



IRISH CATTLE BREEDING FEDERATION

ICBF Dairy Industry Meeting

20th January 2010.

Agenda.

- New CIS proofs – RE & DB.
- Genomics research & evaluations – DB & FK.
- New Calving proofs – FK.
- Routine evaluations & ICBF Active Bull List – AC.
- Future developments in GEN€ IRELAND – AC, N McH & S McP.
- AOB.

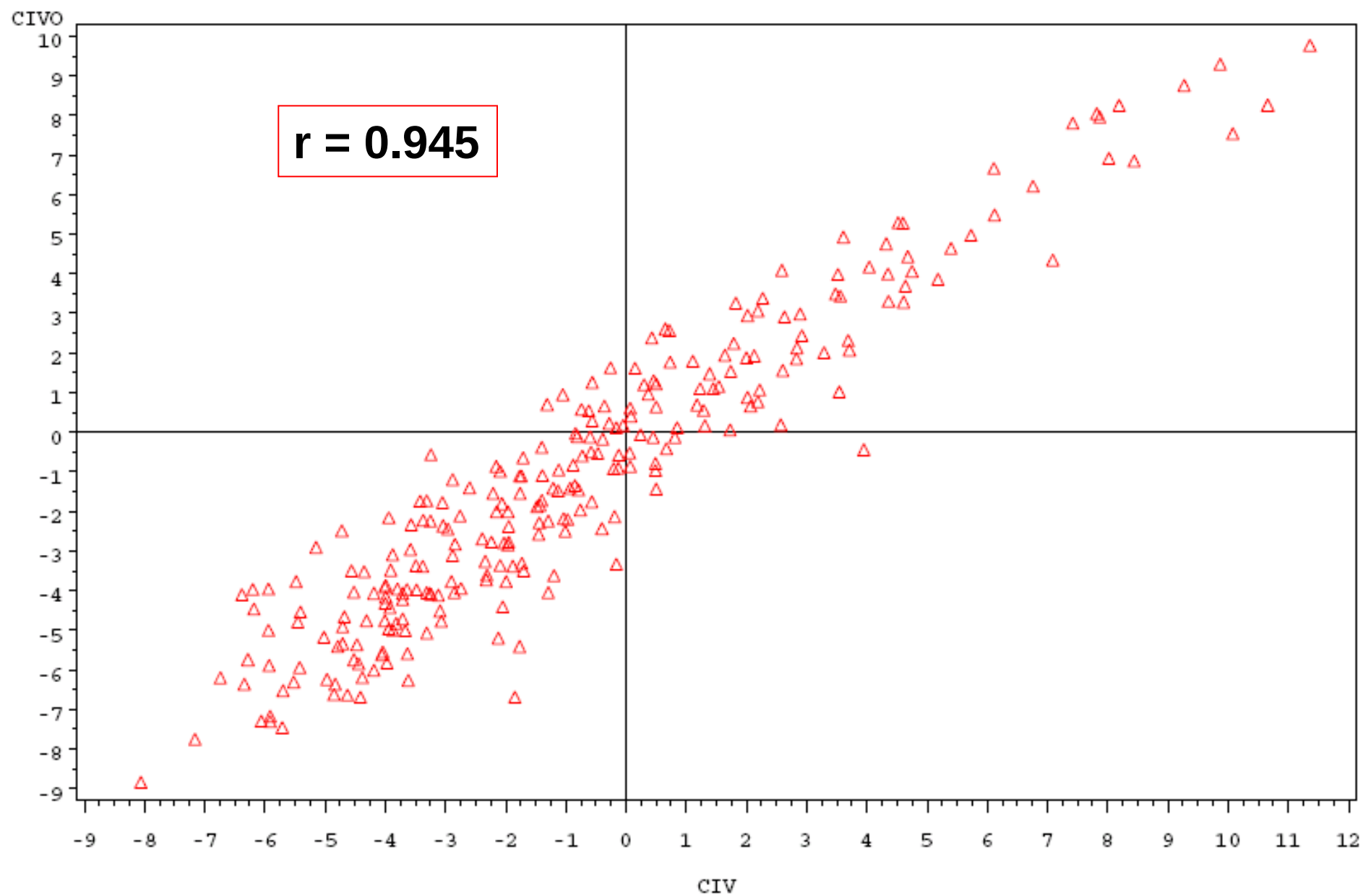
New fertility evaluation Update

- Extra traits: parity 4,5, CFS, NS
- New genetic parameters
- New software
- Increase CIS cut-off limit 600-800 day
- CMMS update July 09
- Cows with no milk recording 1 to 5

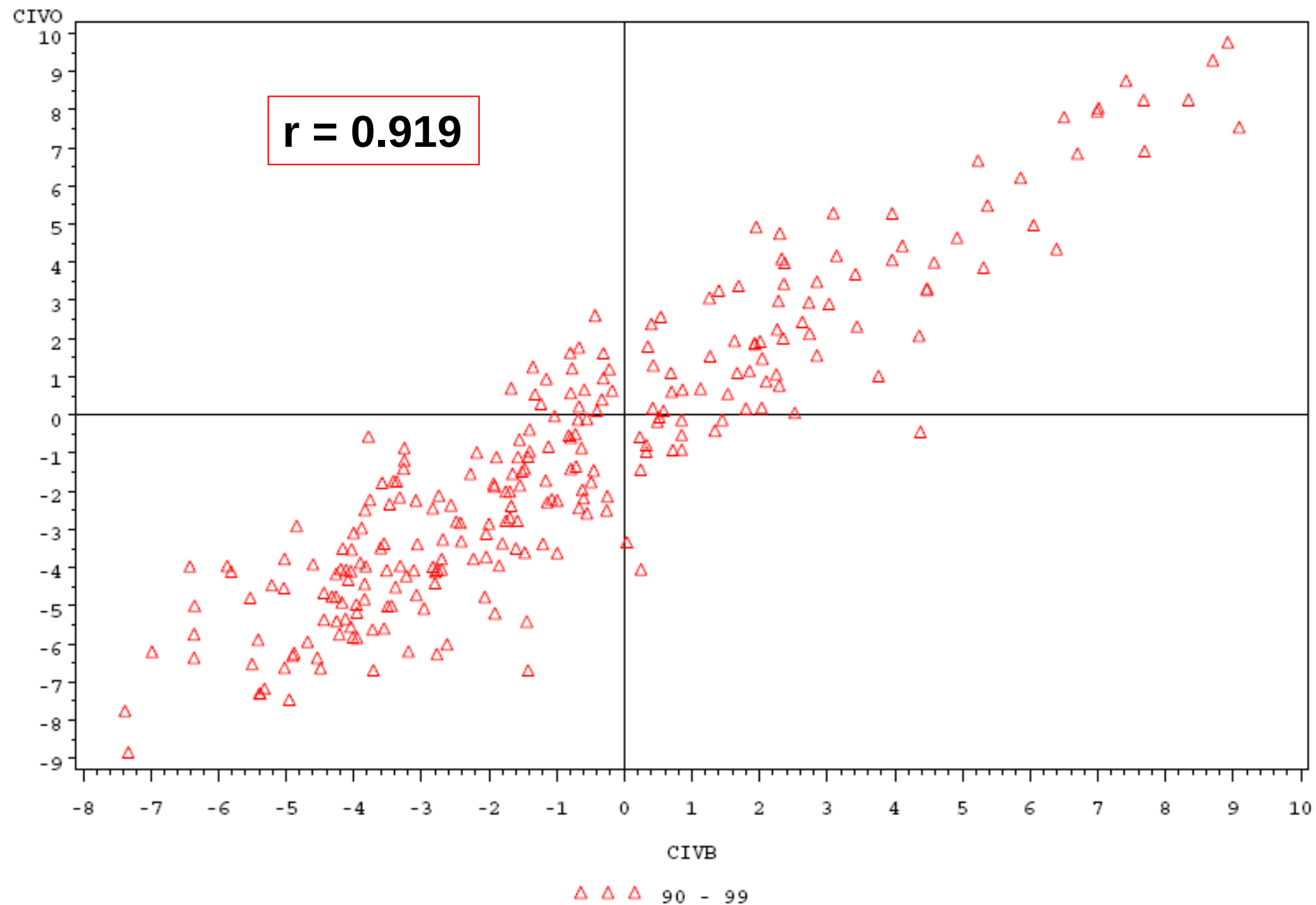
Test Runs.

- Detailed investigation of changes nearing completion
- 12 test runs carried out since last meeting
- Correlations have improved for both calving interval and survival
- Still too much re-ranking concerns to switch to new yet

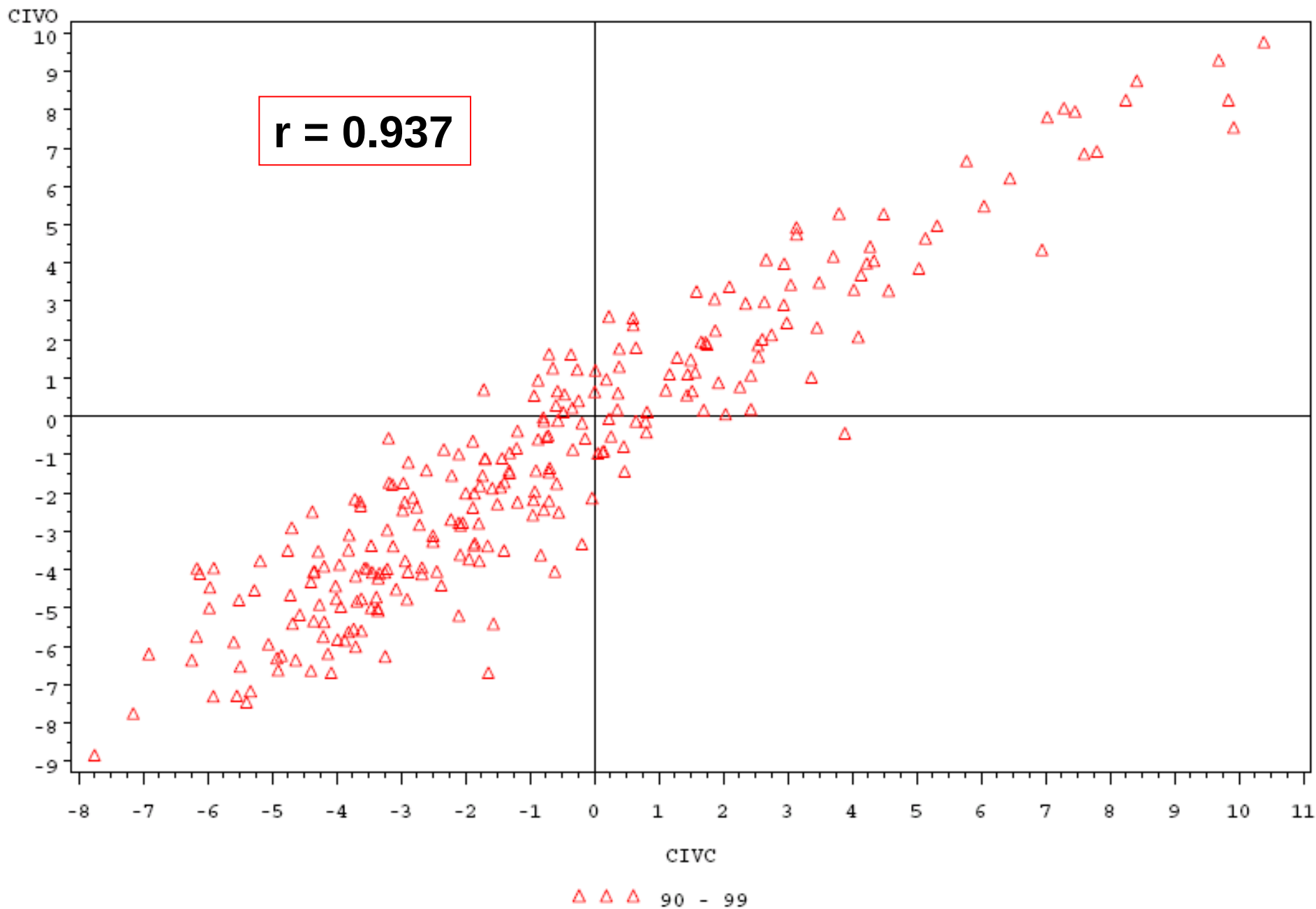
AI sires CIV combined old v new 1st 3 par



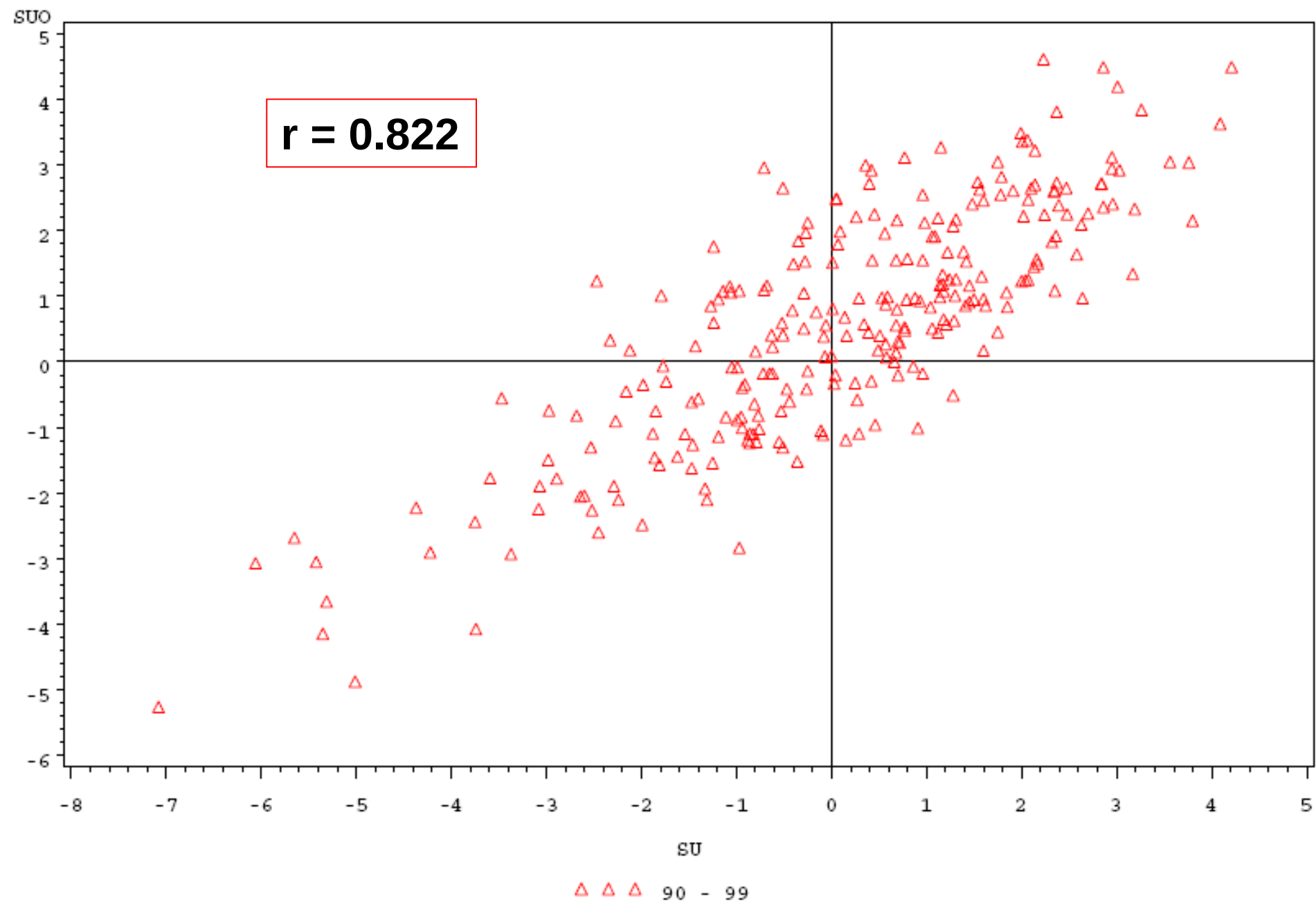
AI sires CIV combined old v new 1st 5 par



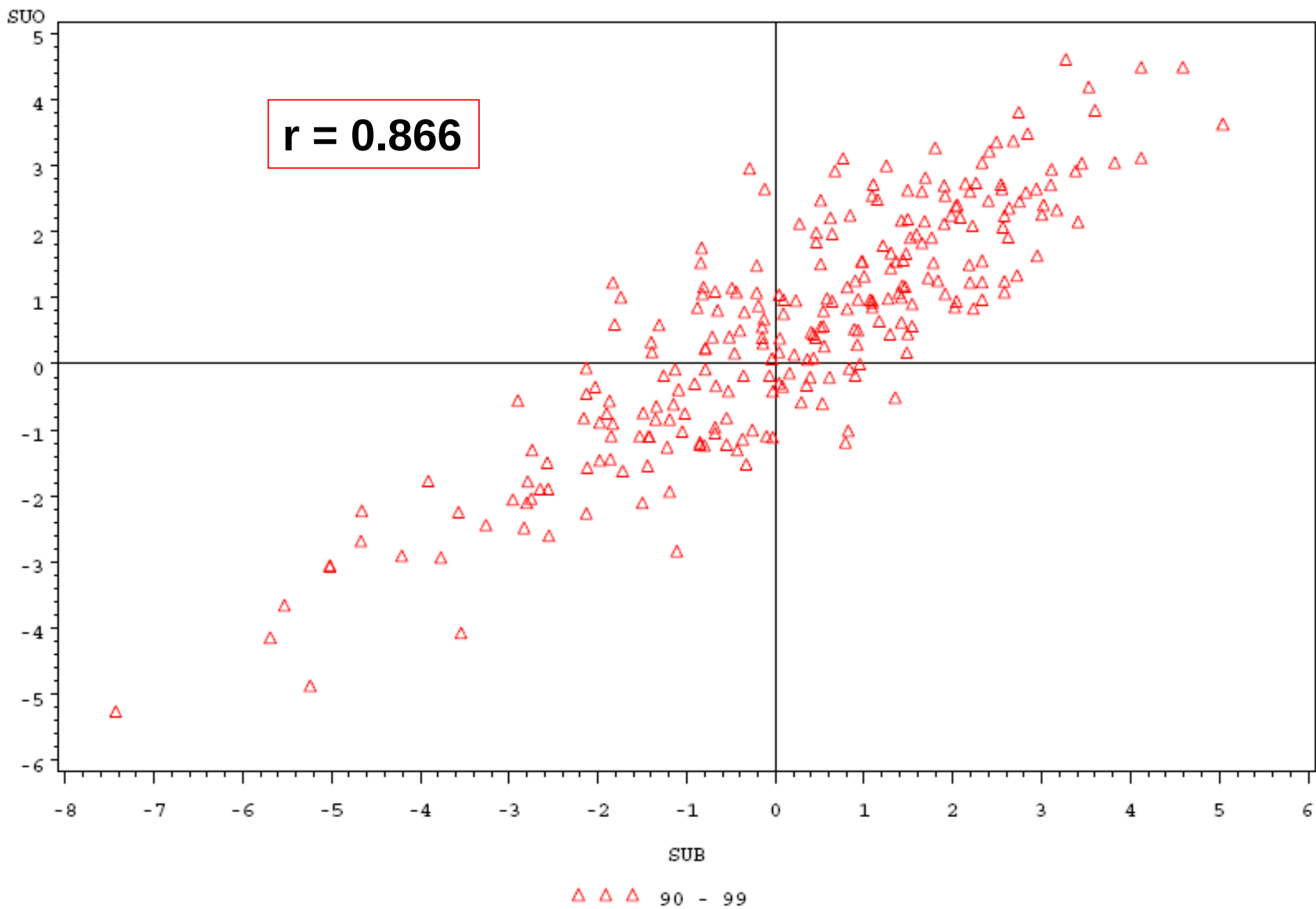
AI sires CIV combined old v new 1st 5 par wgt



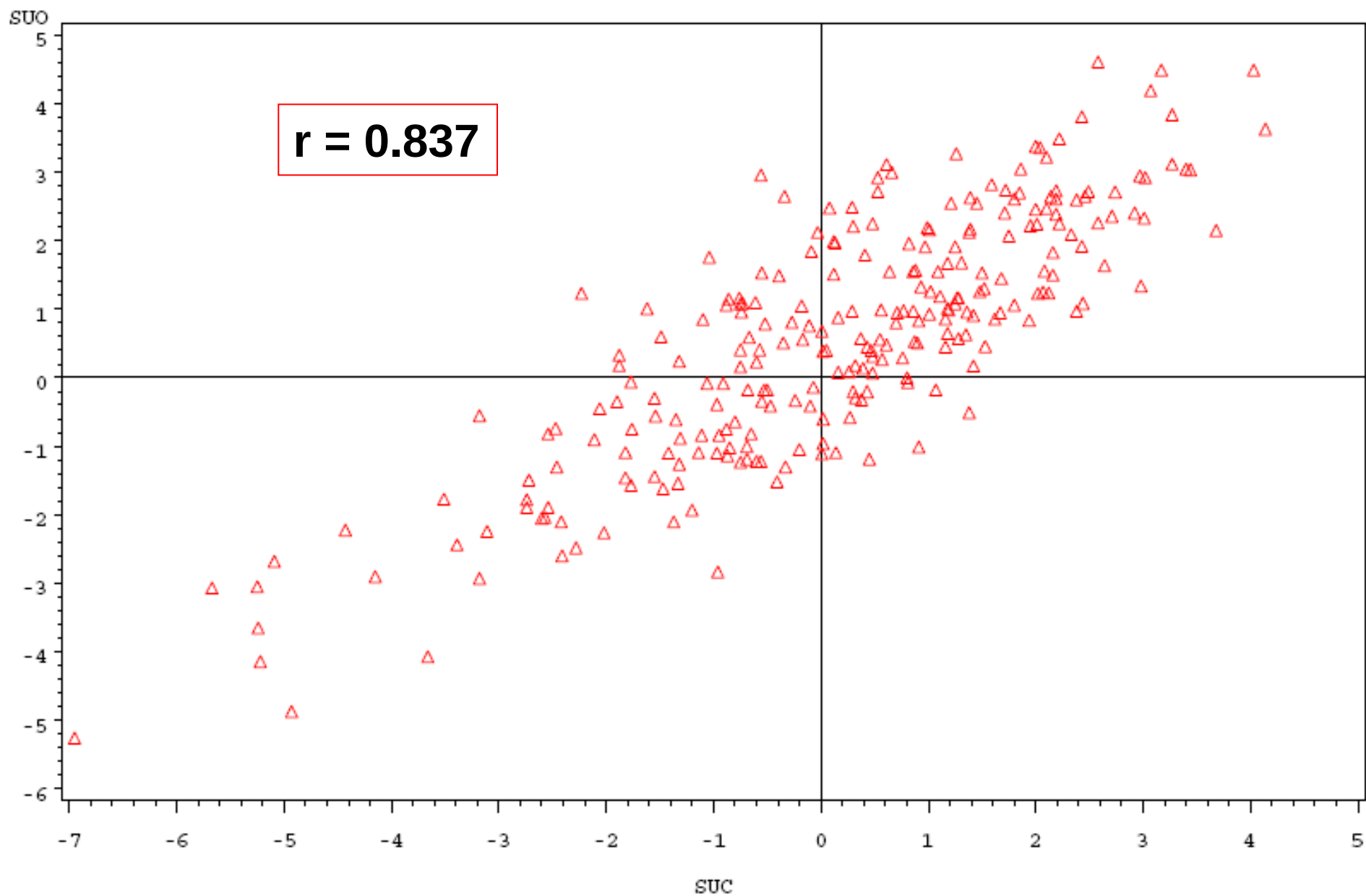
AI sires SU combined old v new 1st 3 par



AI sires SU combined old v new 1st 5 par



AI sires SU combined old v new 1st 5 par wgt



△ △ △ 90 - 99

Reasons for re-rank

- Extra traits: parity 4,5: minimal impact
- Extra traits: CFS, NS: no impact, high rel
- New genetic parameters: **impact on su**
- New software: **could be having impact**,
 - upgrade of PEST software ordered
- 600-800 day: increasing variance of proofs
- CMMS update July 07: minimal impact
- Cows with no milk recording 1 to 5: minimal impact

Next phase

- More iterations in MIX99
- Run new model in upgrade of PEST
- Get reliabilities going in software chosen
- Test specific heterosis effects
- Work is nearing completion
- Deadline passed so old model will be used for Spring dairy proofs
- Updated evaluation ran in old model
 - 0.98 for CIV, 0.97 for SUV
- Introduce later in year – April or August.
 - Improvement especially relevant for cows.

Genomic Selection in Ireland Version 2.1

*Donagh Berry¹, Francis Kearney²,
& Andrew Cromie²*

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On-going research

Slide from 5th Nov 2009

- SNP calling
 - *Issue of calling difference across labs and time* ✓
- Speed up SNP editing (looking forward to 660,000 SNPs and 3,000,000,000 SNPs) ✓....
- More genotype swapping
 - *UK, Poland, LIC, Switzerland, eurogenomics??* ✓....
- New methods of genomic evaluation ✓....
- INTERBULL MACE evaluations ✓....
- Cows in the genomic evaluation
- Across breed genomic evaluation
- SNP identification (Illumina chip) ✓....

SNP calling

- Different types of SNPs calls
 - *Forward allele*
 - *TOP allele*
 - *AB allele*
- Different laboratories call “Forward alleles” differently
- Genomic selection in Ireland now based on “AB allele”
- SNP index and SNP name also change between laboratories

SNP calling

- Data required from genotyping laboratories and swapping partners
 1. SNP name
 2. Chromosome
 3. Position
 4. Allele1_AB
 5. Allele2_AB
 6. GT_Score (GenTrain score)
 7. GC_score

SNP editing

- **Previously:** $\sim 1,500$ animals $\times 54,000$ SNPs
 - *81 million records*
 - *~ 3 days to edit SNP data*
- **With MACE:** $\sim 6,000$ animals $\times 54,000$ SNPs
 - *325 million records*
- **The future:** $> 20,000$ animals $\times 0.5$ m SNPs
 - *$> 10,000$ million (> 10 billion)*

SNP editing - current (1)

- Import all genotypes from all sources separately and appending
- Recoding SNPs from A's and B's to 0,1,2
- Removing sex-chromosome and SNPs of unknown position on the genome
- Check parentage and remove SNPs and animals with >5% discrepancies between offspring-parent
- Rectify parentage errors
- Derive haplotypes (sequence of consecutive SNPs for imputing missing SNPs)
- Estimating population haplotype frequencies

SNP editing - current (2)

- Removing SNPs that are
 - Monomorphic (no difference among animals)
 - Minor allele frequency ($<2\%$; minimal difference among animals)
 - Not in Hardy-Weinberg equilibrium (may be a "poor" SNP)
 - High level of heterozygosity relative to homozygosity and vice versa (may be a "poor" SNP)
 - In linkage disequilibrium (>1 SNP are identical and therefore adding no additional information)
- Impute missing SNPs

SNP editing - proposed (1)

- Inbreeding threshold increased from 10% to 12% and applied to all populations
- Recode and remove unwanted SNPs as new SNP file is received and append on to existing data
- Recode SNPs to match position on the genome
- Chromosome threshold decreased from 5% to 2% with parentage checking undertaken as new genotypes are received
- Determine if any SNPs are missing for imputation
- Estimating population haplotype frequencies

SNP editing - proposed (2)

- Removing SNPs that are
 - Monomorphic (no difference among animals)
 - Minor allele frequency ($<2\%$; minimal difference among animals)
 - Not in Hardy-Weinberg equilibrium (may be a "poor" SNP)
 - High level of heterozygosity relative to homozygosity and vice versa (may be a "poor" SNP)
 - SNPs in LD are not removed - BIG time saver
- Impute missing SNPs
 - Imputing takes better account of parents' genotypes

6074 samples & 54001 SNPs

18 "poor" duplicated samples removed

2419 sex-chromosome/unknown position SNPs removed

Parentage checking

230 "bad" SNPs

3785 monomorphic SNPs

3415 with MAF <2%

21 with poor clustering

693 not in Hard-Weinberg

1518 with poor call rate

168 samples with poor call rate or not aligned with parents

Duplicate SNPs per animal discarded

5740 animals & 41920 SNPs

LAST YEAR: 1209 animals & 42598 SNPs

More genotype swapping

- **Currently**
 - Moorepark 1157
 - LIC: 2290
 - Swiss: 719
 - UK: 25
 - Poland: 14
 - ICBF: 962
 - Irish AI organisations: 457
 - ROBUSTMILK; www.robustmilk.eu: 571
- **In progress**
 - Poland (217)
- **Discussions**
 - Eurogenomics, UK, Australia

New methods of genomic evaluation

- Currently use “G-BLUP” or “Genomic-BLUP”
- Method of choice (with modifications) in most genomic evaluations
- Based on calculating genomic relationship matrix and replacing the average expected relationship matrix in traditional BLUP
- Modify the method of calculating Genomic relationship matrix
 - New method appears to be used by most
 - Probably more amenable to implement in across-breed evaluation
- Algorithms inefficient for memory usage

Estimation of genomic relationships

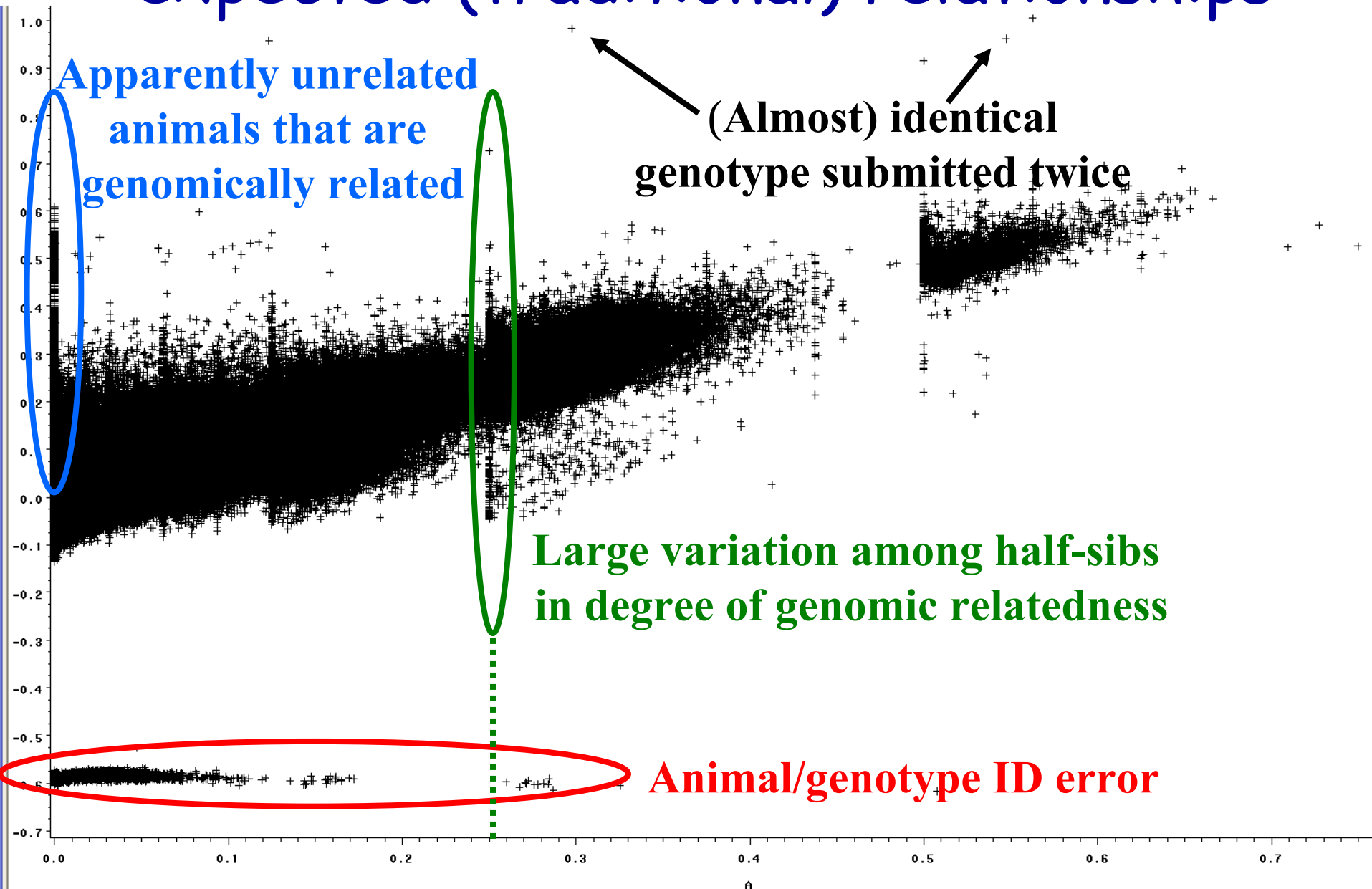
$$\mathbf{G} = \frac{\mathbf{XX}' - 4 \sum_i^n P_i^2 \mathbf{1}\mathbf{1}'}{2 \sum_i^n P_i (1 - P_i)} \quad \text{Habier et al. (2007)}$$



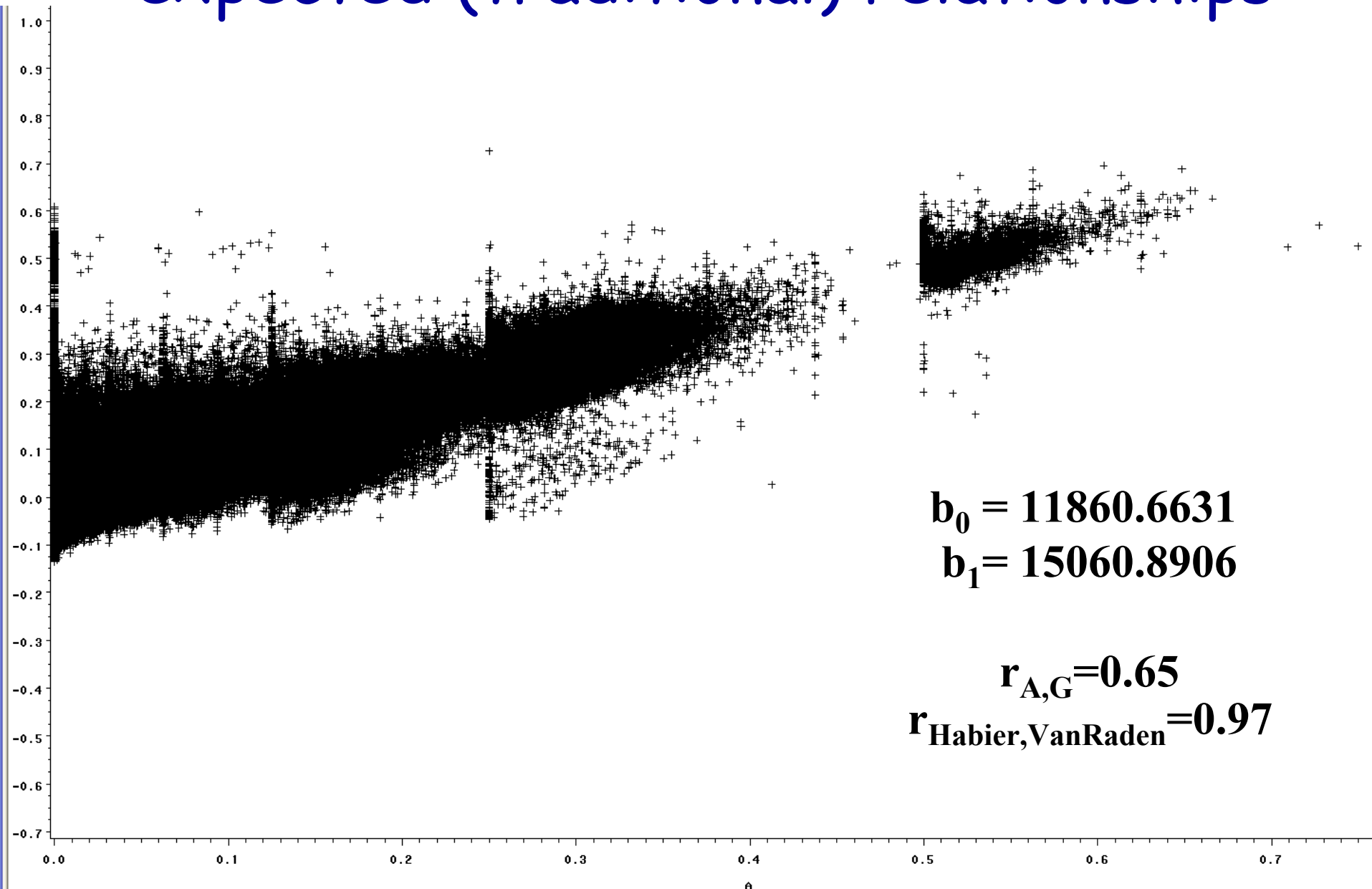
$$\mathbf{G} = \frac{\mathbf{XX}' - b_0(\mathbf{1}\mathbf{1}')}{b_1} \quad \& \quad \begin{bmatrix} n^2 & \sum_i^n \sum_j^n \mathbf{A}_{ij} \\ \sum_i^n \sum_j^n \mathbf{A}_{ij} & \sum_i^n \sum_j^n \mathbf{A}_{ij}^2 \end{bmatrix} \begin{bmatrix} b_0 \\ b_1 \end{bmatrix} = \begin{bmatrix} \sum_i^n \sum_j^n (\mathbf{XX}')_{ij} \\ \sum_i^n \sum_j^n (\mathbf{XX}')_{ij} \mathbf{A}_{ij} \end{bmatrix}$$

VanRaden (2008)

Genomic relationships v average expected (traditional) relationships



Genomic relationships v average expected (traditional) relationships



Testing of genomic selection

- Impact of new method to derive genomic relationship matrix
- Impact of revised weighting factor
- Impact of MACE evaluations
 - Milk production, SCC, Calving interval & survival

Testing of genomic selection

- Forward prediction

- Correlation
- Bias

Training Population:

Bulls born pre
1997/1996 with
adjusted reliability
>40% and >40
daughters in
Ireland

- Implementation

- Achievable reliability
- Weighting on genomics

Training Population:

All bulls with
adjusted reliability
>40%/ >50%

Milk production & fertility: domestic only versus MACE evaluations

Correlations

	PA	Domestic			MACE		
		Training size	DGV	GEBV	Training size	DGV	GEBV
Milk yld	0.74	883	0.66	0.69	3204	0.77	0.77
Fat yld	0.68	883	0.65	0.65	3204	0.73	0.72
Protein yld	0.74	883	0.67	0.69	3204	0.77	0.77
SCC	0.49	883	0.41	0.47	3204	0.60	0.63
Calv. int.	0.73	542	0.66	0.69	1447	0.73	0.73
Survival	0.50	542	0.55	0.58	1108	0.58	0.59

Milk production & fertility: domestic only versus MACE evaluations

Bias

	PA	Domestic			MACE		
		Training size	DGV	GEBV	Training size	DGV	GEBV
Milk yld	31.2	883	36.7	46.3	3204	35.8	37.6
Fat yld	-1.59	883	-0.88	-0.58	3204	-0.36	-0.25
Protein yld	-0.33	883	-0.14	0.30	3204	0.40	0.62
SCC	0.01	883	0.02	0.02	3204	0.02	0.02
Calv. int.	0.34	542	-1.13	-1.29	1447	-1.11	-1.17
Survival	-0.06	542	0.54	0.76	1108	0.60	0.71

Calving performance: *Correlations and Bias*

	Training Size	Correlations			Bias		
		PA	DGV	GEBV	PA	DGV	GEBV
Direct calv. Diff.	1272	0.49	0.37	0.39	0.24	-0.22	-0.40
Maternal calv. Diff.	876	0.67	0.56	0.59	-0.22	0.38	0.65
Gestation length	1068	0.62	0.62	0.64	0.19	-0.12	-0.19
Calf mortality	304	0.45	0.23	0.29	0.23	0.40	0.32

Predictive ability increased when reliability of training population increased from >40% to >50%

Estimates based on 50% reliability shown above

Beef performance: *Correlations and Bias*

	Training Size	Correlations			Bias		
		PA	DGV	GEBV	PA	DGV	GEBV
Carcass wt.	768	0.41	0.35	0.39	-3.18	-6.95	-7.28
Cull cow wt.	720	0.75	0.68	0.70	-1.41	-4.72	-4.70
Carcass conf.	735	0.78	0.74	0.76	-0.32	-0.55	-0.58
Carcass fat	735	0.77	0.74	0.77	-0.03	-0.03	-0.03

Predictive ability increased when reliability of training population increased from >40% to >50%

Estimates based on 50% reliability shown above

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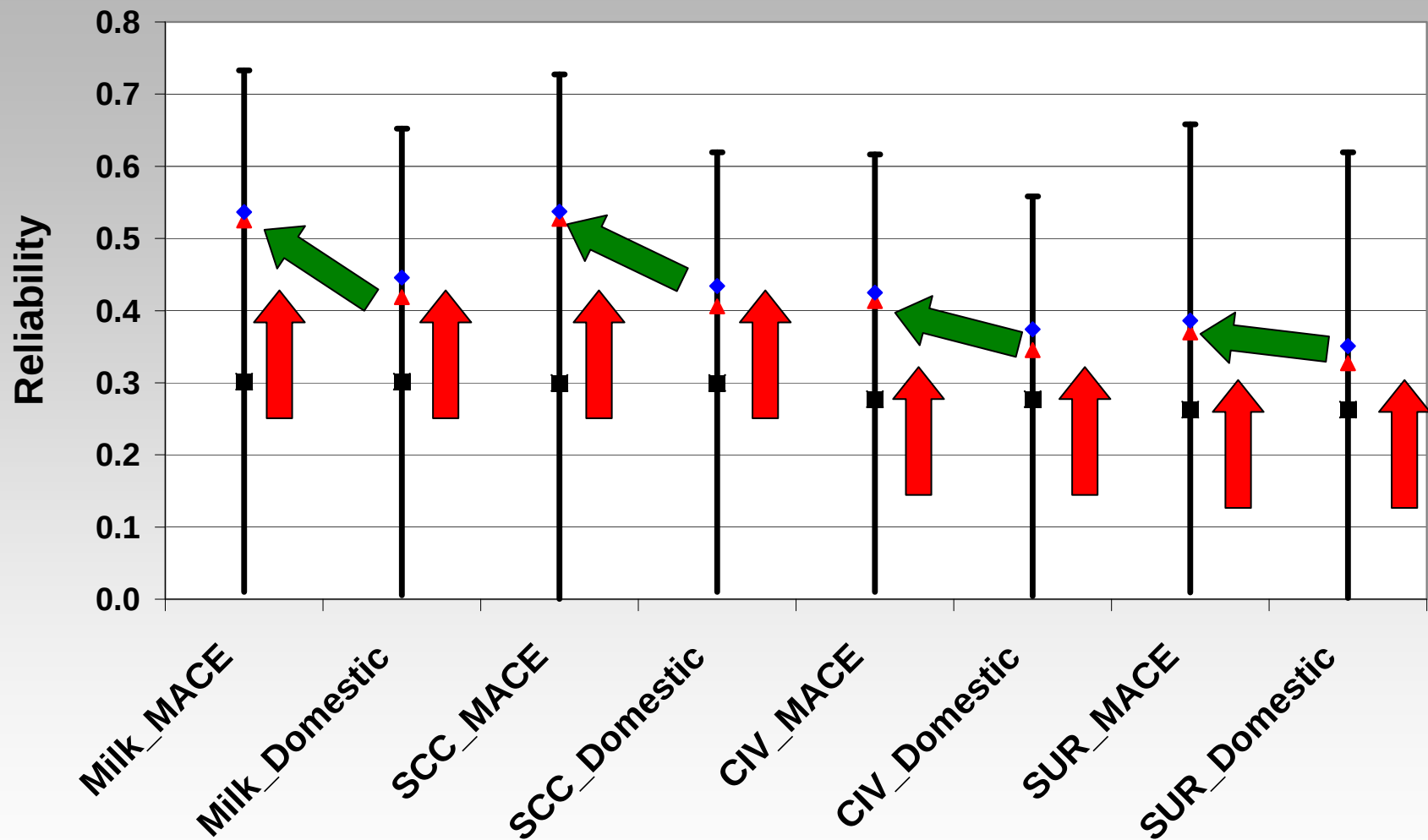
Correlations and Bias

	Training	Correlations			Bias		
	Size	PA	DGV	GEBV	PA	DGV	GEBV
Locomotion	454	0.58	0.84	0.86	-0.05	-0.04	-0.01
Feet & legs	675	0.68	0.54	0.57	0.16	-0.16	-0.10
Mammary	675	0.66	0.72	0.74	-0.57	-0.38	-0.33
Overall type	675	0.72	0.72	0.74	-0.03	-0.34	-0.28

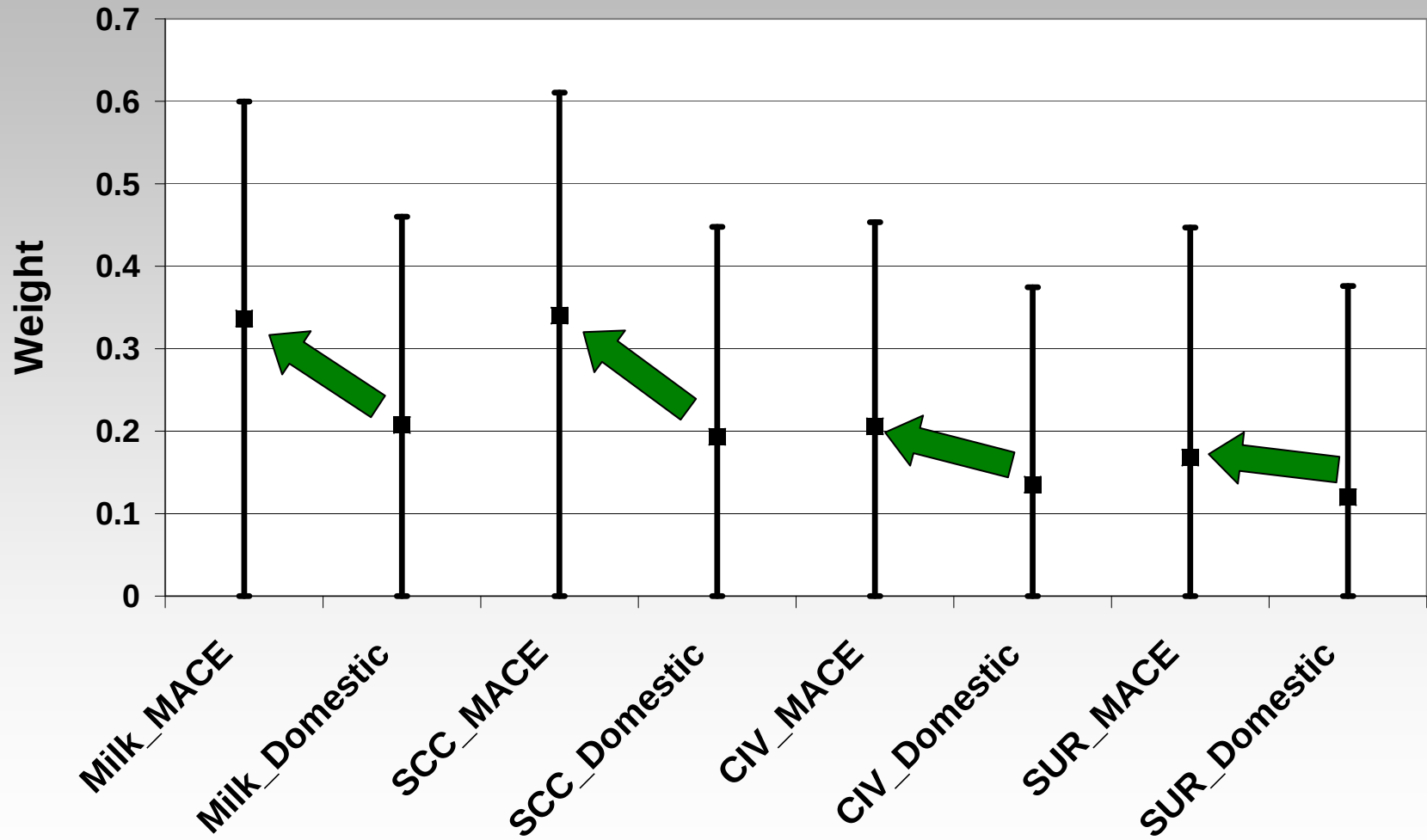
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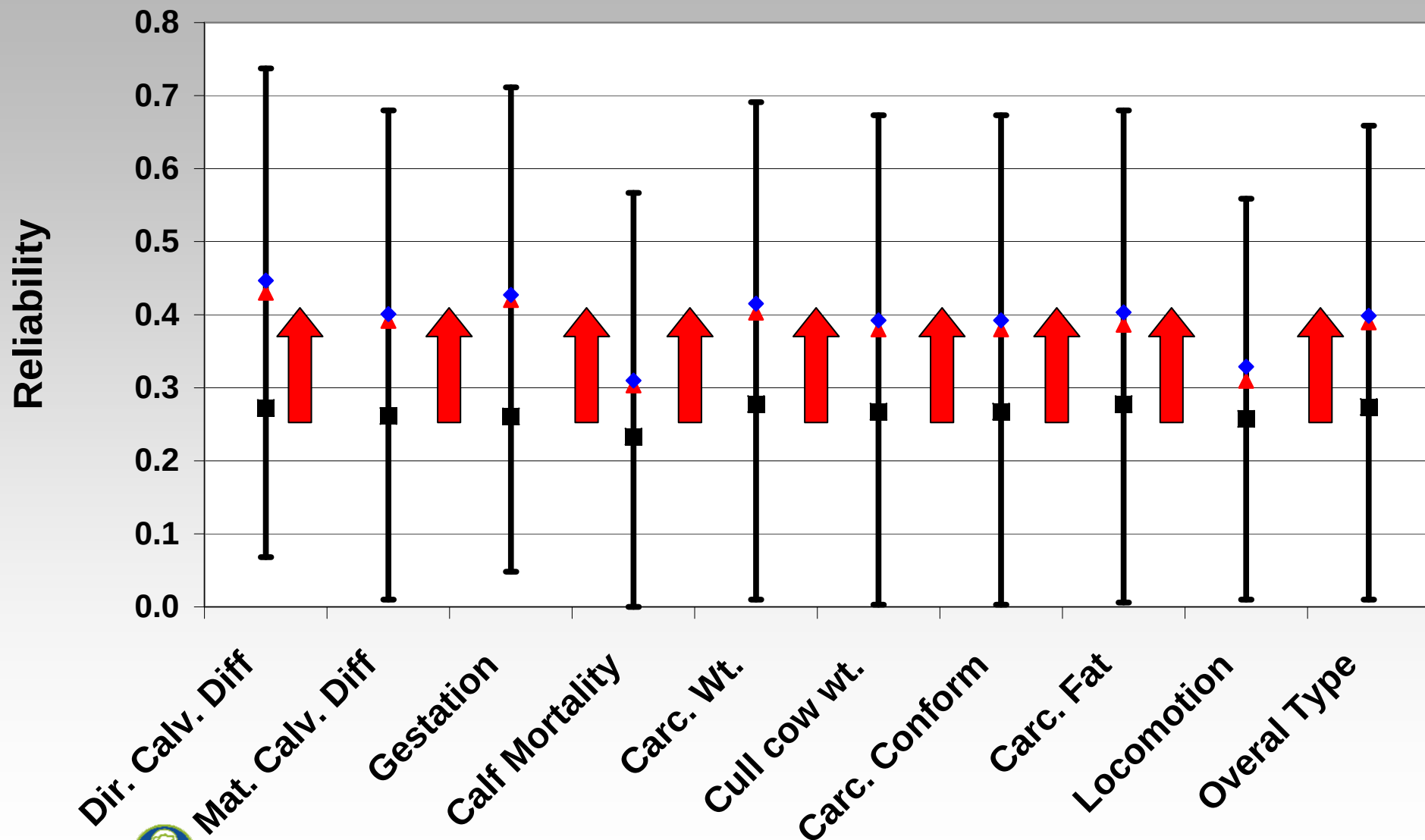
Impact on young bulls: *Reliabilities*



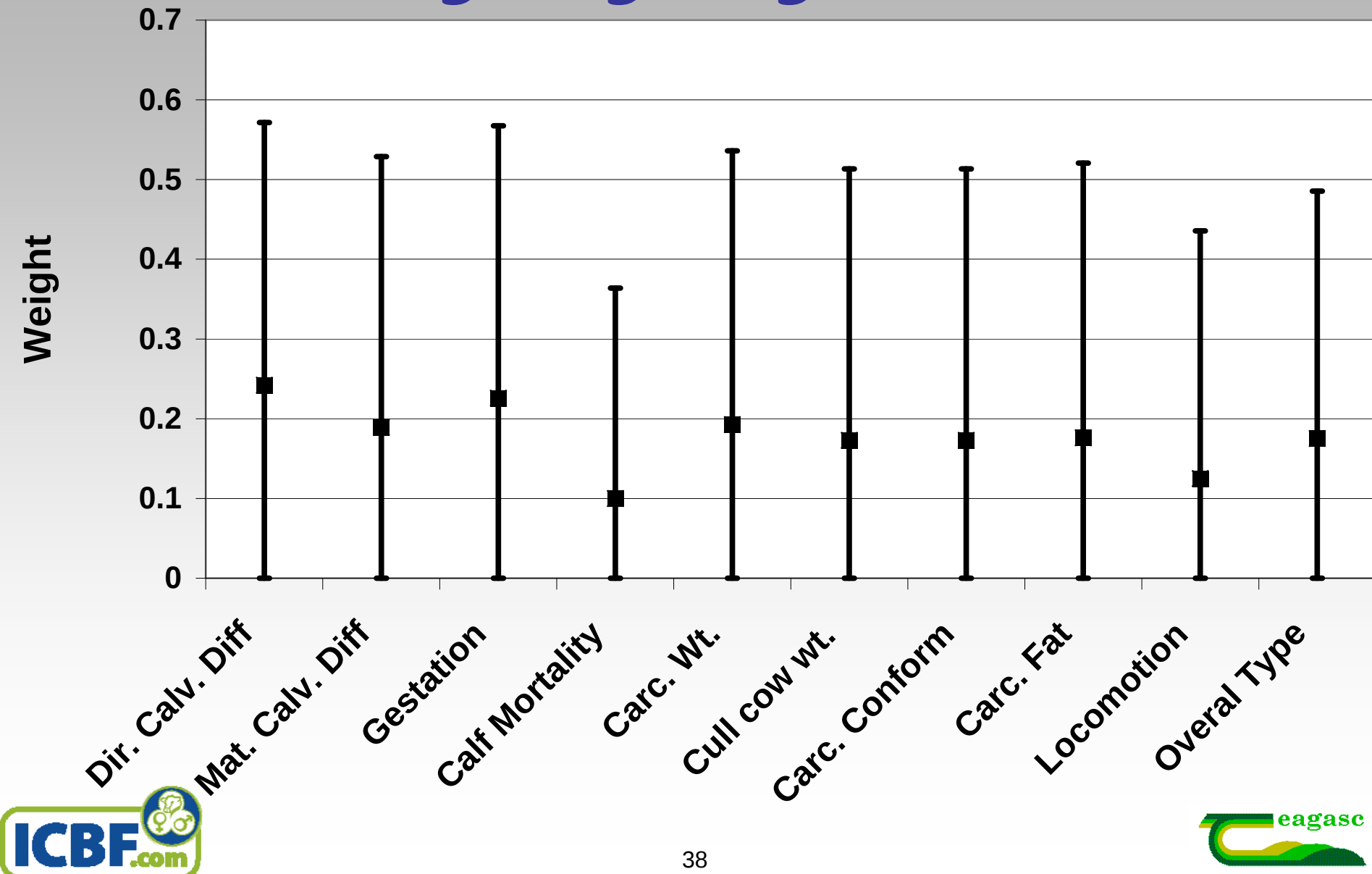
Impact on young bulls: *Weighting on genomics*



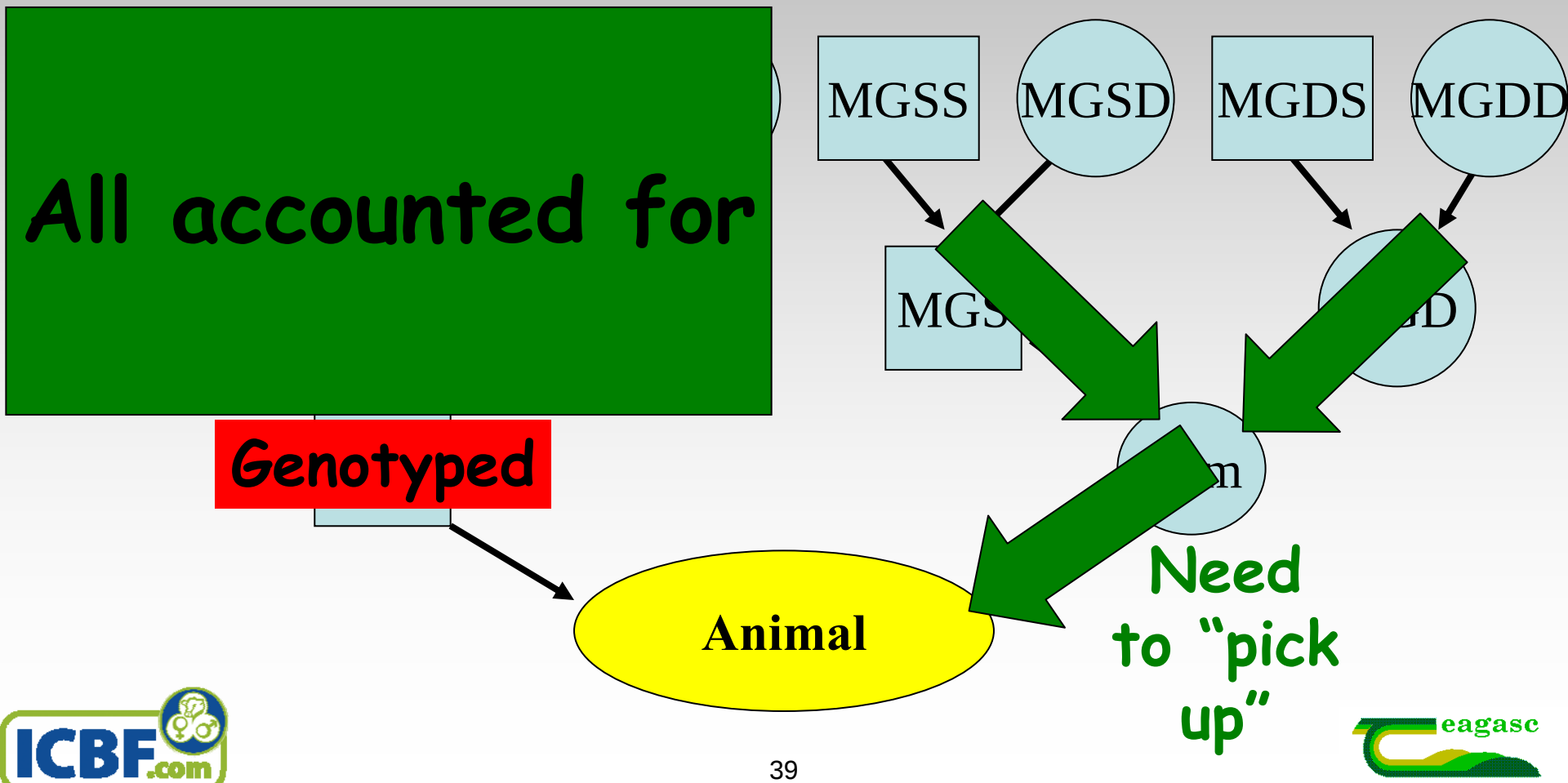
Impact on young bulls: *Reliabilities*



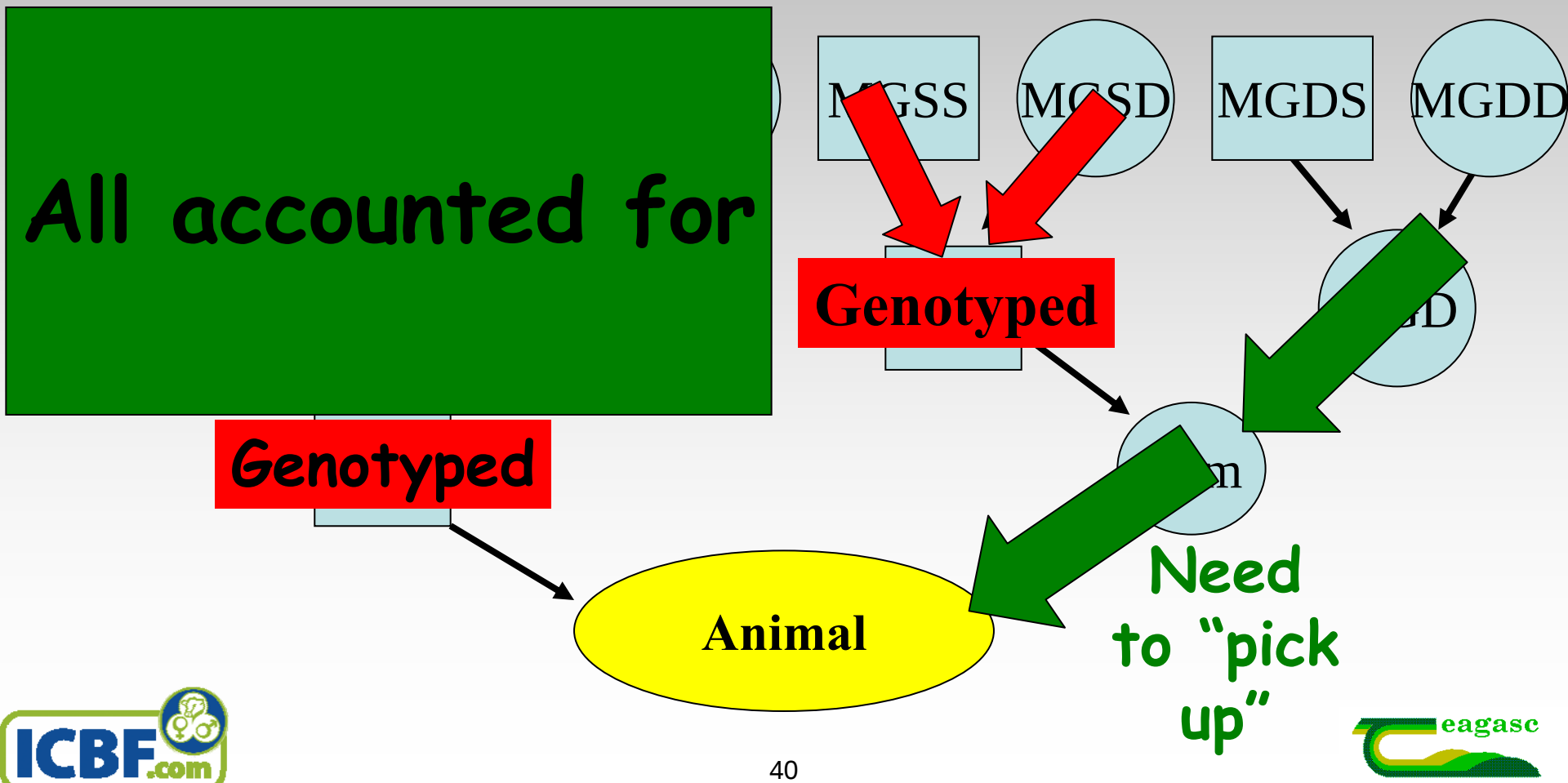
Impact on young bulls: *Weighting on genomics*



Blending of genomic and traditional evaluations



Blending of genomic and traditional evaluations



Blending of genomic and traditional evaluations - Examples

- Direct genomic value (DGV)
 - Estimate of EBV based on genotyped pedigree (EBV_genotype)
 - Parental average (PA)
-
- All the following examples assume almost identical reliabilities for each

Blending - In "simple" terms

- *If the EBV_genotype says the animal is good and the DGV says it's good then the genotype information adds nothing more over and above the PA*
- *If the EBV_genotype says the animal is poor but the DGV says it's good then it's approx the DGV better than the PA*
- **Weighting on genomics is influenced by respective reliability estimates**

Blending - Examples

- High DGV (e.g., EBI=€200)
- Low EBV_genotype (e.g., EBI=€0)
- Low PA (e.g., EBI=€0)
- High GEBV near DGV (€196)

Blending - Examples

- High DGV (e.g., EBI=€200)
- High EBV_genotype (e.g., EBI=€200)
- Low PA (e.g., EBI=€0)
- Low GEBV near PA (€4)

Blending - Examples

- High DGV (e.g., EBI=€200)
- High EBV_genotype (e.g., EBI=€200)
- High PA (e.g., EBI=€200)
- High GEBV near all (€200)

Blending - Examples

- High DGV (e.g., EBI=€200)
- Low EBV_genotype (e.g., EBI=€0)
- High PA (e.g., EBI=€200)
- Very high GEBV (€392)

SNP identification – new SNPchip

- Identified and supplied 102 SNPs in candidate genes for milk production, fertility and growth to the new larger Illumina SNP chip
- Released in April 2010
- >500,000 SNPs
 - All may not be segregating in *Bos Taurus*
- Need to re-genotype ~50% of animals (influential descendents) and impute SNPs in remainder
- Funding secured

Genomic selection output

- Traditional estimated breeding value (Parental average)
- Direct Genomic Value (DGV)
- Genomic breeding value (GEBV; blended value)
- Traditional EBV reliability
- DGV reliability
- Blended reliability
- Weighting on genomic information

Input from AI organisations and breed societies

- Still need semen from bulls not already sourced
- ICBF sent out list of bulls required specific to each AI organisation
 - *Also on ICBF website*
(<http://www.icbf.com>)
- Benefits of larger training population are obvious

Conclusions

- Genomic selection process improved (speed and quality control)
- Large benefit of including MACE evaluations for milk production and fertility...calving performance??
- Immediate future - impact of cows in genomic selection & acrossbreed evaluation



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Calving Performance Evaluations

Calving Performance

- Currently based on parameters that were estimated a number of years ago
- Large increase in data in the last number of years
- Estimates of heritability based on records across all lactations
- Is heifer calving/gestation a different trait?

Current Model

- Evaluate calving difficulty, maternal calving difficulty, gestation, mortality
- No correlation between traits except a negative 0.7 correlation between direct and maternal calving difficulty
- Historical calving data used as a correlated trait for each trait

Heritabilities

Current Estimates

	heritability
Calving Diff	0.25
Gestation	0.40
Mortality	0.01

New Estimates

	heritability
<u>Calving Diff</u>	
1 st	0.13
Later	0.07
<u>Gestation</u>	
1 st	0.45
Later	0.40
Mortality	No estimate

New estimates in line with those in the literature

Correlations

	CD	MCD	Gestation
1 st – Later	0.72	0.29	0.93

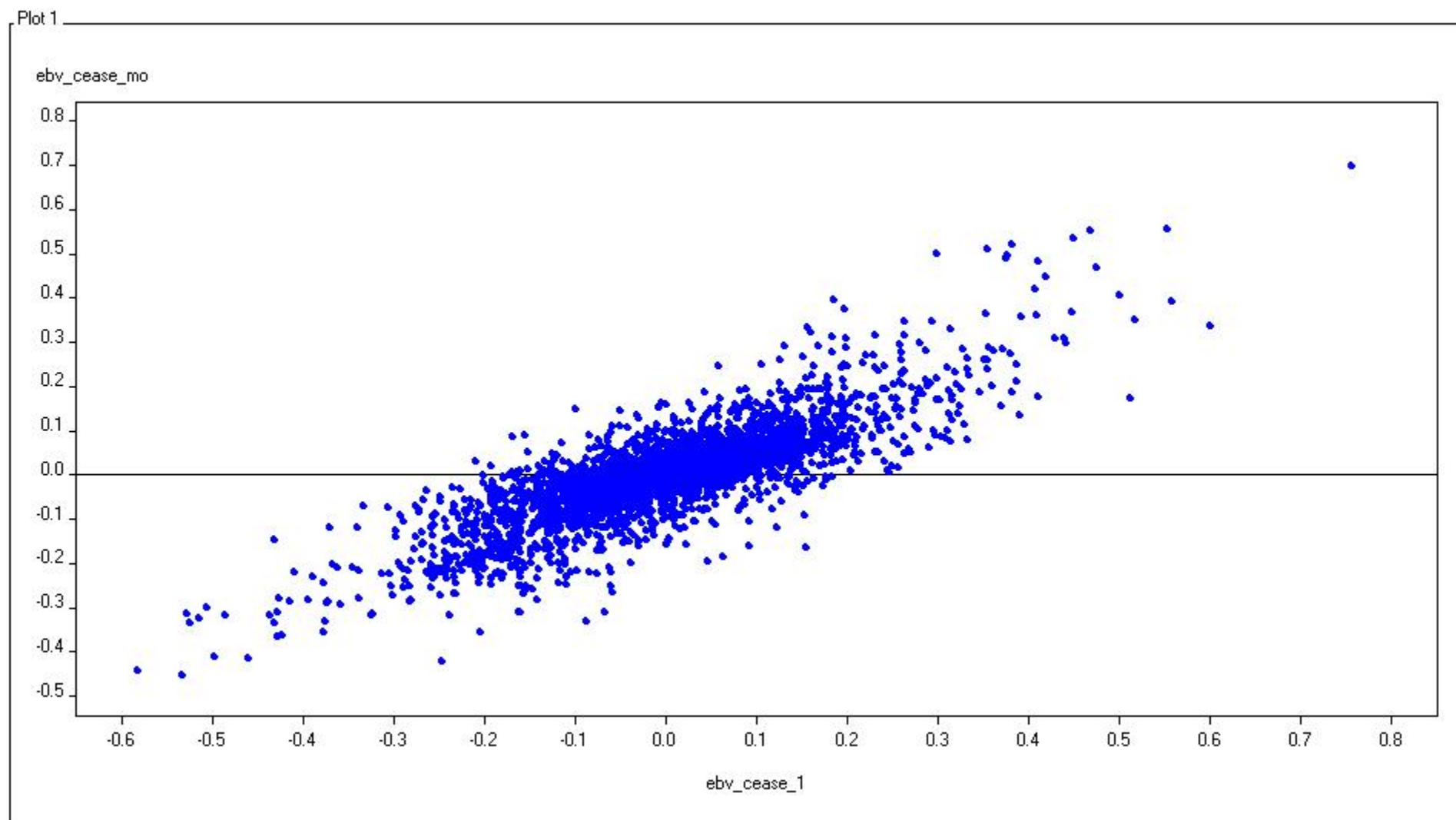
Correlation between two traits less than 0.8 indicate traits are not controlled by the same genes

Correlations

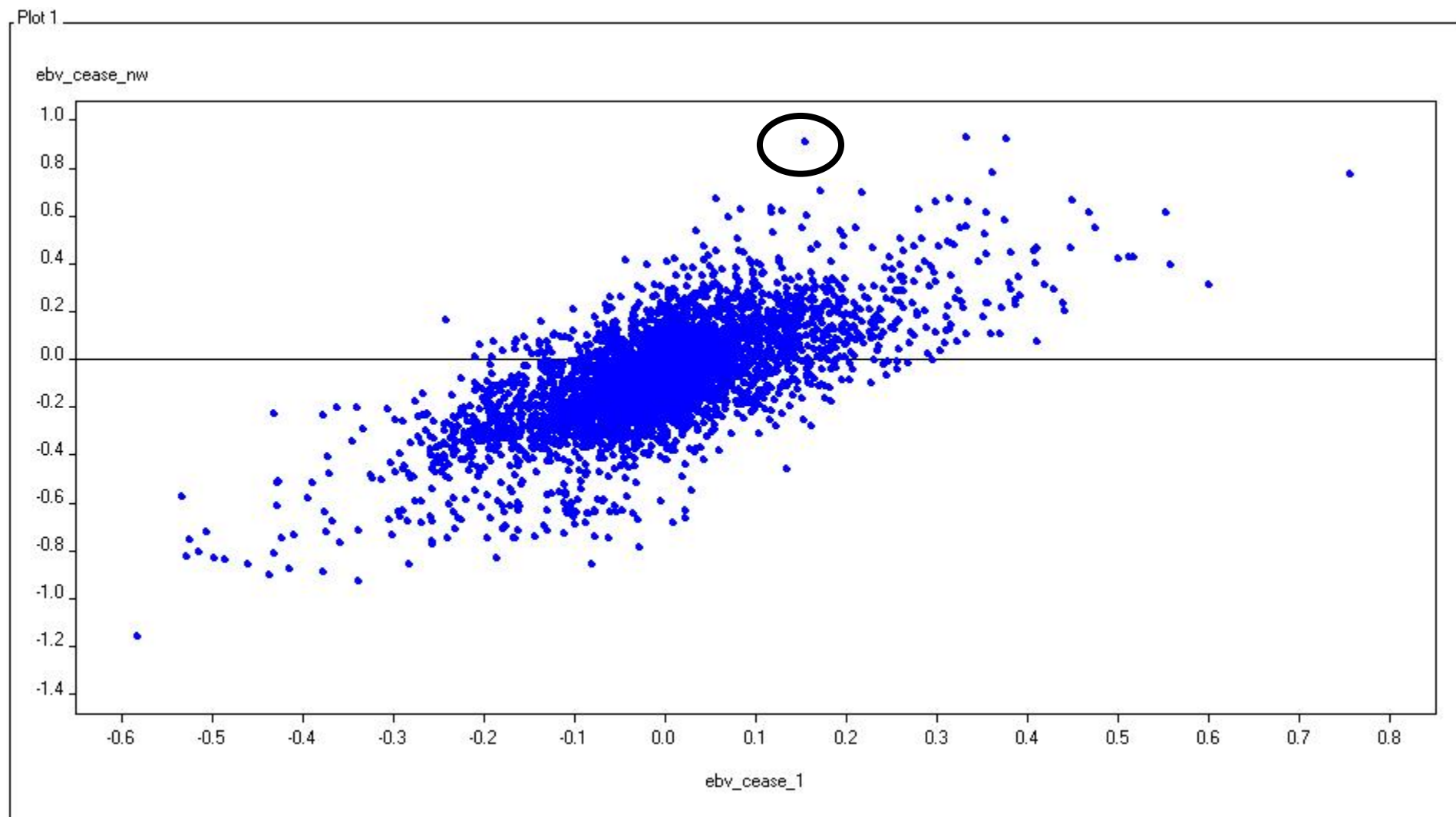
Correlation between direct and maternal – current estimates indicate that daughters of bulls that are easy calving have difficulty calving themselves

	Current	New
CD-MCD	-0.7	
CD-MCD -1 st		-0.48
CD-MCD - later		-0.24

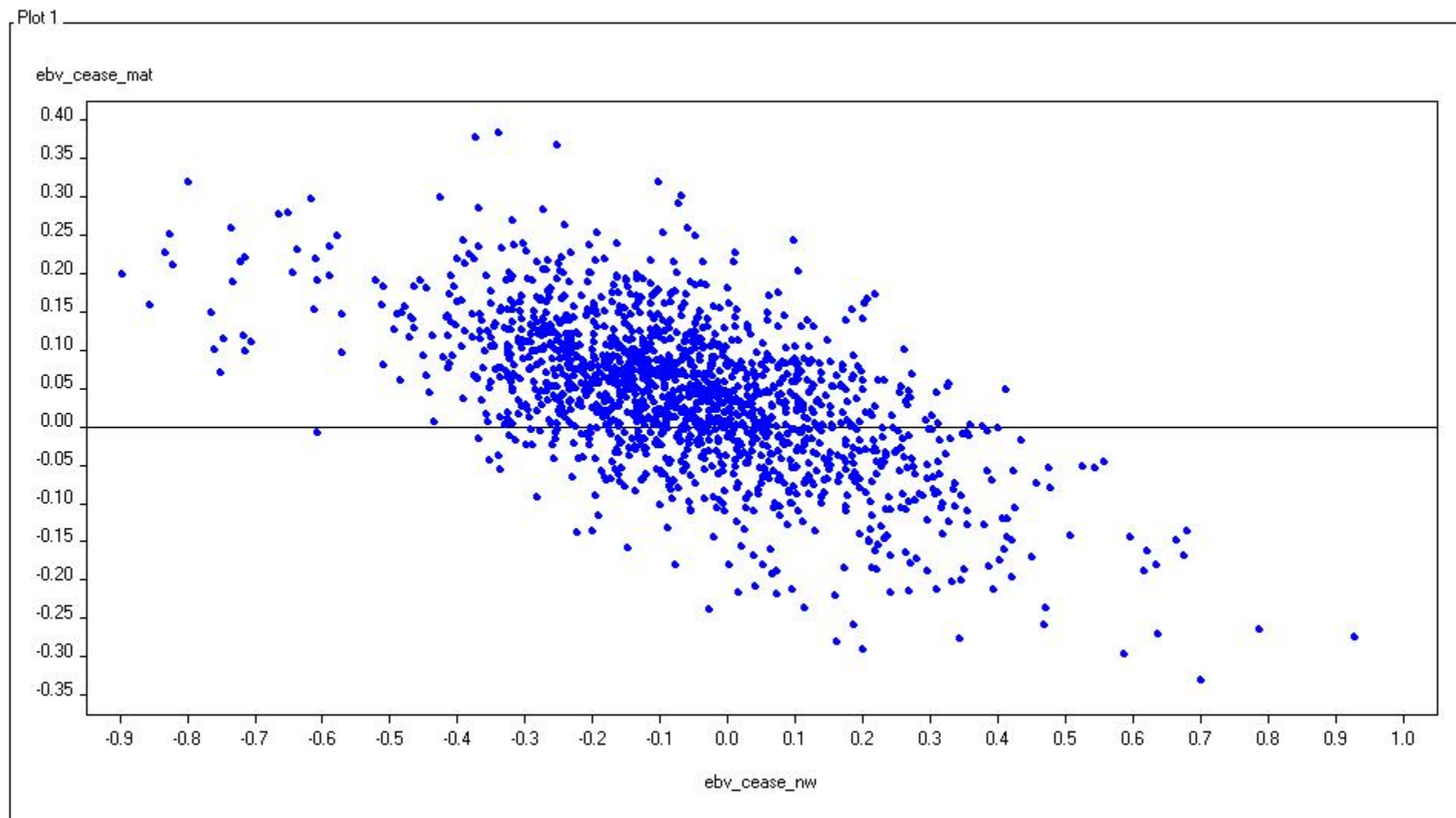
Results



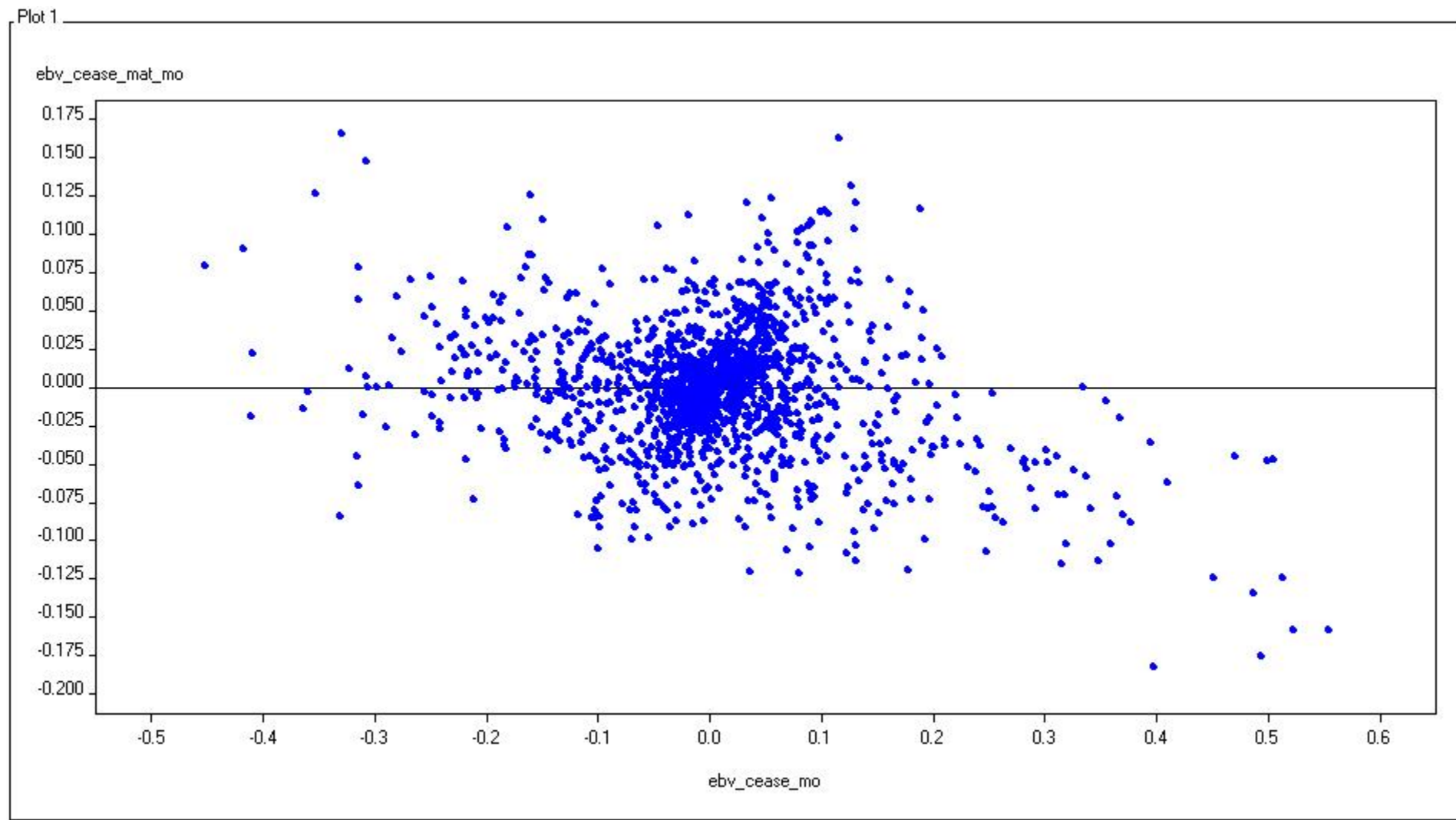
Results



Results



Results



Implications

- Lower heritabilities for calving diff will result in lower reliabilities especially for new test bulls
- Biologically a model with 1st and later parities evaluated separately should be used for CD, MCD
- Weighting between 1st parity and later parities must be calculated
- Direct calving will have less of an impact on maternal calving due to a lower correlation

Implementation

- More research on how best to combine the traits
- Further testing of proofs (e.g., bulls harder calving in later lactation animals?)
- Implementation later in the year after feedback from the industry

Routine evaluations.

- Release date = 1st February.
- Key changes:
 - Updating EBI values.
 - Maintenance sub-index.
 - Improvements in genomic evaluations.
- Further research will continue:
 - New CIS proofs (use of insemination data)
 - New Calving proofs (and sub-index).
 - Health traits....

ICBF Active Bull List – Spring 2010

- Content - Same as Spring 2009.
 - Minimum EBI reliability of 35%.
 - Includes DP & GS bulls.
 - Includes semen limits for GS bulls.
 - EBI rel 35%-50% = 3,000 doses.
 - EBI rel >50% - 5,000 doses.
- Layout - Small change to layout.
 - Inclusion of maintenance sub-index.

ICBF Active Bull List – Spring 2010

- Updating – Change in approach.
 - List being compiled 1st week February.
 - ICBF will contact all AI organisations re: bulls for published listing (IFJ) & advise how to update “live” listing on ICBF website.
 - “Live” listing for season; code, availability & price.

GENE IRELAND – Future developments.

- Procurement service.
 - User-pays service for AI companies.
 - Top cow list, pregnancies...
 - DRAFT contracts being developed.
- Genomics Service.
 - User-pays service for industry.
 - Two levels; (i) Genotype + Genomic EBI service, & (ii) Genomic EBI service only.
 - Volume discounts to apply.
 - DRAFT contracts being developed.

GENE IRELAND – Future developments.

- Progeny Test Service.
 - Started for 2010.
 - Target – 80 bulls @ €170.
- Research work.
 - Balancing EBI gain & genetic diversity.
 - Contract mating females this Spring.
 - Optimal Program for Ireland.

Producing Elite Young Test Bulls for GENE IRELAND

*Sinéad Mc Parland,
Kearney, Evans, Cromie & Berry*

Objective

Design a mating scheme to generate
ELITE bull calves annually for entry into
GENE IRELAND

Focus:

1. Continually improve genetic gain
2. Maintain genetic diversity

3 Steps Involved

1. Identify elite bulls to act as bull sires
 - Sought globally
2. Identify elite cows to act as bull dams
 - National data base
3. Identify best combination of matings between elite bulls and cows

Bull Selection

1. All bulls with Interbull proofs considered
 - $\text{€BI} > \text{€120}$
 - Reliability $> 50\%$
 - Positive Milk and Fertility SI
 - Prominent sire lines removed
 - OJI, HNS, UYC, GMI



Top 64 potential bull sires

Variable	Mean	Std Dev	Minimum	Maximum
EBI (€)	153	21	120	215
EBI Reliability (%)	64	12	50	98
Milk SI (€)	53	22	0	102
Fertility SI (€)	85	33	20	170
Calving SI (€)	19	7	5	36
Health SI (€)	3	6	-6	16
Carcass SI (€)	-7	5	-24	8
R-value (%)	1.70	0.61	0.01	2.94

3 Steps Involved

- ✓ 1. Identify elite bulls to act as bull sires
 - Sought globally
2. Identify elite cows to act as bull dams
 - National data base
3. Identify best combination of matings between elite bulls and cows

Selection of Bull Dams

- Milk production
 - Genetic and phenotypic
- Fertility
 - Genetic and phenotypic
- EBI > €120
- 2 complete generations of ancestry recorded
- Prominent sire lines removed
- Top 150 daughters & granddaughters per bull



Top 2000 potential bull dams

Variable	Average	Minimum	Maximum
EBI (€)	142	128	194
Milk SI (€)	68	1	152
Fertility SI (€)	60	0	152
Milk (kg)	6,336	3,505	10,269
Solids (kg)	496	300	784
Fat (%)	4.22	2.66	6.65
Protein (%)	3.64	3.11	4.31
Calving interval	365	301	400

3 Steps Involved

- ✓ 1. Identify elite bulls to act as bull sires
 - Sought globally
- ✓ 2. Identify elite cows to act as bull dams
 - National data base
3. Identify optimum combination of matings between elite bulls and cows

Determine optimum matings

- Elite bull dams and elite bull sires are entered into computer programme
 - Computer generated “phantom” matings
 - All combinations of bull sire and bull dam
 - $64 \text{ Bulls} * 2000 \text{ cows} = 128,000 \text{ mating combinations}$



Determine optimum matings

- Screen all mating combinations for the best sire-dam combinations
- Dual objective defined which accounts for
 - Parent average EBI (+ve)
 - Relatedness to future females (-ve)
 - Holstein-Friesian females
 - Incl Foetuses
 - Weight $2 \times \text{EBI}$: $-1 \times \text{R-value}$
- Balanced for milk and fertility

Top 1000 Potential Offspring

Variable	Mean	Std Dev	Minimum	Maximum
EBI	161	14	134	204
Milk SI	56	13	32	99
Fertility SI	88	18	36	129
Calving SI	21	6	3	34
Health SI	2	3	-8	12
Carcass SI	-6	4	-19	5
R-value	1.45	0.60	0.19	2.54

Bulls Used (n=28)

Variable	Mean	Std Dev	Minimum	Maximum
EBI	168	19	140	215
EBI Reliability	62	10	50	88
Milk SI	49	21	0	94
Fertility SI	102	31	39	170
Calving SI	19	8	5	35
Health SI	3	6	-6	16
Carcass SI	-5	5	-13	8
R-value	1.32	0.60	0.01	2.54

Cows Used (n=1000)

Variable	Mean	Std Dev	Minimum	Maximum
EBI (€)	148	12	129	194
Milk SI (€)	67	25	4	152
Fertility SI (€)	67	21	7	152
Calving SI (€)	22	7	2	41
Health SI (€)	-1	4	-11	9
Carcass SI (€)	-7	6	-25	13
R-Value (%)	1.00	0.53	0.11	2.69

Cows Used (n=1000)

Variable	Mean	Std Dev	Minimum	Maximum
Milk (kg) Parity 1	5716	898	3550	8577
Milk (kg) Parity 2	6658	964	3704	10232
Milk (kg) Parity 3	7122	1047	4257	10819
Protein(%) Parity 1	3.60	0.19	3.06	4.17
Protein(%) Parity 2	3.66	0.20	3.07	4.72
Protein(%) Parity 3	3.67	0.20	3.06	4.94
Fat(%) Parity 1	4.23	0.45	2.18	5.99
Fat(%) Parity 2	4.17	0.46	2.21	5.83
Fat(%) Parity 3	4.20	0.47	2.39	5.60
Average CI	368	12	322	400

In Conclusion

- Identification of elite bull calves with a low average relationship to the population is possible
 - Careful selection of bull sires and bull dams
 - Correct combination of bull sires and bull dams
 - Bull sires should be sought globally for maximum effect
 - Genomic selection will play a key role
 - Use younger bull sires and bull dams

Breeding Programs to exploit Genomic Selection in Ireland

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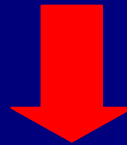
What is genomic selection

- “The most promising application of molecular genetics in livestock populations”
- Involves the use of genetic markers across the genome that ideally lie close to genes
- Ideal situation → all genes are covered by the markers

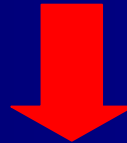
Genomic Selection - the process

Training dataset:

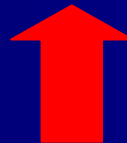
1000s animals with known genotypes (SNPs) and reliable phenotypes (EBVs)



Obtain effects for SNPs for each trait



Accurate GEBVs for young selection candidates



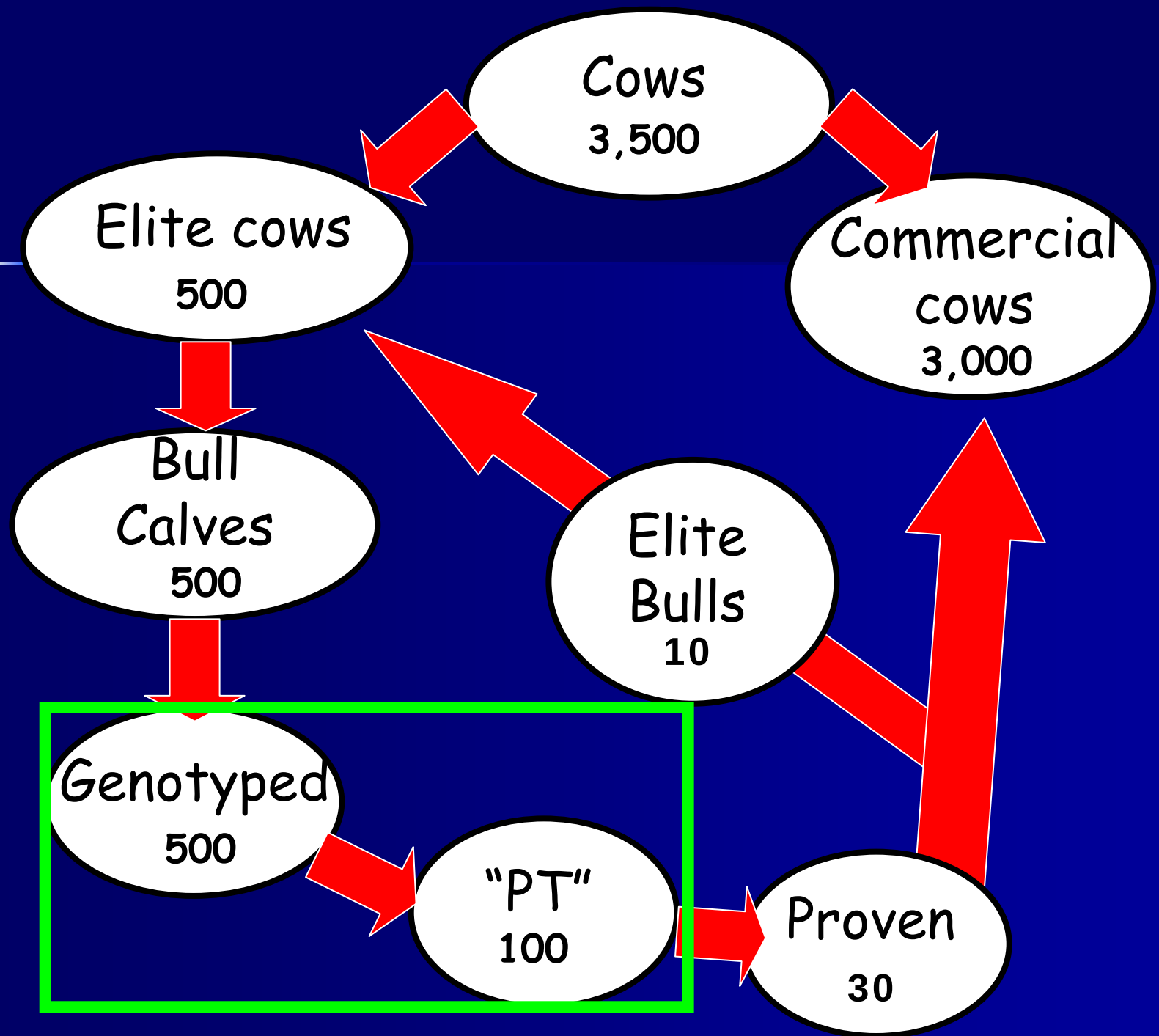
Young selection candidates with known genotypes (SNPs) but without performance records

Why use genomic selection

- Current methods of genetic evaluation based on statistical analysis of performance data
- Takes time for a bull to generate sufficient daughters to achieve high reliability
- Tool for more accurately identifying genetically different animals at a younger age, with no phenotypic information required
- Increased genetic gain, reliability and reduces the generation interval

Key Questions for Ireland

- Aim to design a optimal breeding program for Ireland, taking into account costs and benefits and the management of inbreeding
 - How many bull calves should be genotyped per year
 - How many bull calves should be progeny tested
 - How many bulls should be returned to AI
 - Possible role of females within the breeding program



General Scheme

- Initially 3,000 proven animals are genotyped to estimate marker effects
- Genetic marker effects are updated annually as more proven become available
- Population size;
 - Reduction in size of Irish dairy population to 3,500 cows
 - 10 elite bulls chosen as SS
 - 30 bulls chosen as SD
 - ~5% elite females chosen as DS

Variations on General Scheme

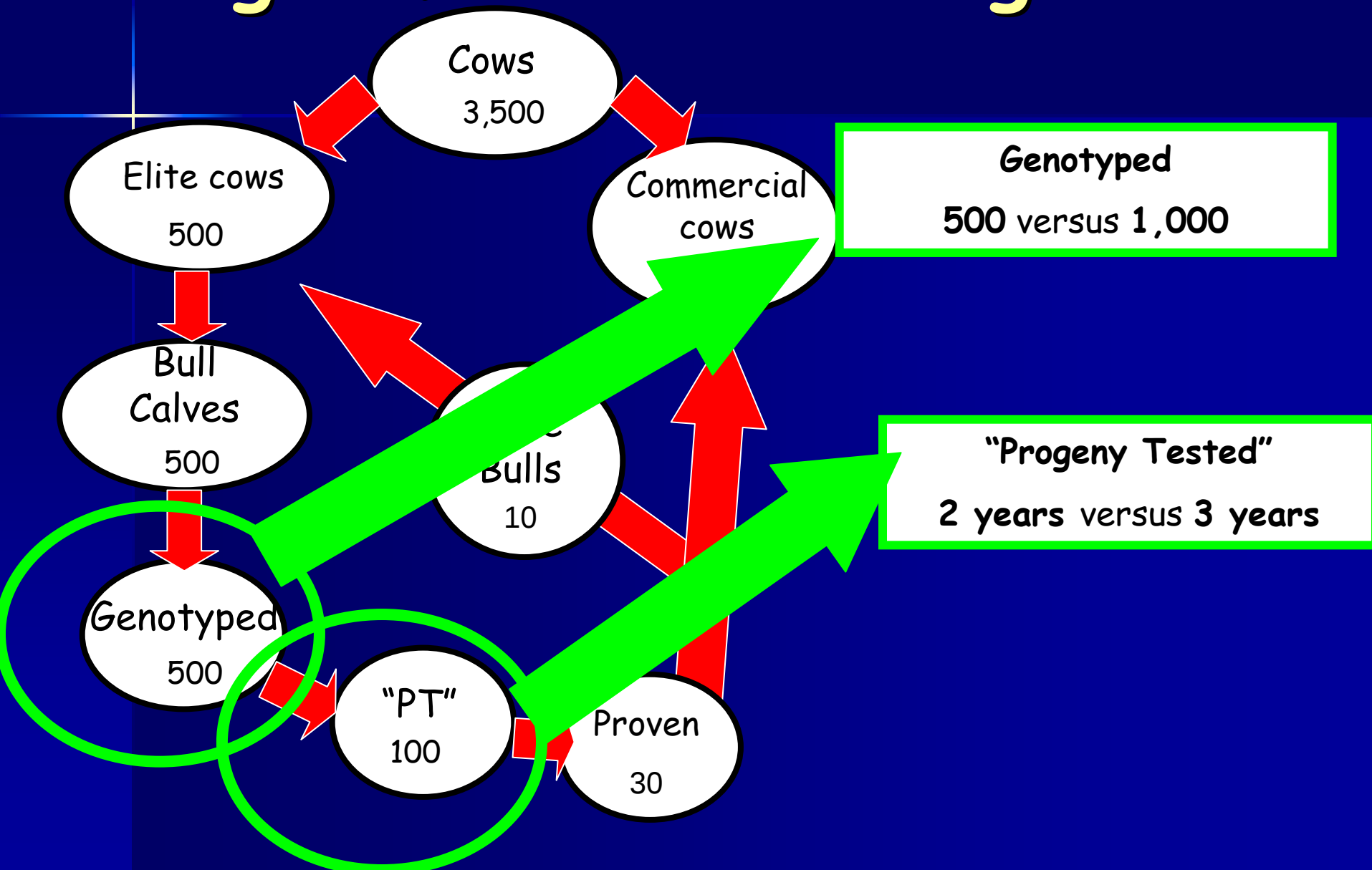
- Age at which bulls enter AI
 - 2 versus 3 years
- Number of bull calves that are genotyped per year
 - 500 versus 1,000
- Number of bull calves entering AI per year
 - 30 → 60 → 100

Genome Structure

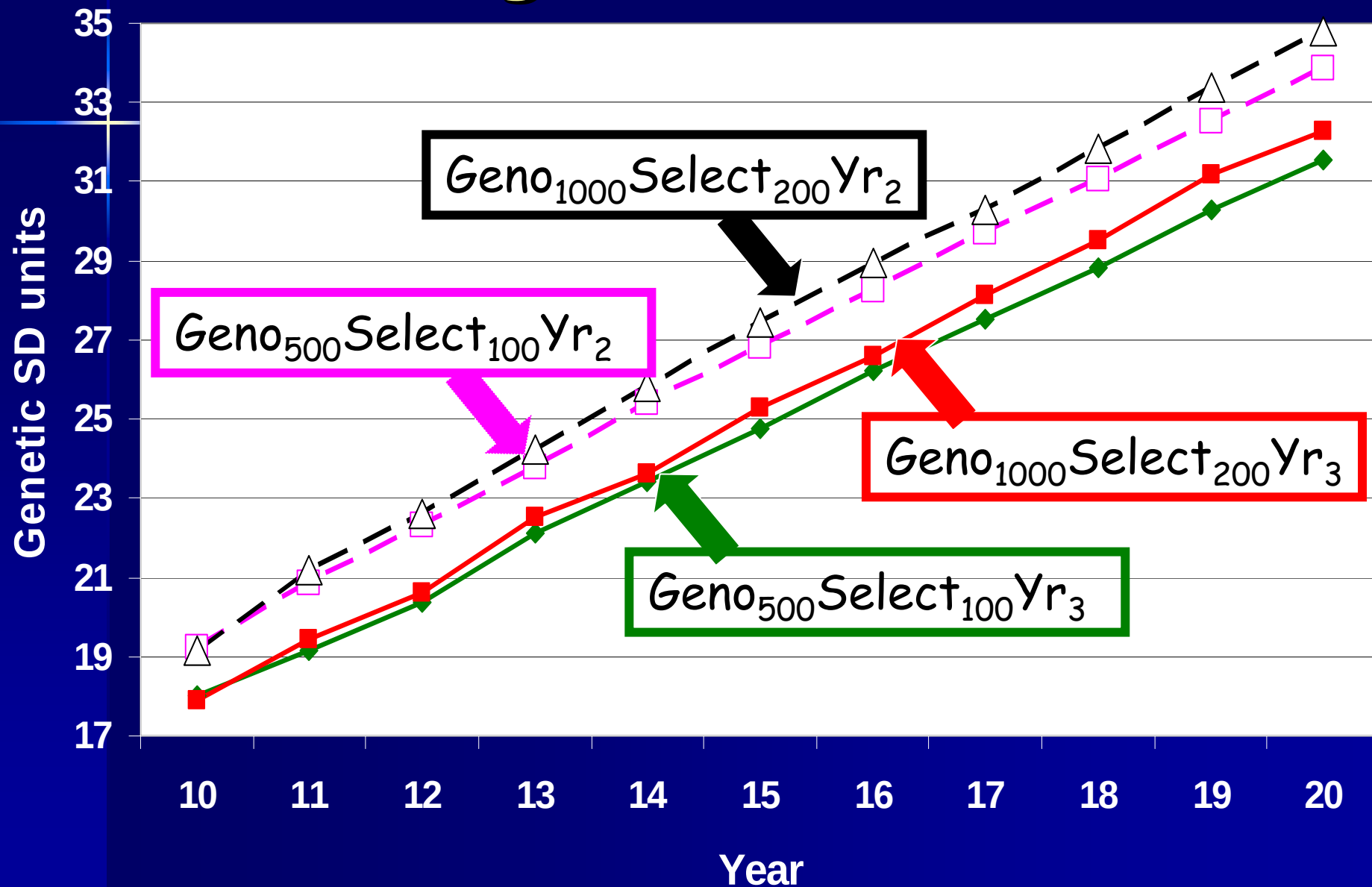
- Genome assumed 3,000 cM in length
- 15,000 SNPs → density 5,000 SNPs/cM
- 3,000 QTL (100 per chromosome)
- Marker effects estimated using GW-BLUP
- Historical effective population size 200 animals
- Heritability of trait 0.15

Age of Bulls entering AI

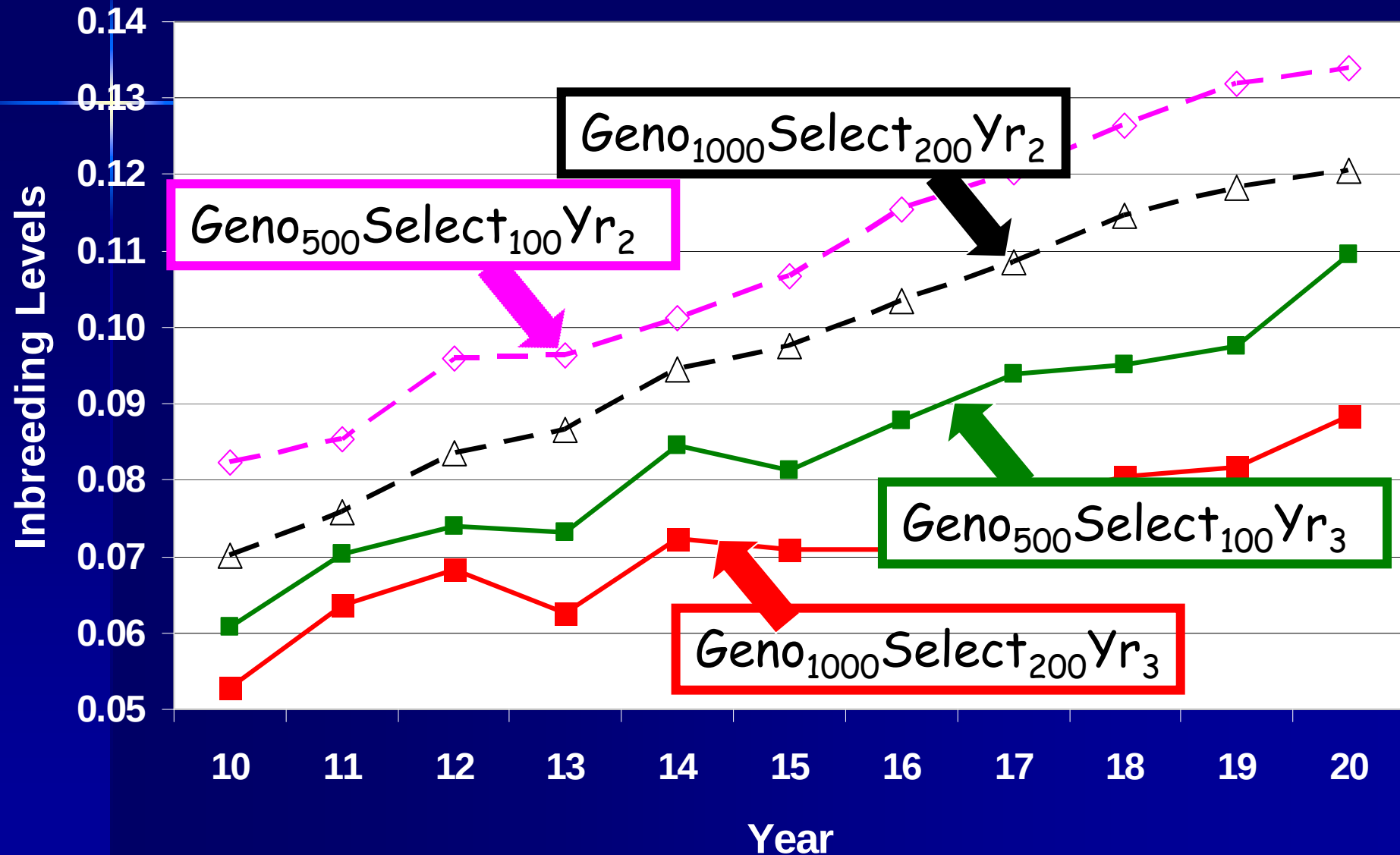
Age of Bulls entering AI



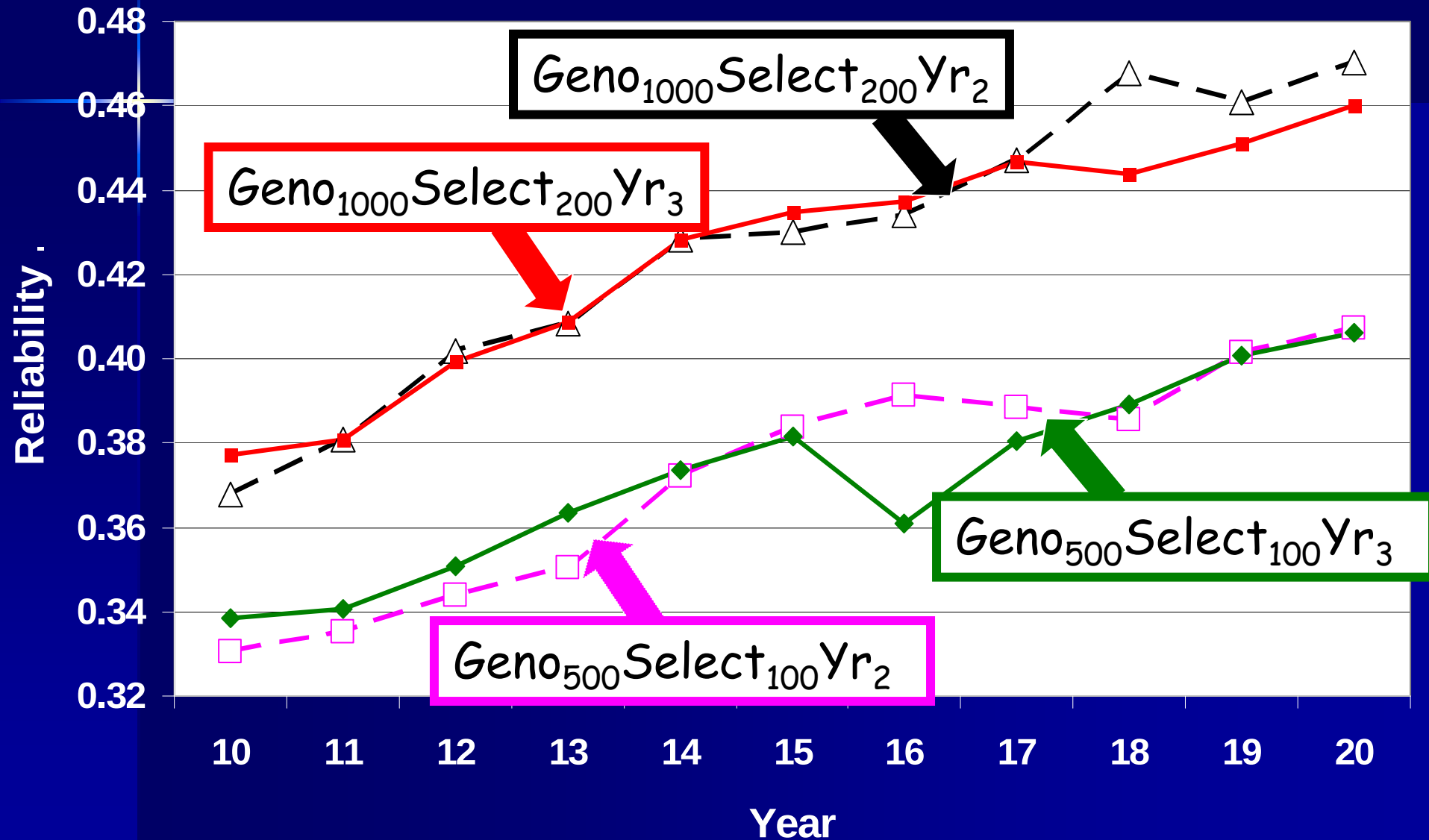
Genetic gain



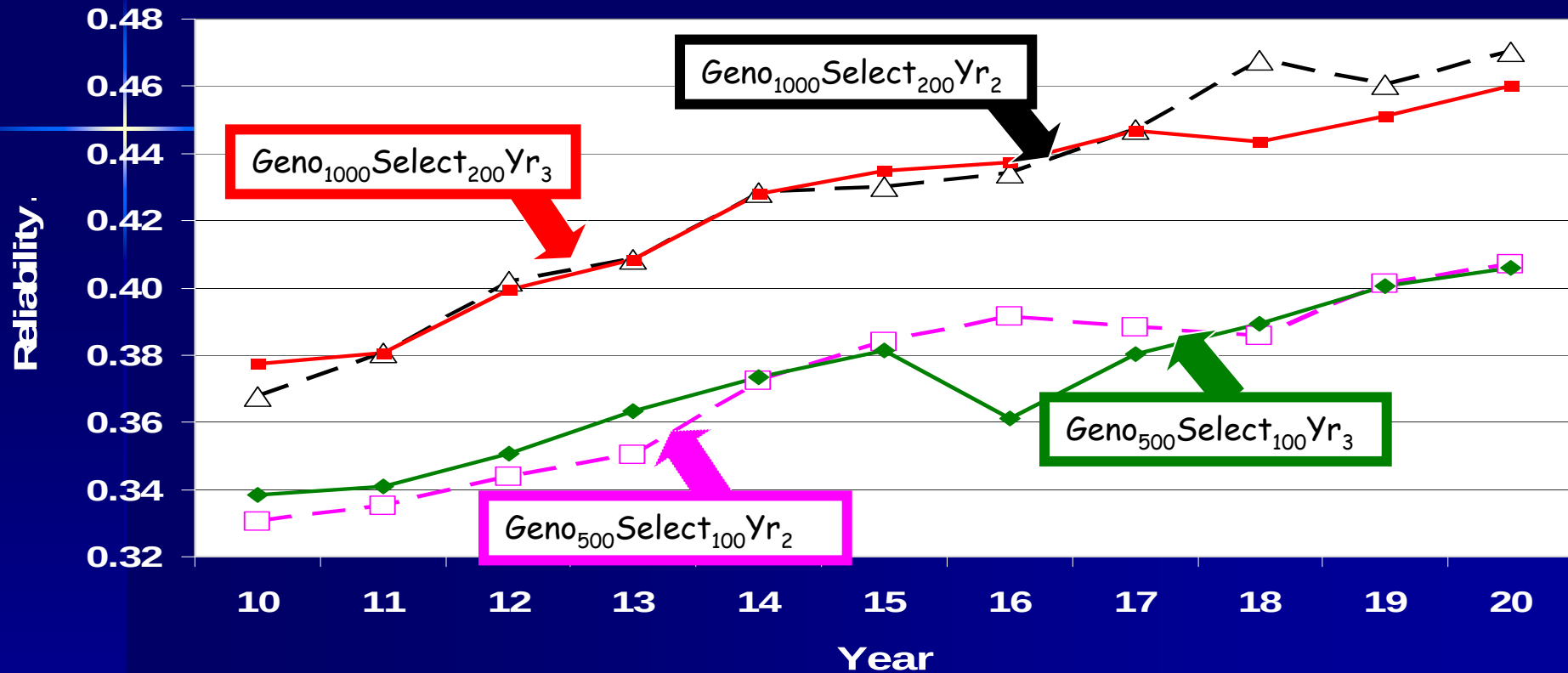
Inbreeding Levels



Reliability



Reliability



Size of Training Population

100 selected 3,400

200 selected 3,800

Summary

■ Genetic Gain

- Greater gain when selecting animals for AI at younger age

■ Inbreeding

- Higher inbreeding levels associated with animals selected at a younger age

■ Reliability

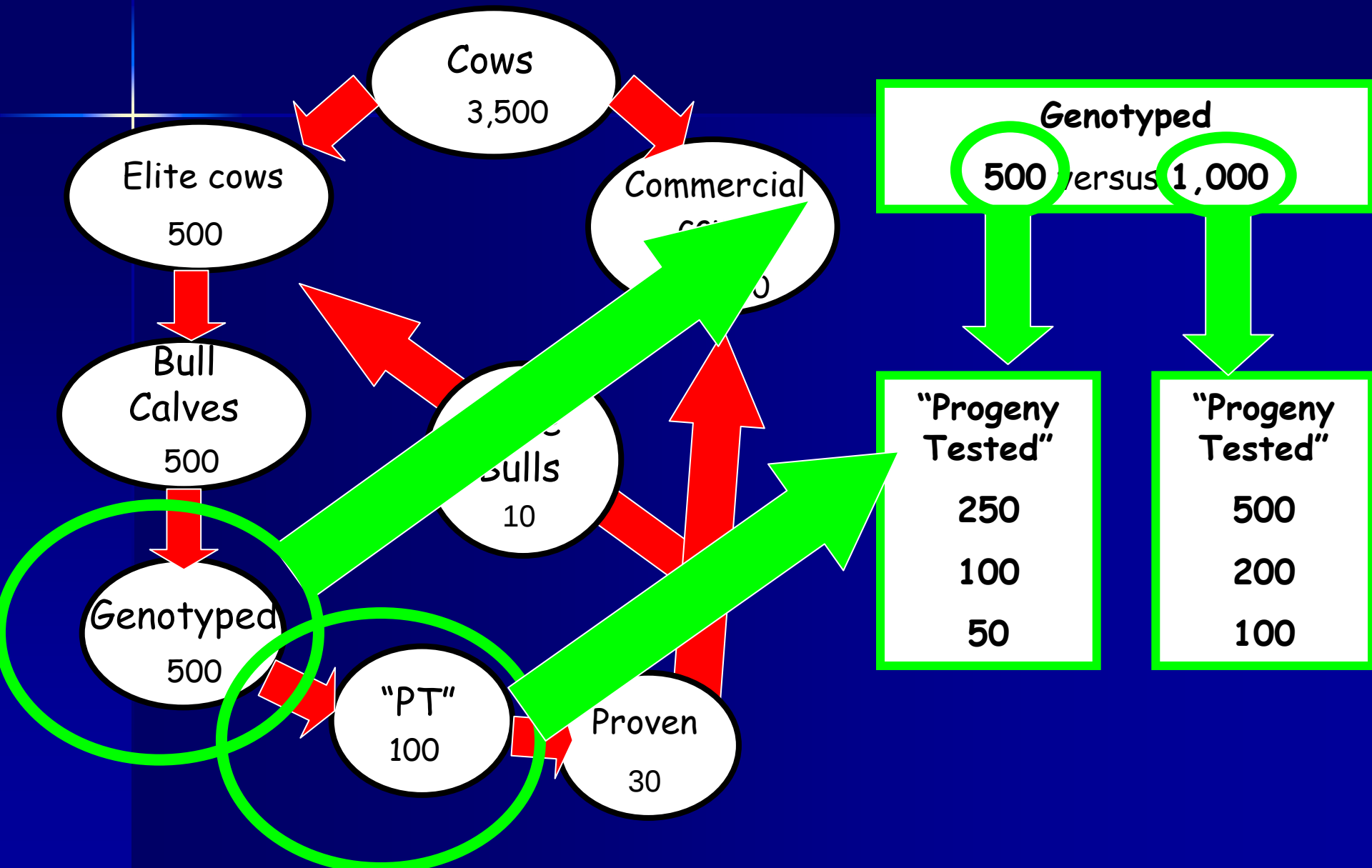
- Greater reliabilities for larger numbers entering "PT"

■ Generation Interval

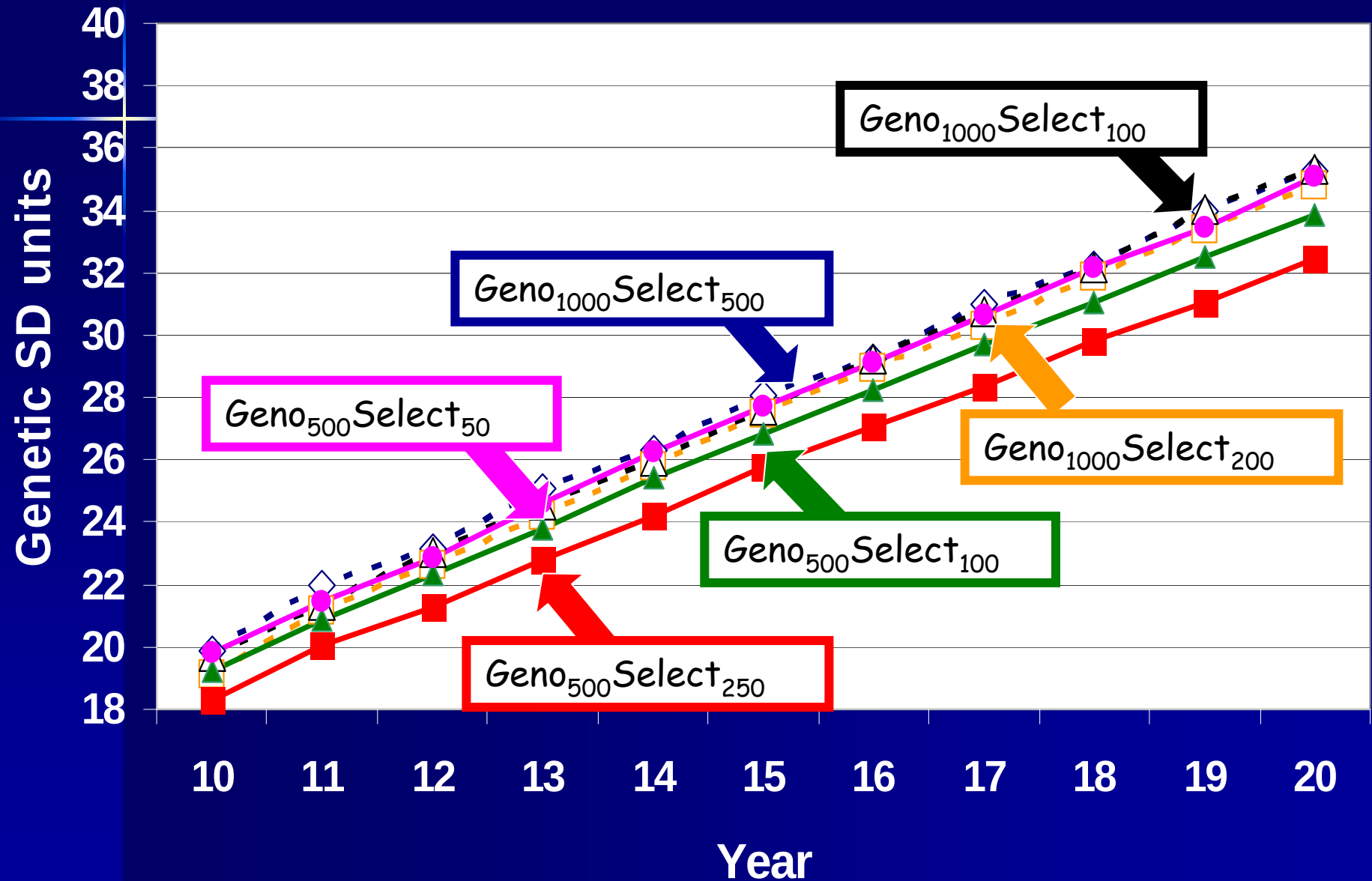
- Lower generation intervals for animals selected at a younger age

Number of Potential Candidates

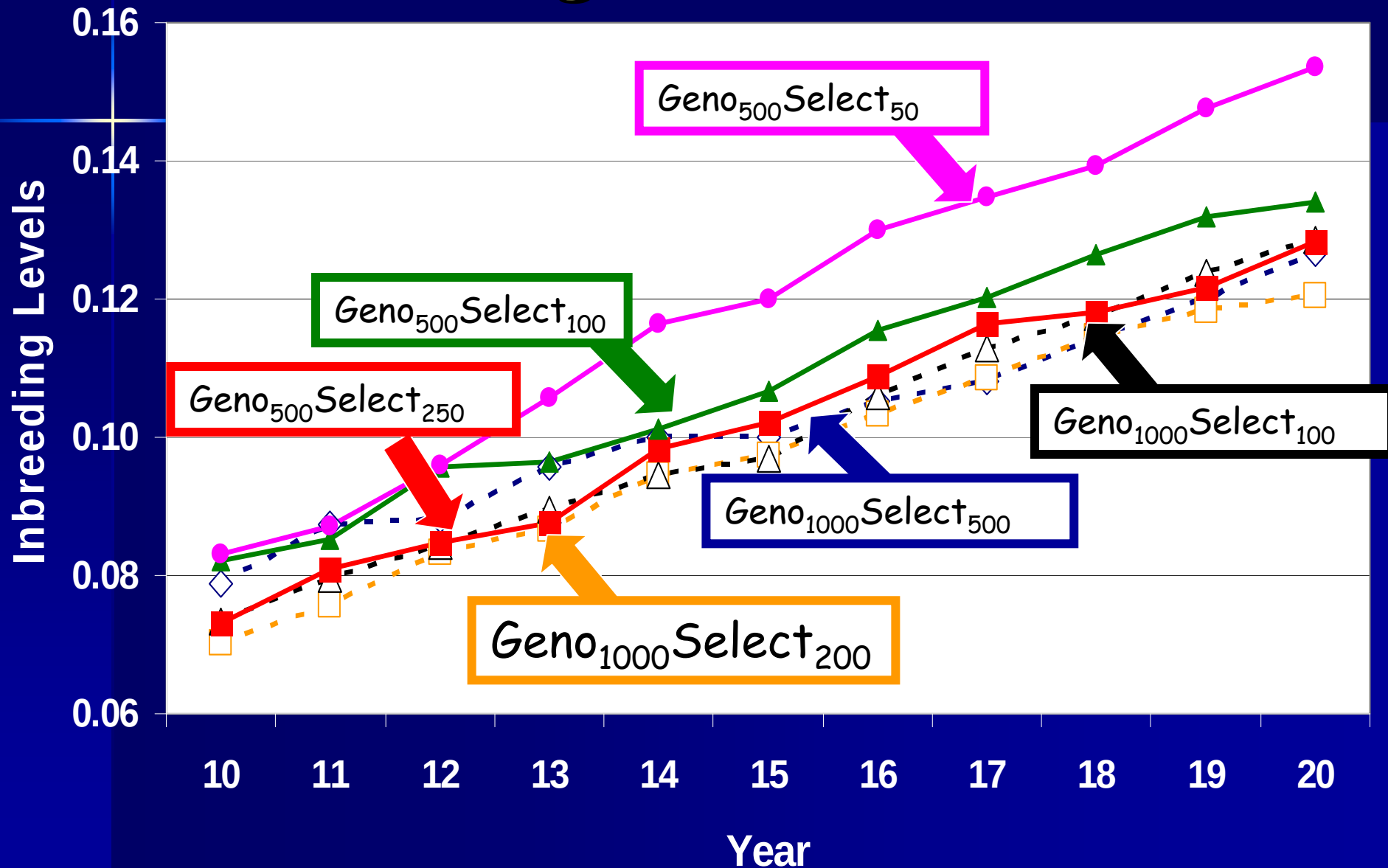
Number of Potential Candidates



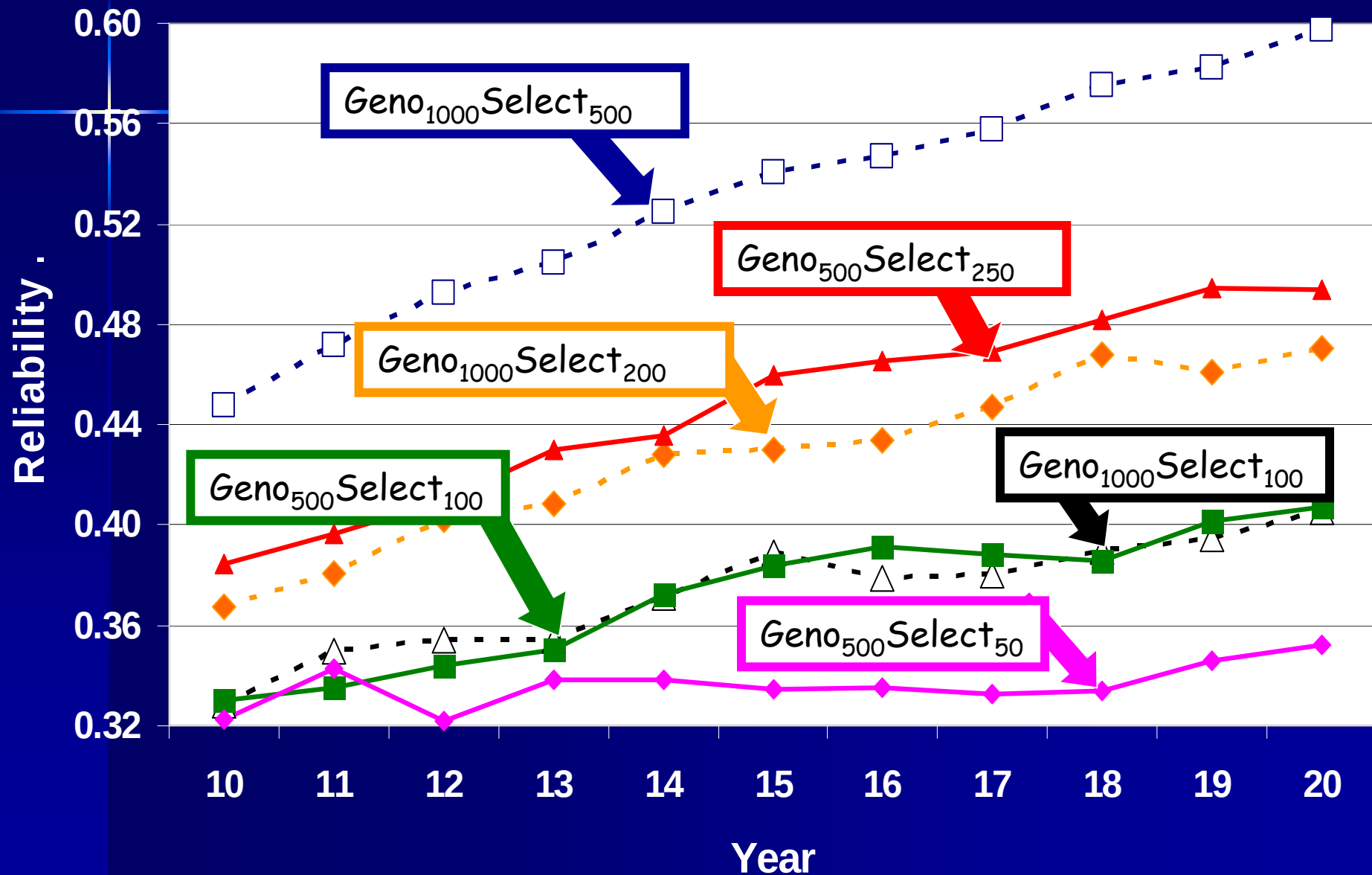
Genetic Gain



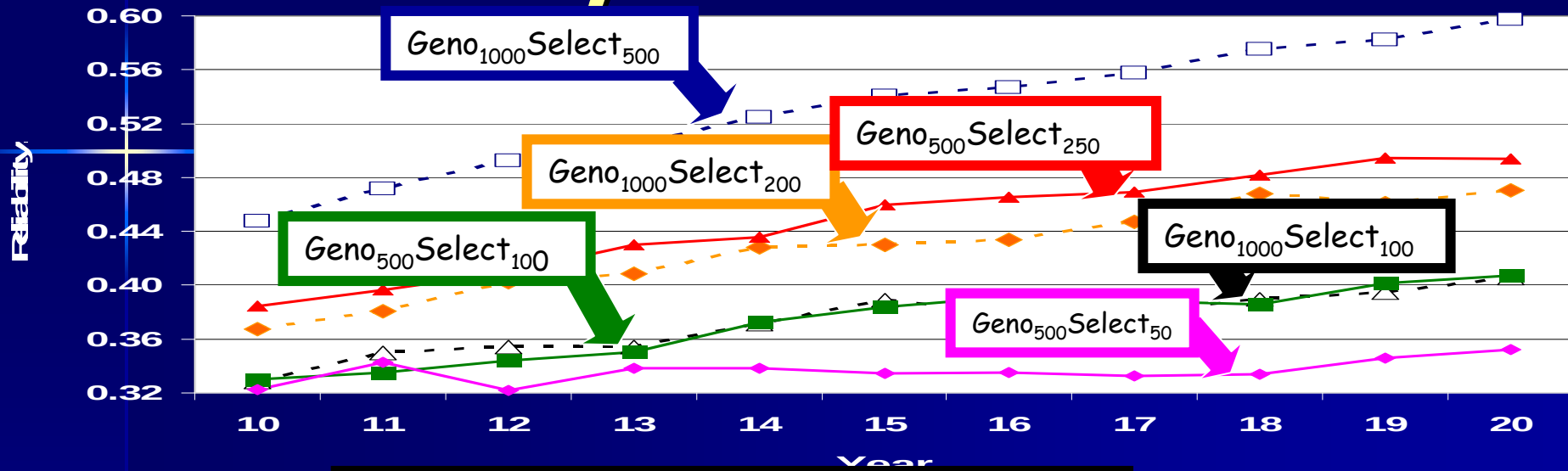
Inbreeding Level



Reliability



Reliability



Size of Training Population

50 selected 3,200

100 selected 3,400

200 selected 3,800

250 selected 4,000

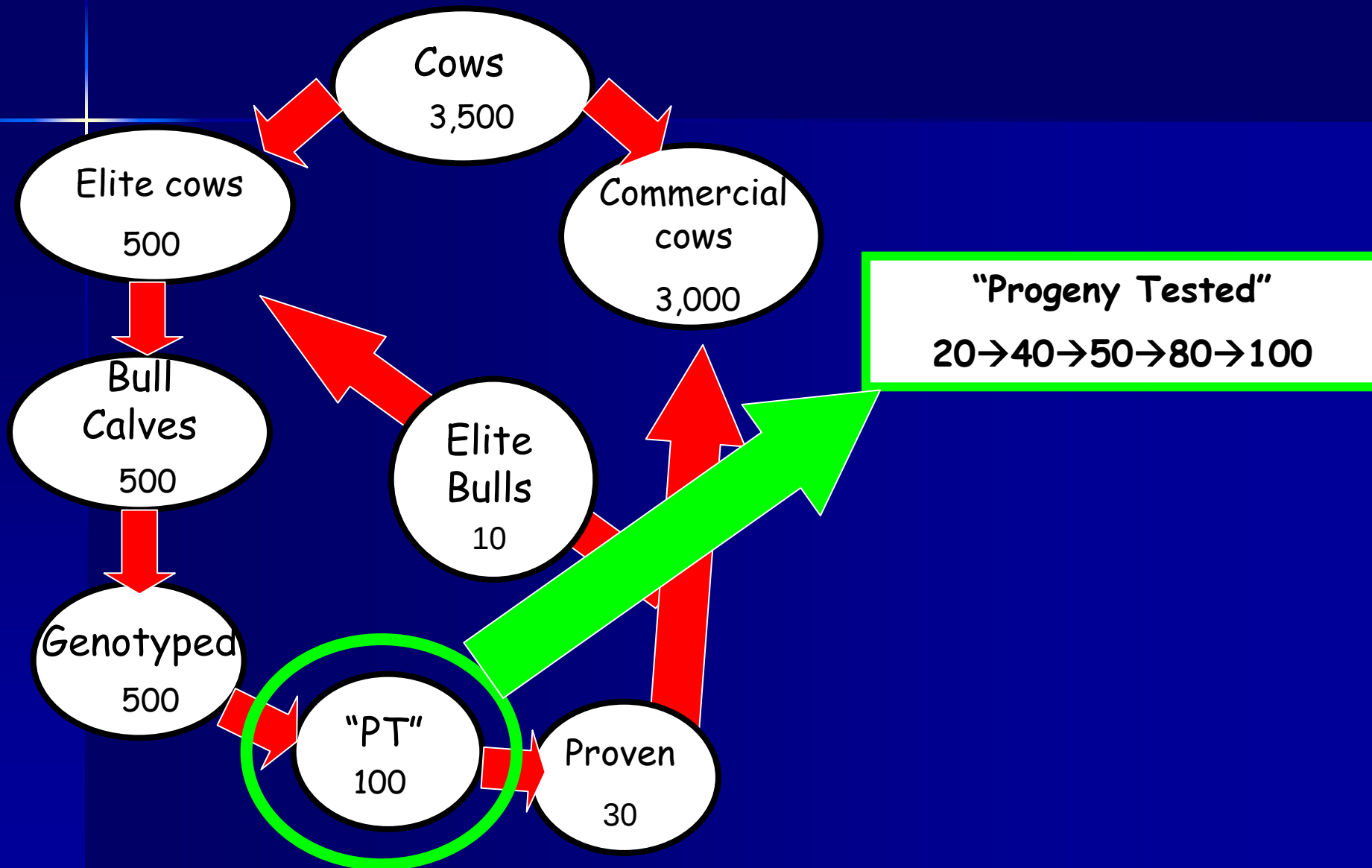
500 selected 5,000

Summary

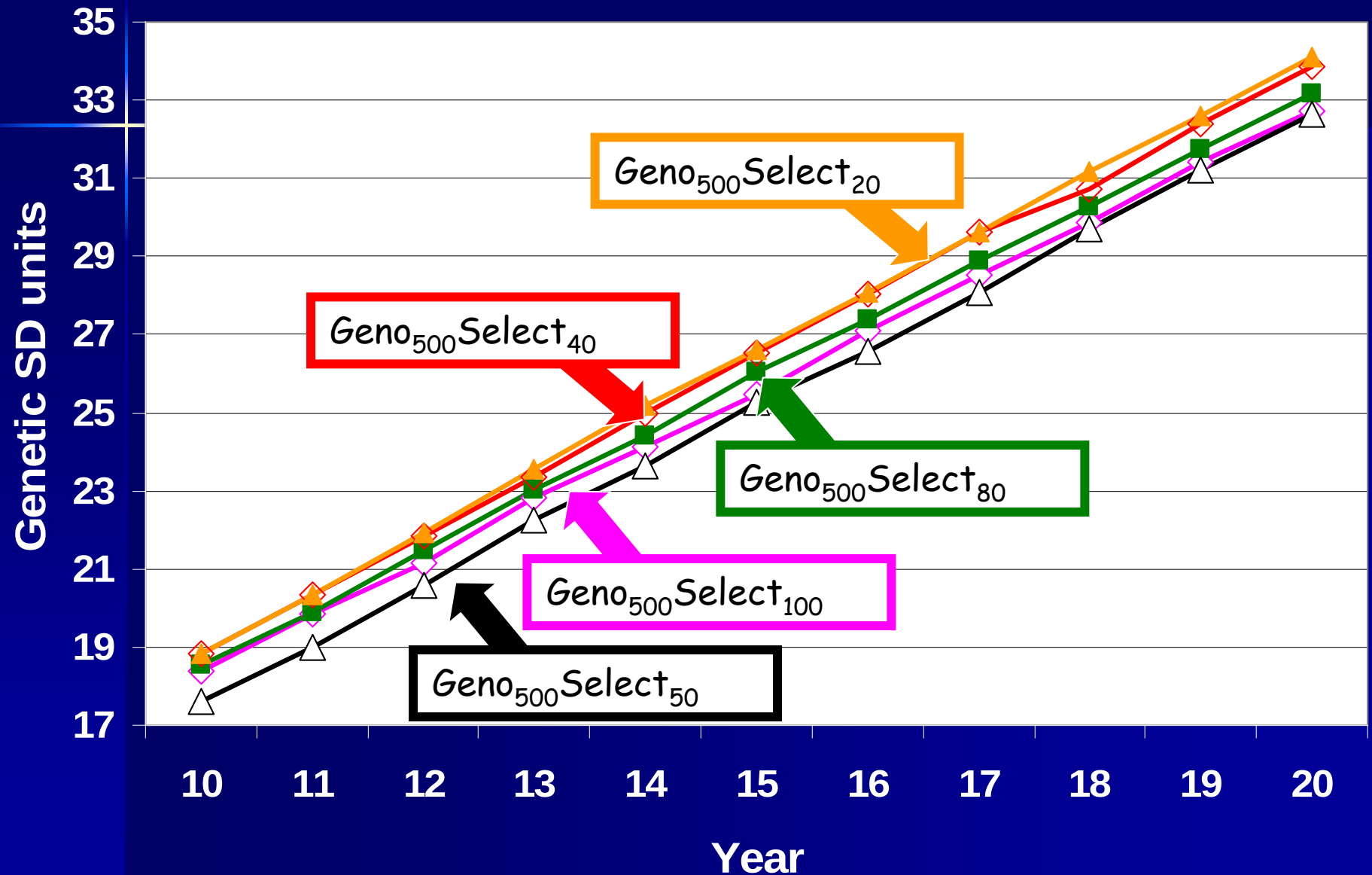
- Genetic gain
 - High selection intensity the greater gain
- Inbreeding
 - Lower numbers selected leads higher inbreeding
- Reliability
 - Greater numbers selected = greater reliabilities
- Generation Interval

**Number of Bulls Progeny
Tested**

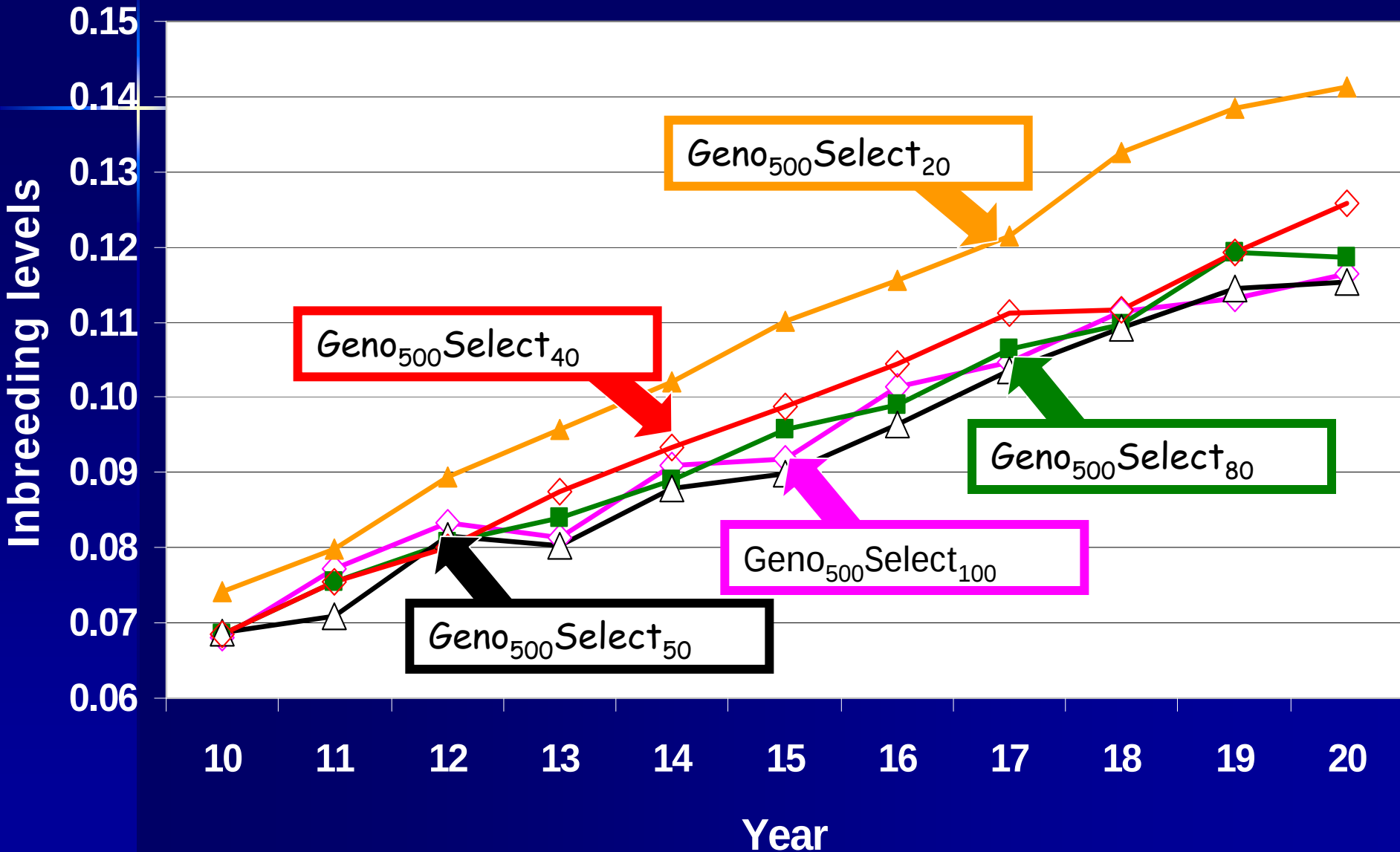
Number of Bulls Progeny Tested



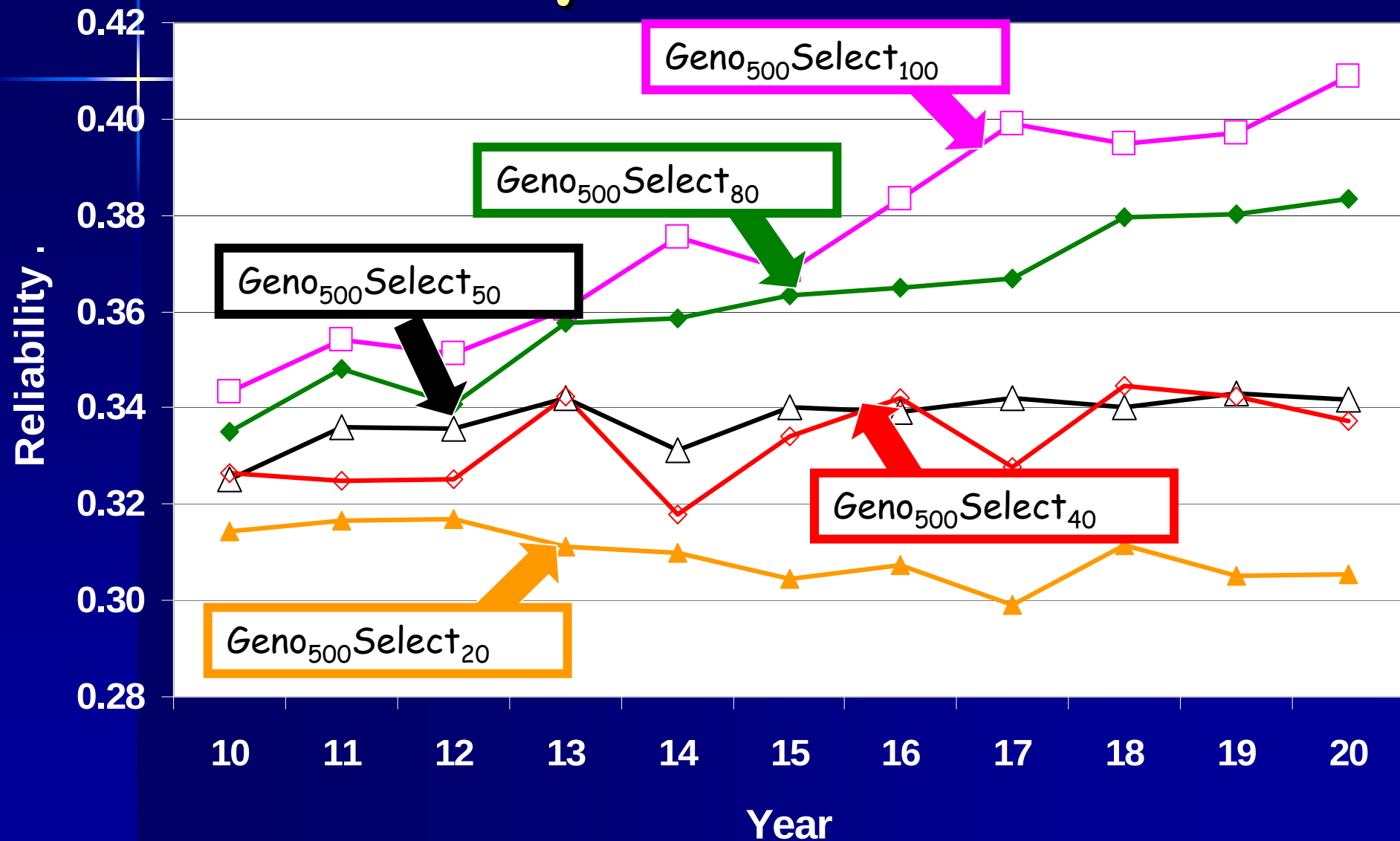
Genetic gain



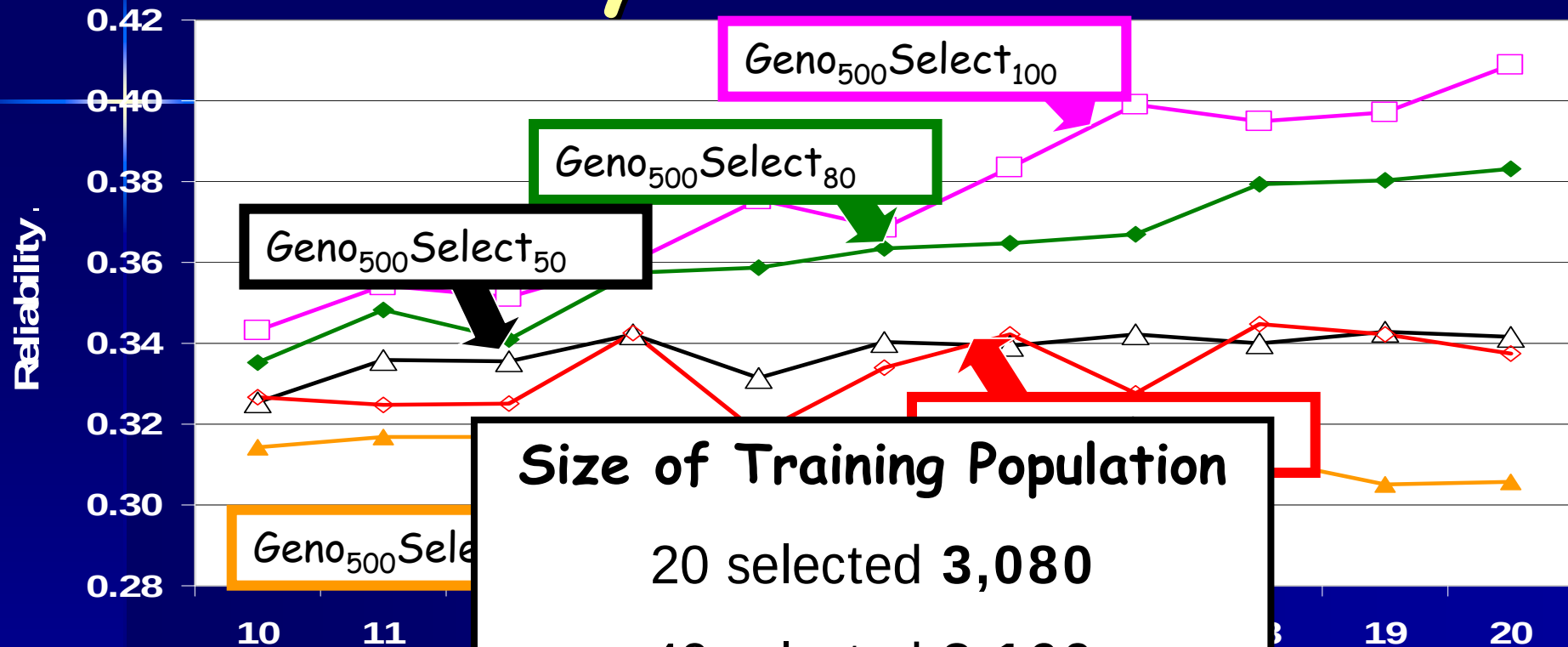
Inbreeding Levels



Reliability



Reliability



Size of Training Population

20 selected 3,080

40 selected 3,160

50 selected 3,200

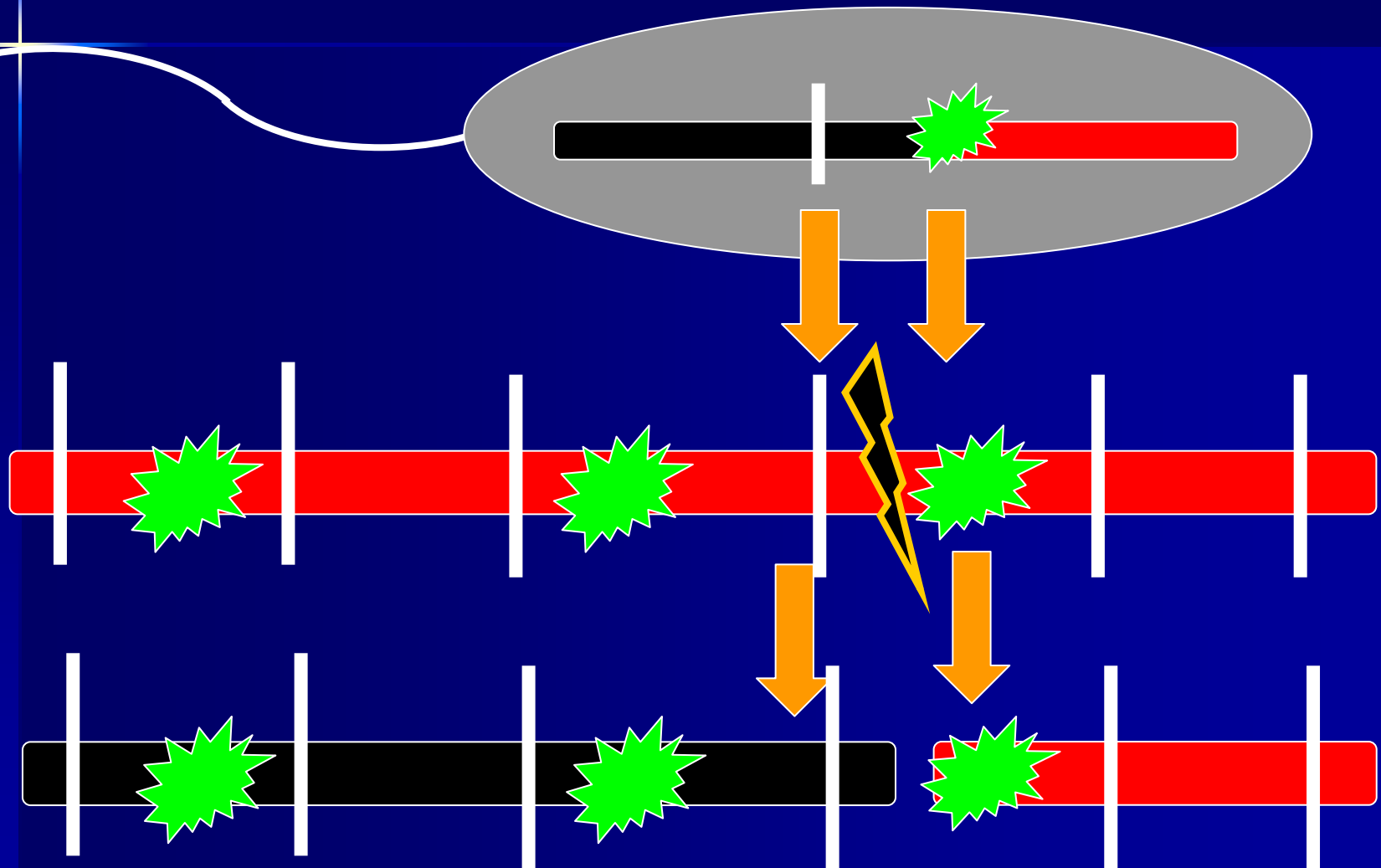
80 selected 3,320

100 selected 3,400

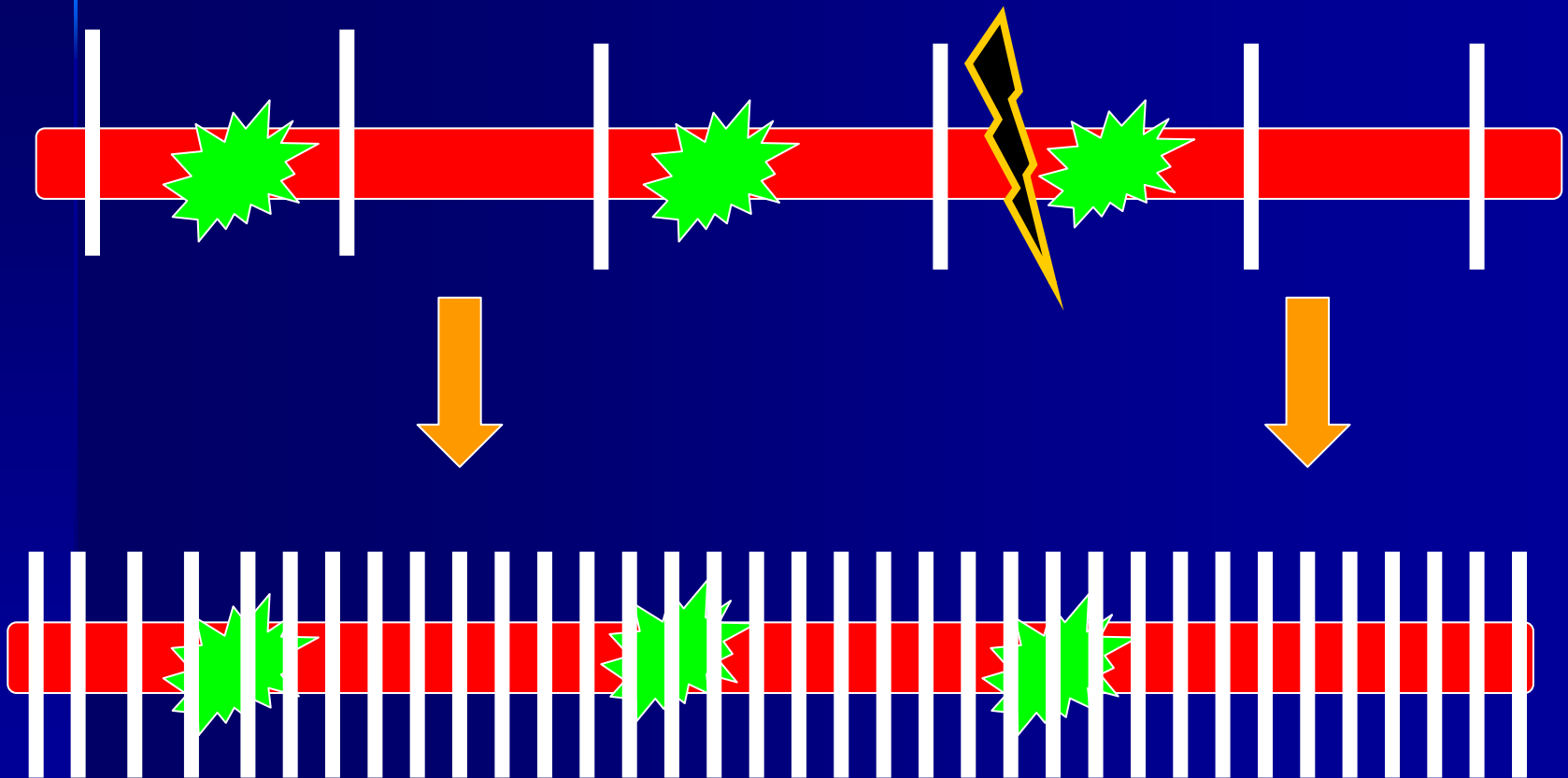
Summary

- Genetic gain
 - Little difference between schemes
- Inbreeding
 - Lower the number of animals selected
→ greater inbreeding
- Reliability
 - Higher numbers selected → higher reliability

Why retrain the Chip



Why retrain the Chip



Overall Summary

- To increase genetic gain select animals at a younger age and use high selection intensities
- The greater the number of animals selected the lower the inbreeding. Higher levels associated with younger animals
- Reliability is a function of the number of animals selected

Conclusions

- Extra genetic gain is achievable by selecting bulls at a younger age and genotyping larger numbers
- Greater reliabilities are also achievable with increasing numbers genotyped and "PT"
- However the increase in costs associated with increasing numbers genotyped and also rates of inbreeding should also be considered

Further Research

- Role of females within the breeding program
- Modifications to the breeding program?
 - Role of reproductive technologies
 - Different heritabilities
- Increasing size of SNP Chip?

Acknowledgements

ICBF for financial contribution
towards travel and subsistence

Feedback ??