RL	NBorn
1st	ASRF16603R (DU)	0.001	126	127	119	0.05	0.79	- 6.4	- 0.078	0.35	0.75	- 0.09
2nd	ATJS 7076R (DU)	0.033	123	123	108	- 0.01	0.71	- 5.8	- 0.069	0.23	1.01	- 0.32
3rd	BMR 50204R (DU)	0.005	116	116	106	- 0.19	0.25	- 5.4	- 0.059	0.59	0.63	- 0.25
			(pts)	(pts)	(pts)	(%)	(sq cm)	(days)	(kg/kg)	(mm)	(mm)	(pigs)

Sow/Gilt			Predicted EBVs									
	ATJS 59718 (DU)		National Index (Sire)	Sirep	Damp	Yield	LEYEA	Age	FCR	Fat	3-4RL	NBorn
1st	ASRF16603R (DU)	0.000	125	125	123	0.06	0.08	- 6.1	- 0.075	0.31	- 0.19	0.06
2nd	ATJS 7076R (DU)	0.032	122	122	112	0.00	0.01	- 5.5	- 0.066	0.19	0.07	- 0.17
3rd	BMR 50204R (DU)	0.000	115	115	110	- 0.19	- 0.45	- 5.1	- 0.056	0.55	- 0.31	- 0.10
			(pts)	(pts)	(pts)	(%)	(sq cm)	(days)	(kg/kg)	(mm)	(mm)	(pigs)

Sow/Gilt		Predicted EBVs

Thank you !



More information ?

www.ccsi.ca

laurence@ccsi.ca