Monitoring U.S. genetic evaluations for the influence of Genomic Pre-Selection

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Update on 2013 talk plus more

Measuring genomic pre-selection in theory and in practice

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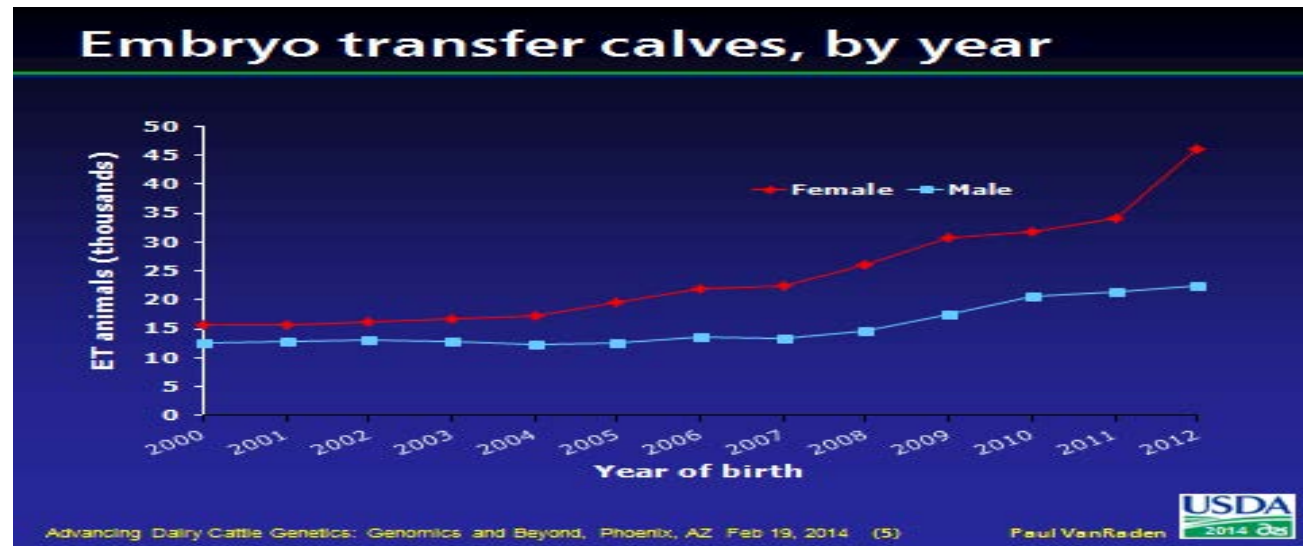
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Plan to keep genetic evaluations unbiased.

- Monitor genetic evaluations for potential sources of bias from genomic pre-selection

- Short term: as we learn more - improve current procedures.

  - Prevent genomic selection from impacting our traditional evaluations.

- Longer term: Develop better genetic evaluation models.

  - Single-Step utilizing recursion to compute the inverse of the genomic relationship matrix

Lots of Genomic Testing

Genotyped				Imputed		Total
Proven Male	**Female with records**	**Young Male**	**Female without records**	Older Female	Young Female	
26748	111685	107053	461699	3221	1499	**711905**

Growth in Embryo Transfer

Embryo transfer calves, by year

Advancing Dairy Cattle Genetics: Genomics and Beyond, Phoenix, AZ Feb 19, 2014 (5)   Paul VanRaden

Decline in number of breeders of bulls

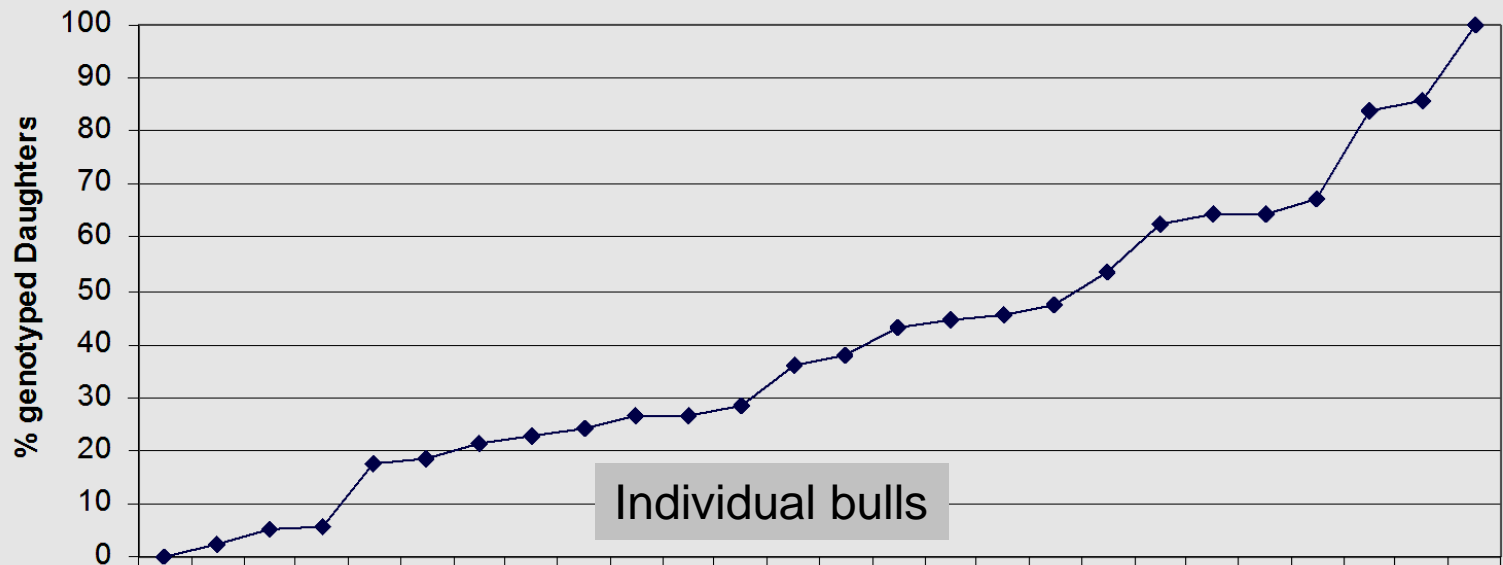| **Bull's Birth Year**		**Breeders**
2010 to 2012	Genomic era	459
2000 to 2006	Pre-Genomic	650

Top Proven Bulls*: Opportunity for Genomic Selection

10 or more genotyped daughters with a record
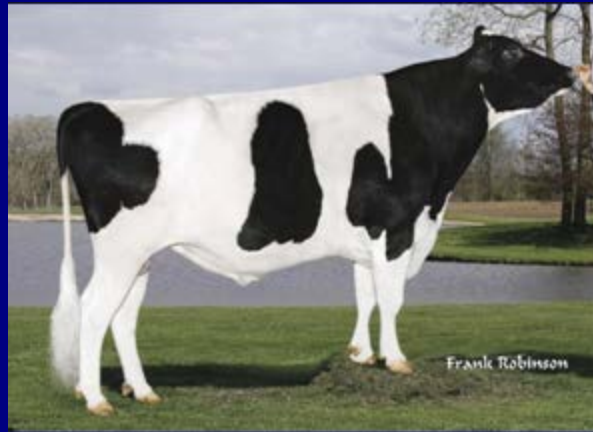
Mates
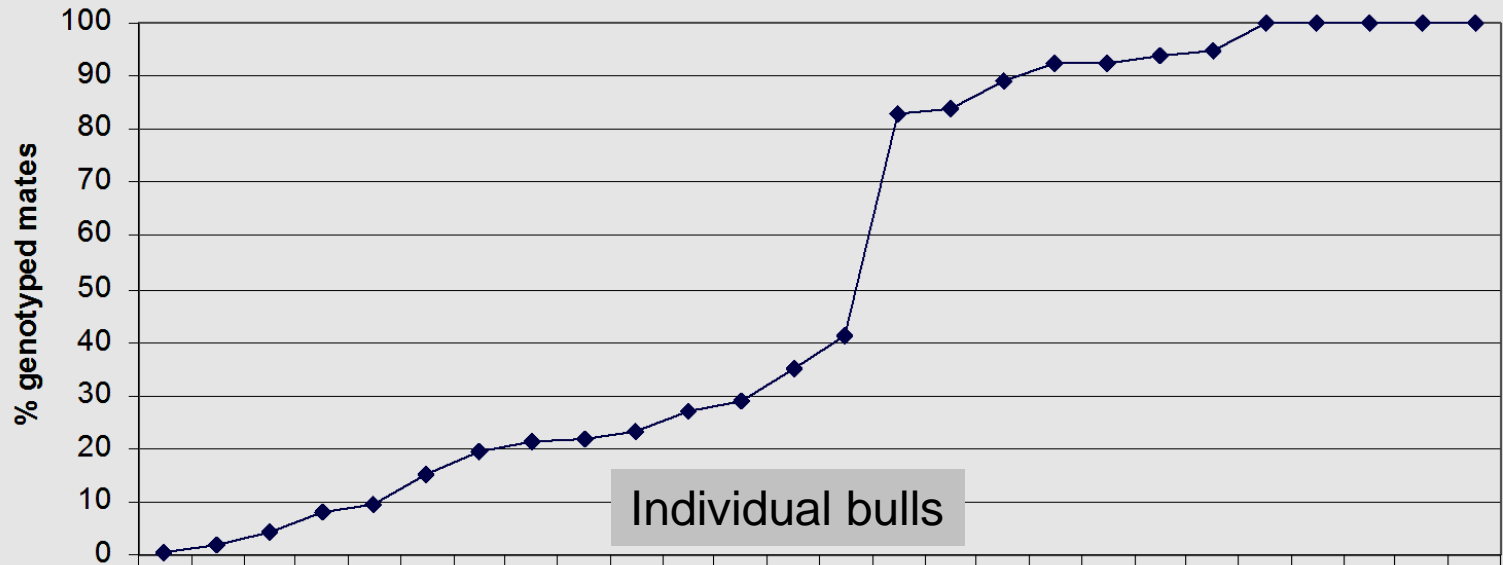
Daughters

Are some bulls being bred to "better" mates ?

- Proven bulls
  - Top 50
  - Daughters have records in 2013
  - Daughters did not have any records in 2010
  - Do Genomic PTAs of the mates differ from their Traditional PTAs?

Frank Robinson

Proven bulls from 2013 talk
Genomic Pre-Selection of mates was small

Group 1 Realized Mate Bias

Trait	Mean	SD	Min	Max
NM$	2	4	-5	13
Protein	0	0	-1	1
Prod Life	.0	.0	.0	.1
Dtr Preg Rate	.0	.0	.0	.1
SCS	.00	.00	-.01	.01
Final Score	.00	.01	-.04	.02
Udder Depth	.00	.01	-.02	.02

Interbull annual meeting, Nantes, France, August 2013 (11)   Paul VanRaden

Genomic PTA – Traditional PTA

Top 50 Proven bulls

August 2013

- Daughters have records in **2013**
- Daughters did not have any records in **2010**

December 2014

- Daughters have records in **2014**
- Daughters did not have any records in **2011**

Do Genomic PTAs of the mates differ from their Traditional PTAs?

Changes to evaluation system (December 2013)
Genomic weighting and deregression improved

- Less weight placed on cow's Traditional PTA

- Deregress the Traditional PTAs jointly across animals
  (use matrix instead of simple one at a time)
  dam only gets credit for own records and non-genotyped progeny, not genotyped sons or daughters

Modifying the deregression procedure can reduce some of the potential source of bias

Little evidence of Genomic Pre-Selection

August 2013

December 2014

Group 1 Realized Mate Bias

Trait	Mean	SD	Min	Max	Mean	SD	Min	Max
NM$	2	4	-5	13	1	2	-1	8
Protein	0	0	-1	1	0	0	0	0
Prod Life	.0	.0	.0	.1	.0	.0	.0	.2
Dtr Preg Rate	.0	.0	.0	.1	.0	.0	.0	.1
SCS	.00	.00	-.01	.01	.00	.00	-.01	.00
Final Score	.00	.01	-.04	.02	-.01	.01	-.05	.00
Udder Depth	.00	.01	-.02	.02	-.01	.01	-.04	.04

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Opportunity to select daughters based upon early genomic results
Progeny of top 50 Proven bulls
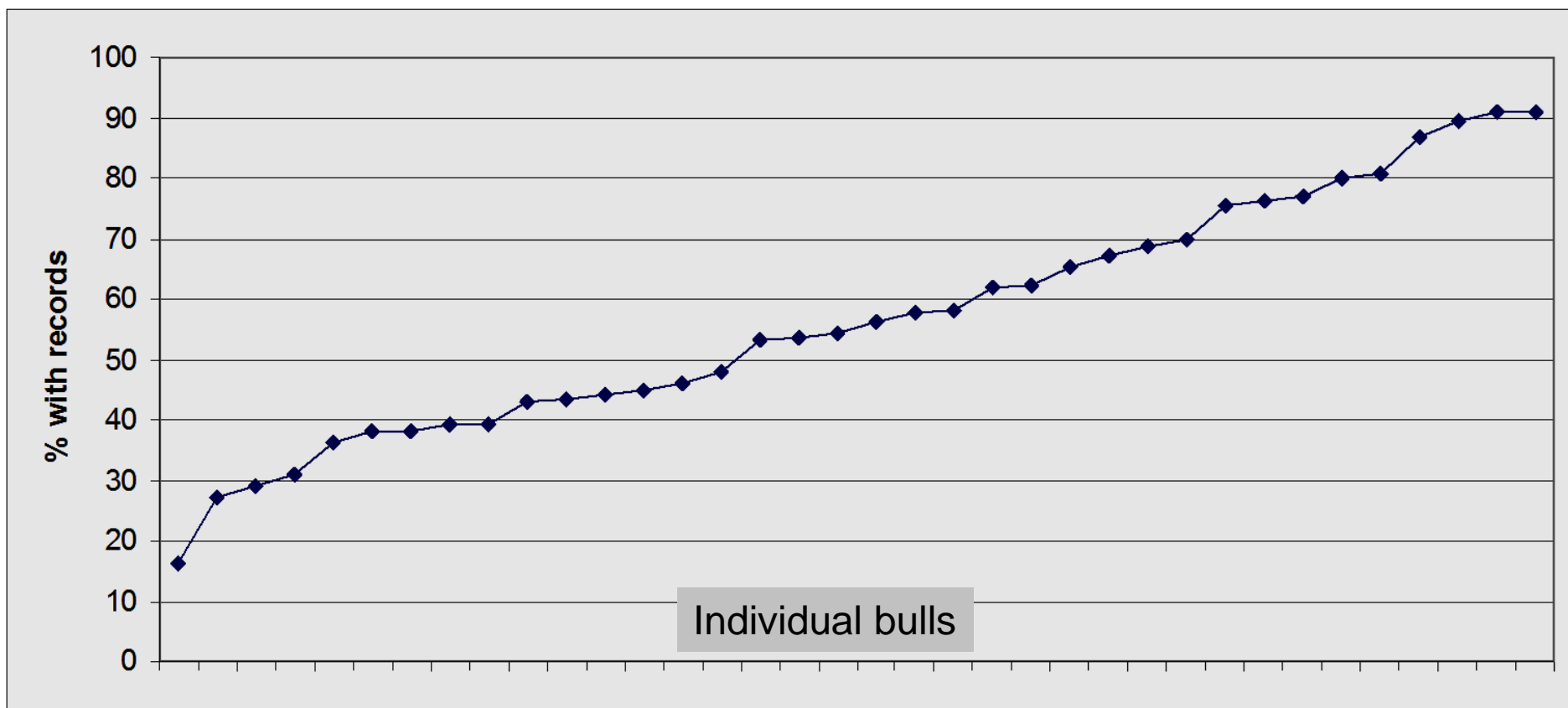
Percent genotyped daughters with Records

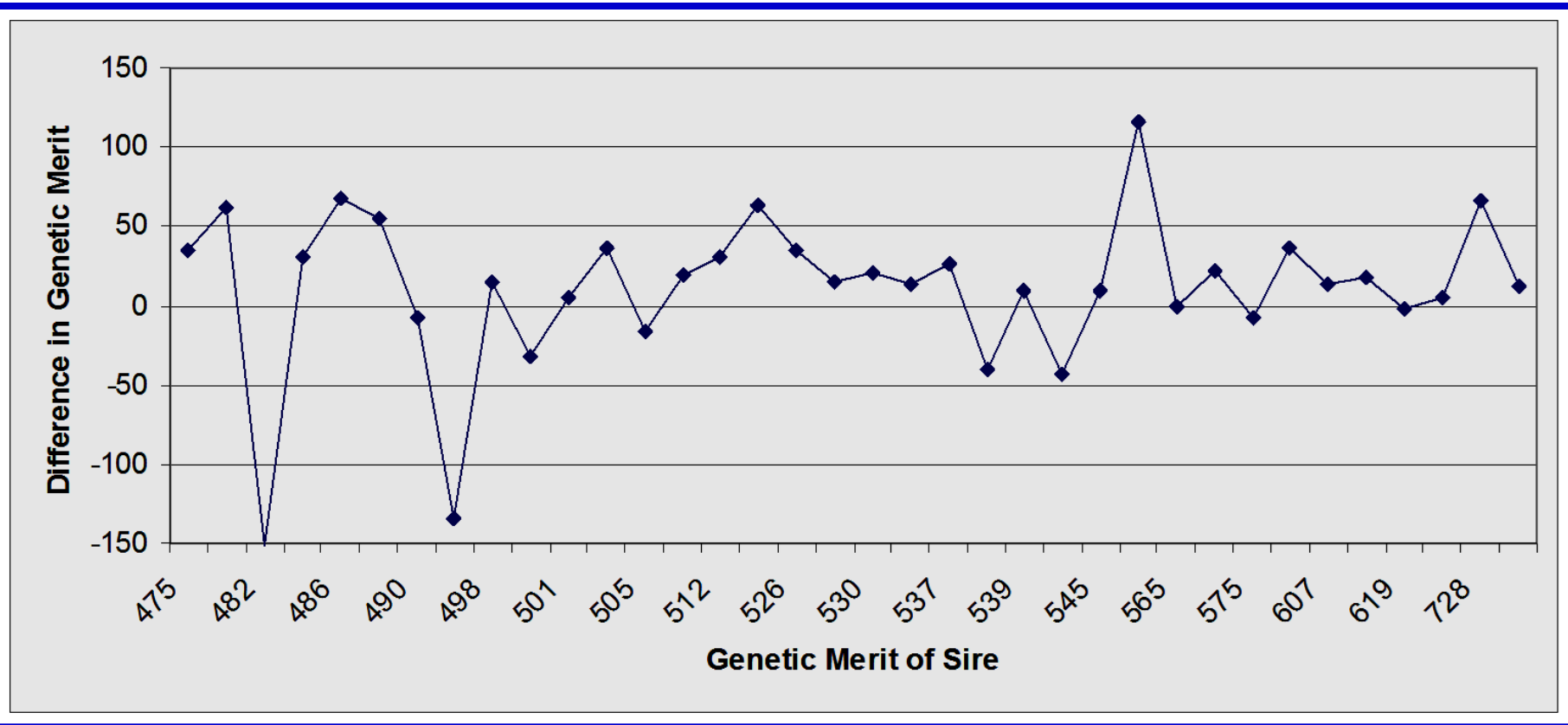# Percent daughters with records is <u>unrelated</u> to genetic merit of the Sire
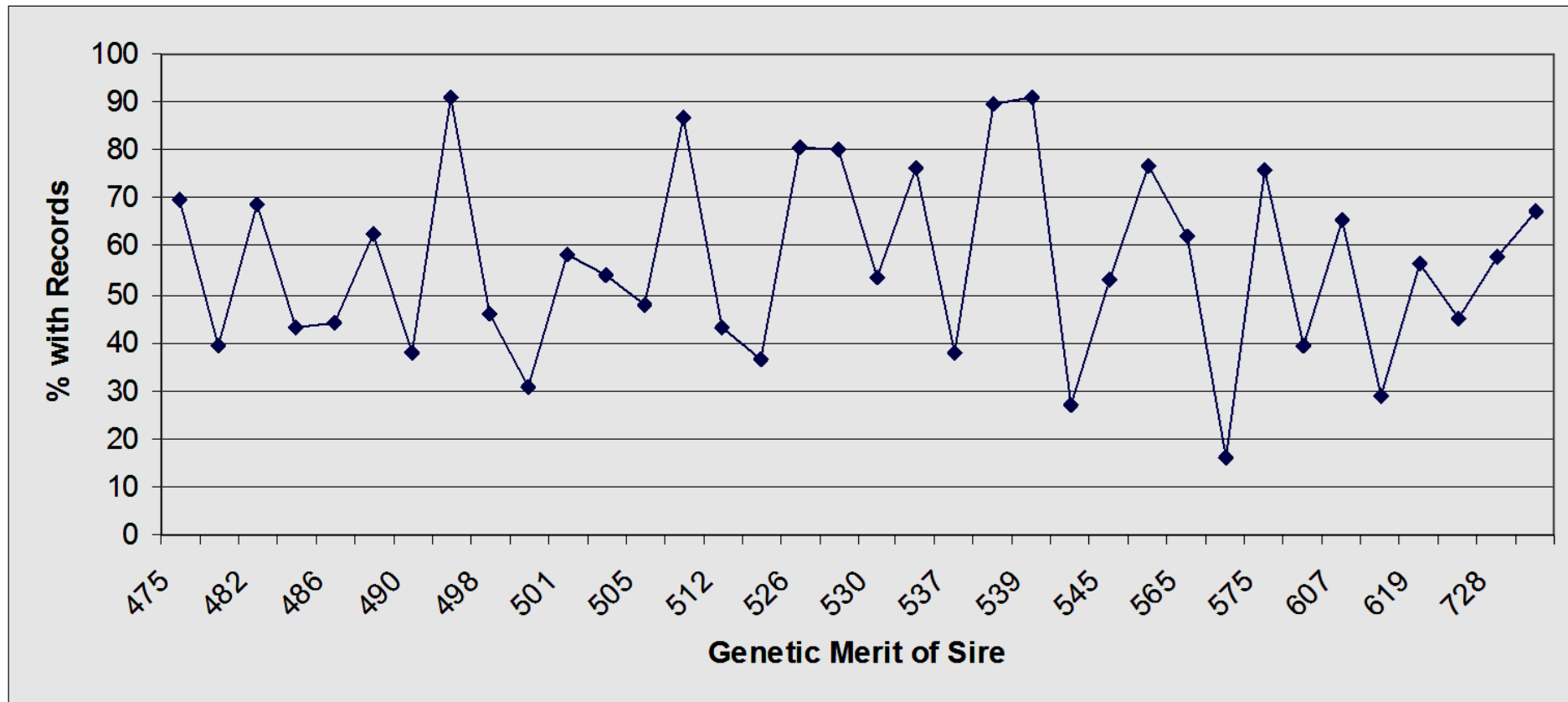
Percent genotyped daughters with Records

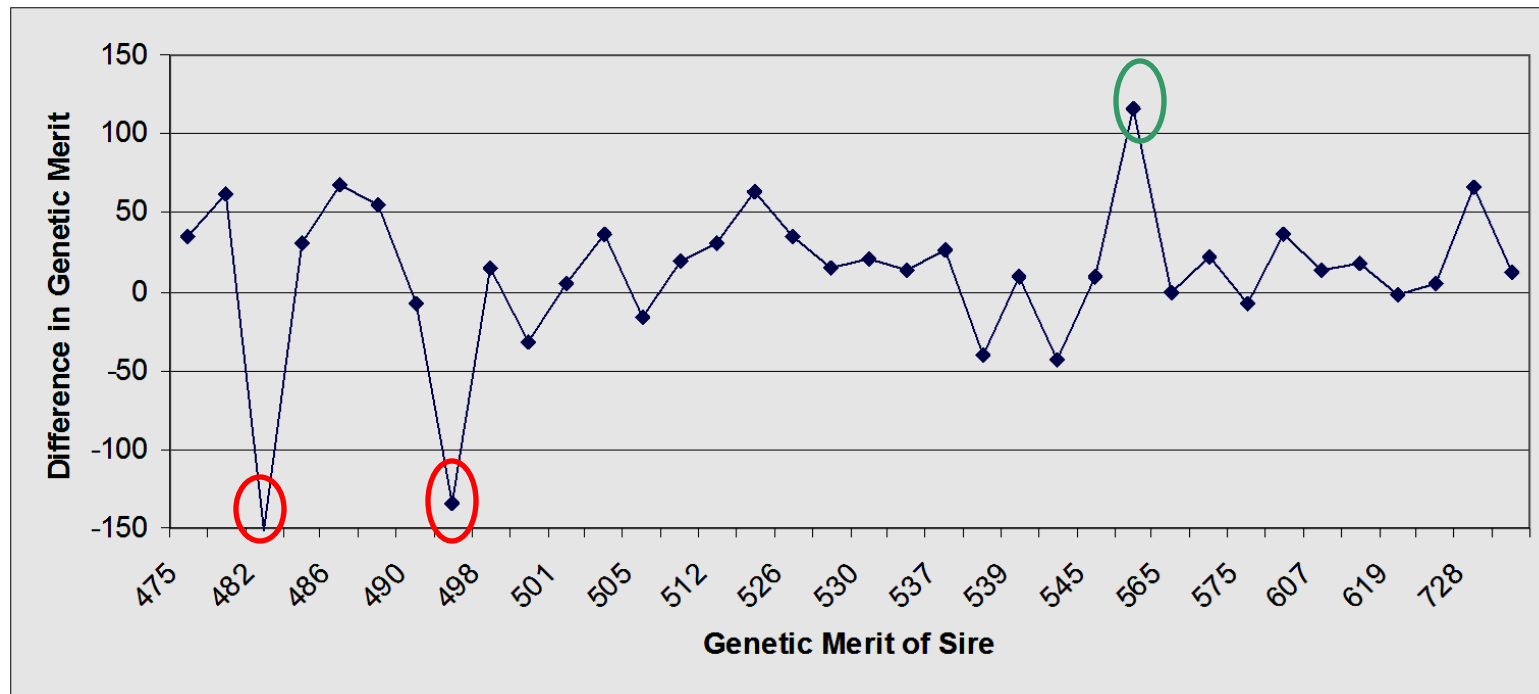# Difference between groups of daughters shows little relationship with Genetic Merit of the Sire

NM$ of daughters <u>with</u> records
versus
NM$ of daughters <u>without</u> records

Best daughters could be selected to obtain a record
or
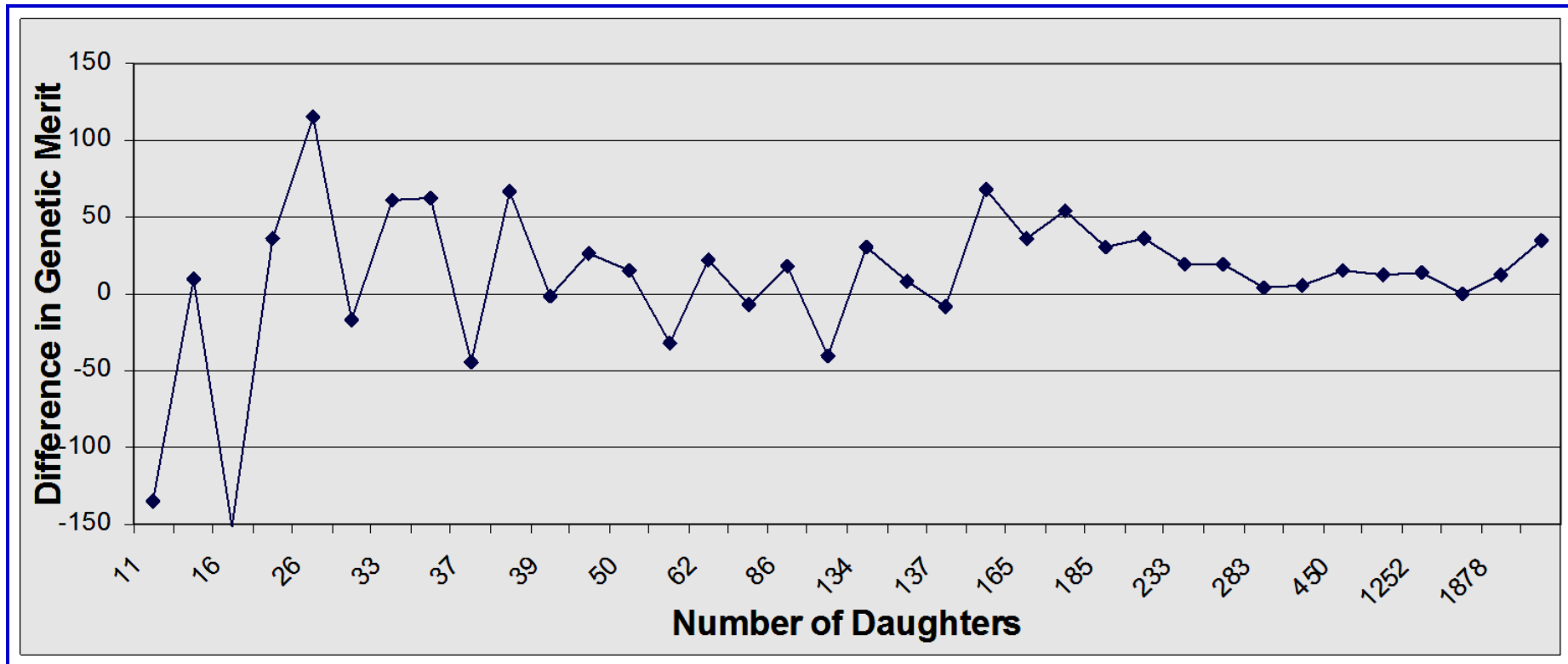# Best daughters could be selected to be flushed

Best daughters
selected to
obtain a record?

Best daughters
being flushed?

No real pattern for the daughters of the top bulls

Largest differences are related to small NUMBER of daughters

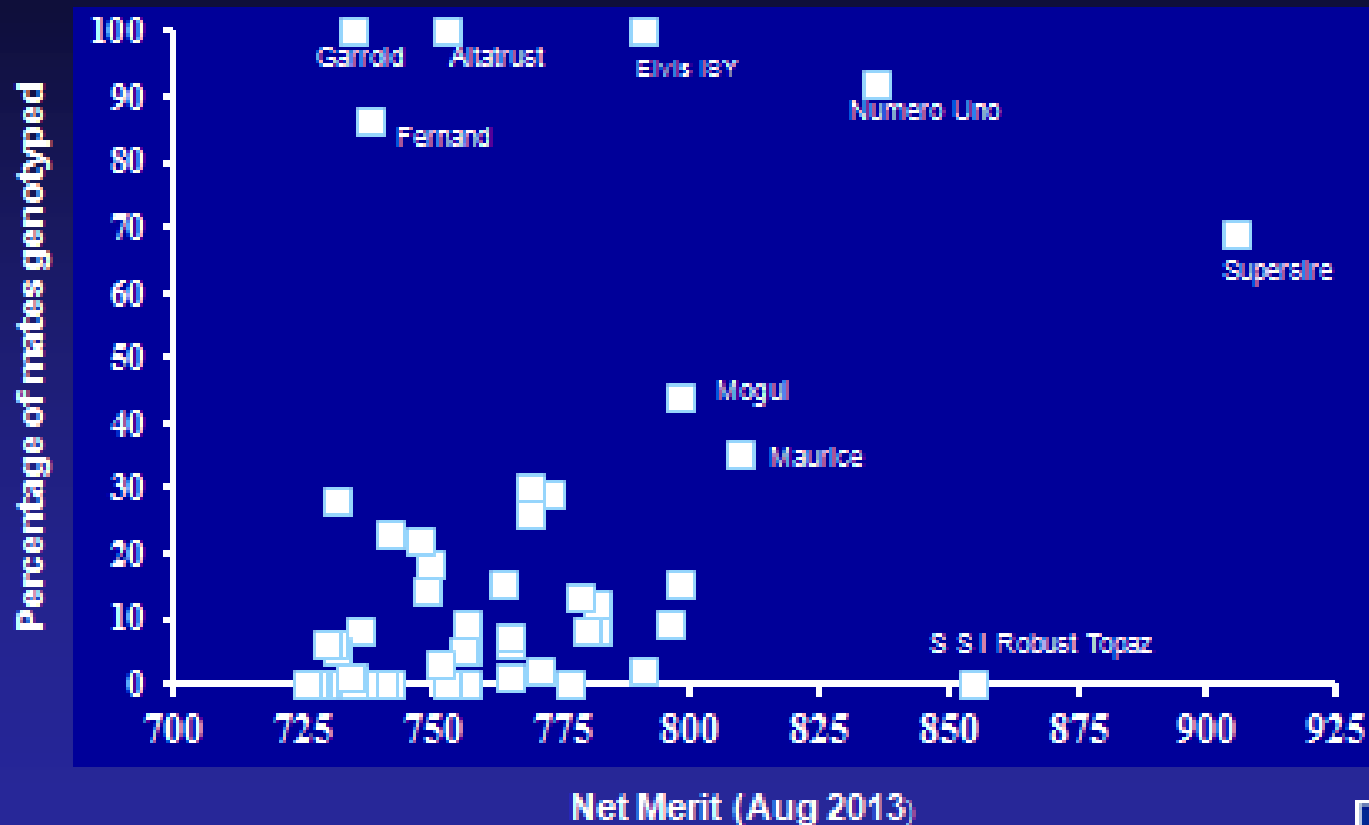Little evidence of Genomic Pre-Selection

Mates of Young Bulls

- Young bulls
  - Top 50, born 2009 and 2010
  - Study calves born in USA
  - Will pre-selected mates cause bias?

Percent mates genotyped and percent offspring born as as result of ET for top young NM bulls, Dec 2014
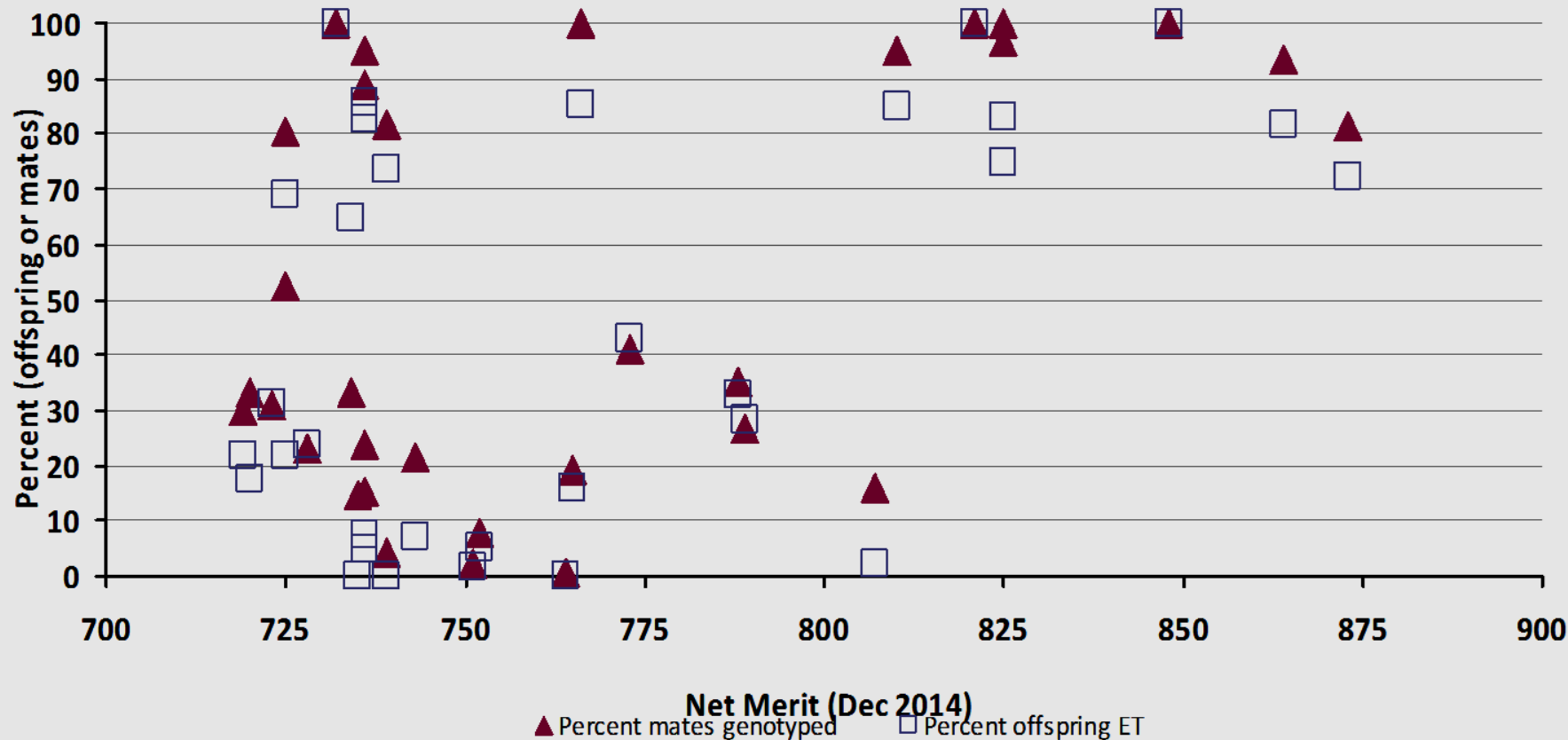
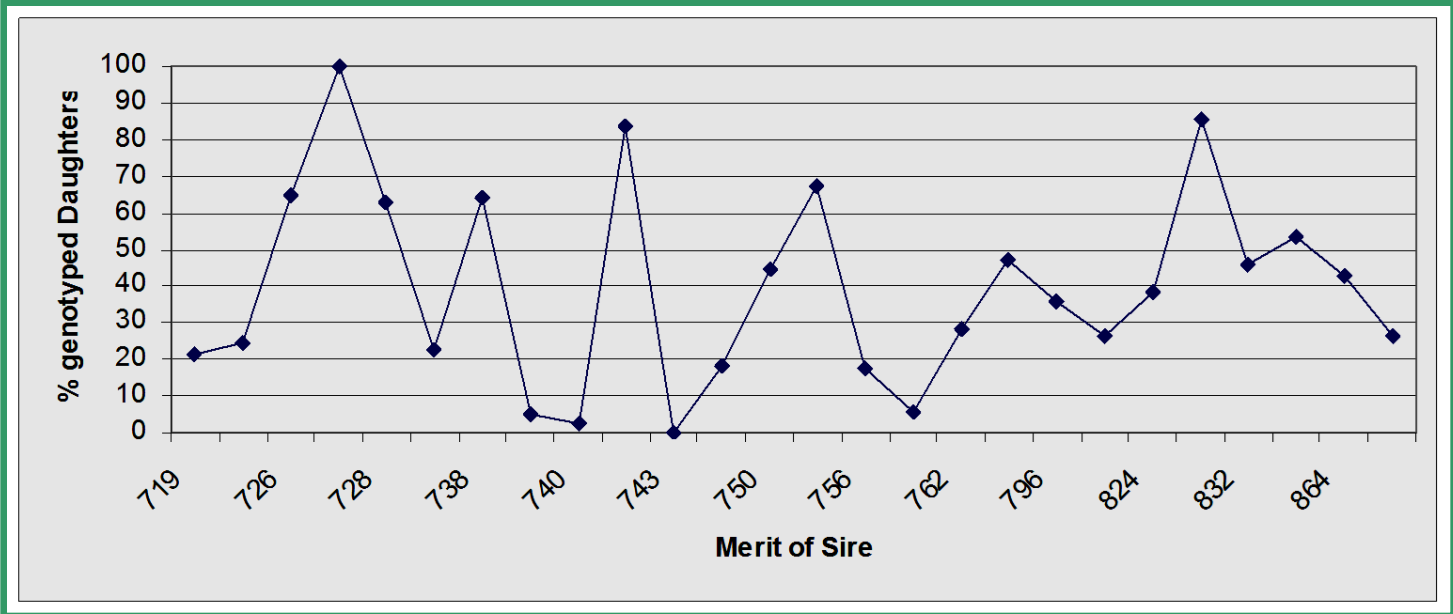# Percentage of genotyping not related to merit of Bull

Mates
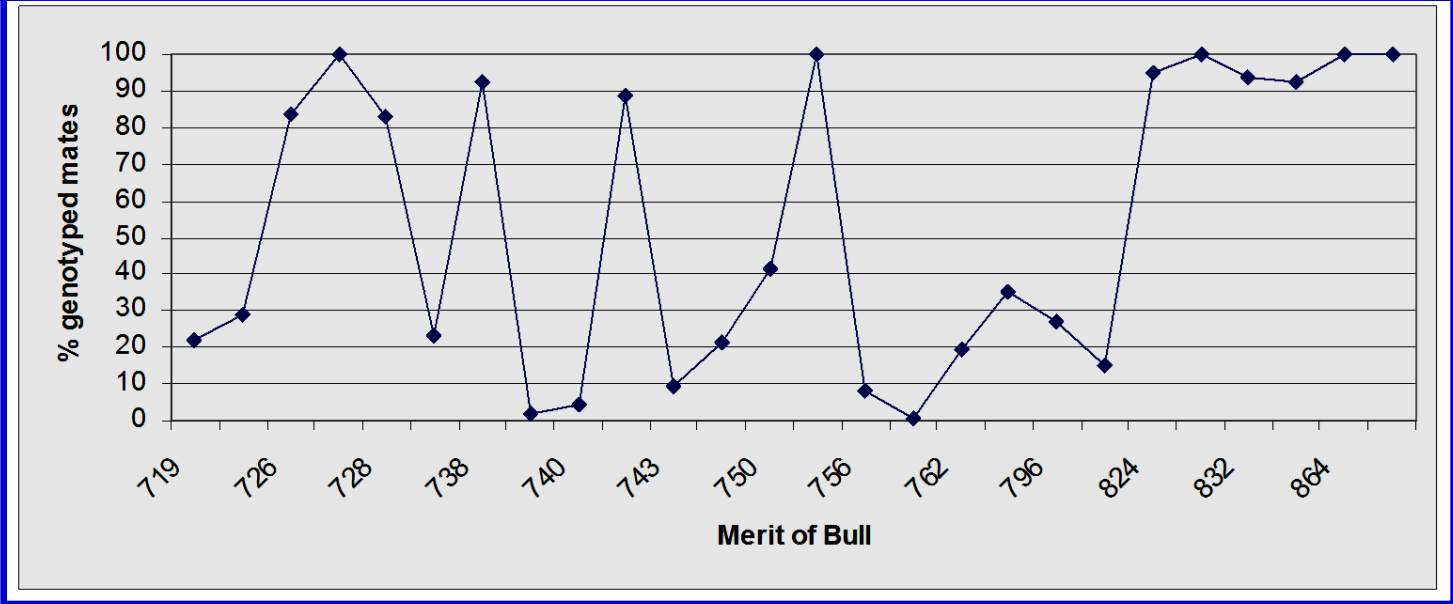
Daughters

Young bulls are used quickly and in high amounts

Little evidence showing top bulls have been selectively bred to mates with higher than "recorded" Mendelian Sampling

August 2013

Group 2 Future Bias from Mates

Trait	Mean	SD	Min	Max
NM$	8	9	0	33
Protein	0	0	0	1
Prod Life	.1	.1	.0	.5
Dtr Preg Rate	.1	.1	.0	.3
SCS	-.01	.01	-.03	.00
Final Score	.02	.03	-.01	.10
Udder Depth	.03	.04	-.01	.13

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December 2014

Mean	SD	Min	Max
5	3	0	11
0	0	0	1
.1	.0	.0	.1
.1	.0	.0	.1
.00	.00	-.01	.00
-.02	.02	-.08	.00
-.01	.01	-.04	.02

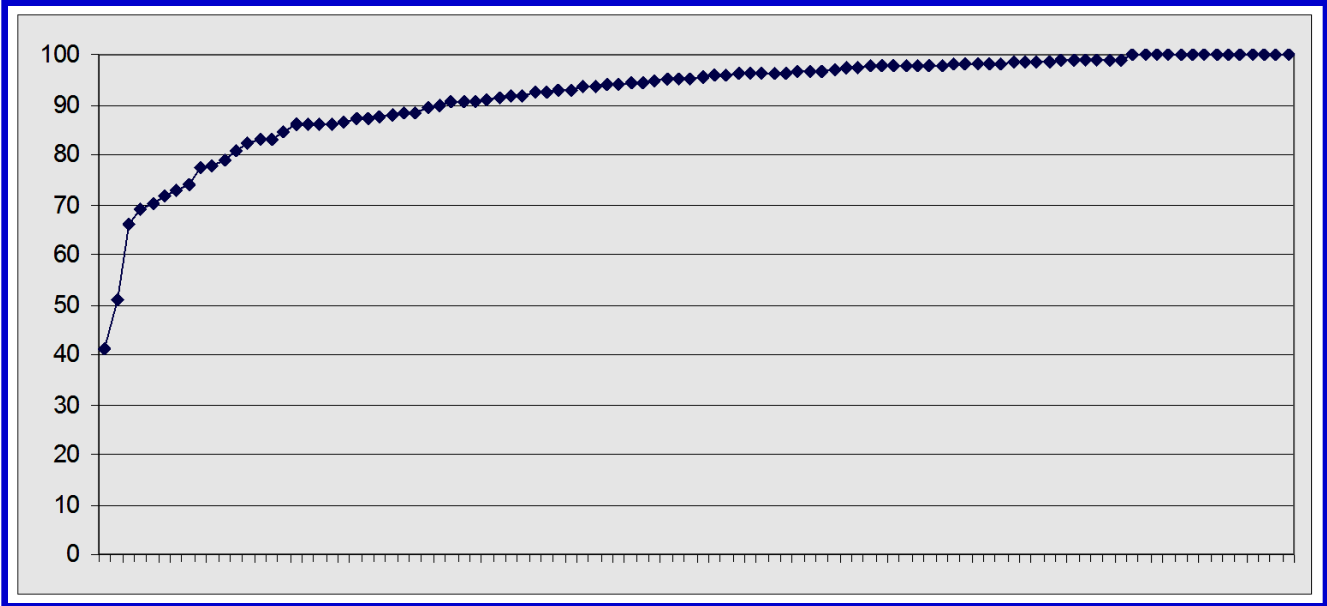*Genomic PTAs are not much different than Traditional PTAs*

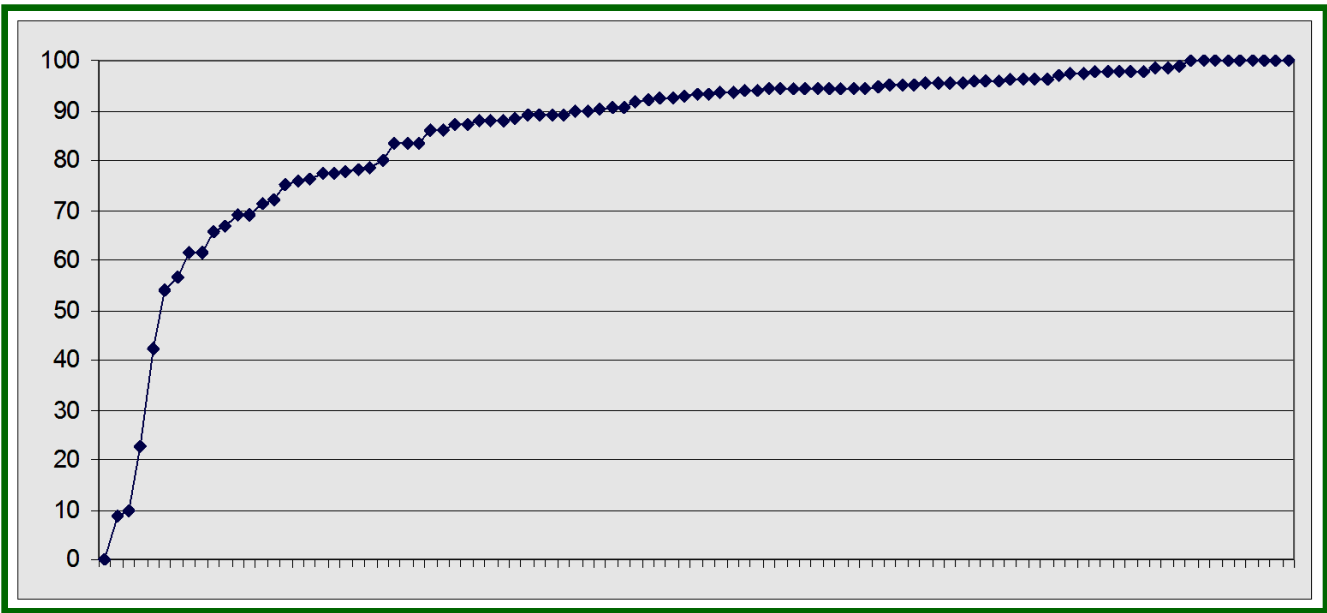# What about elite females?

Dams* with most genotyped daughters.

40 or more genotyped daughters with 10 or more daughters with records

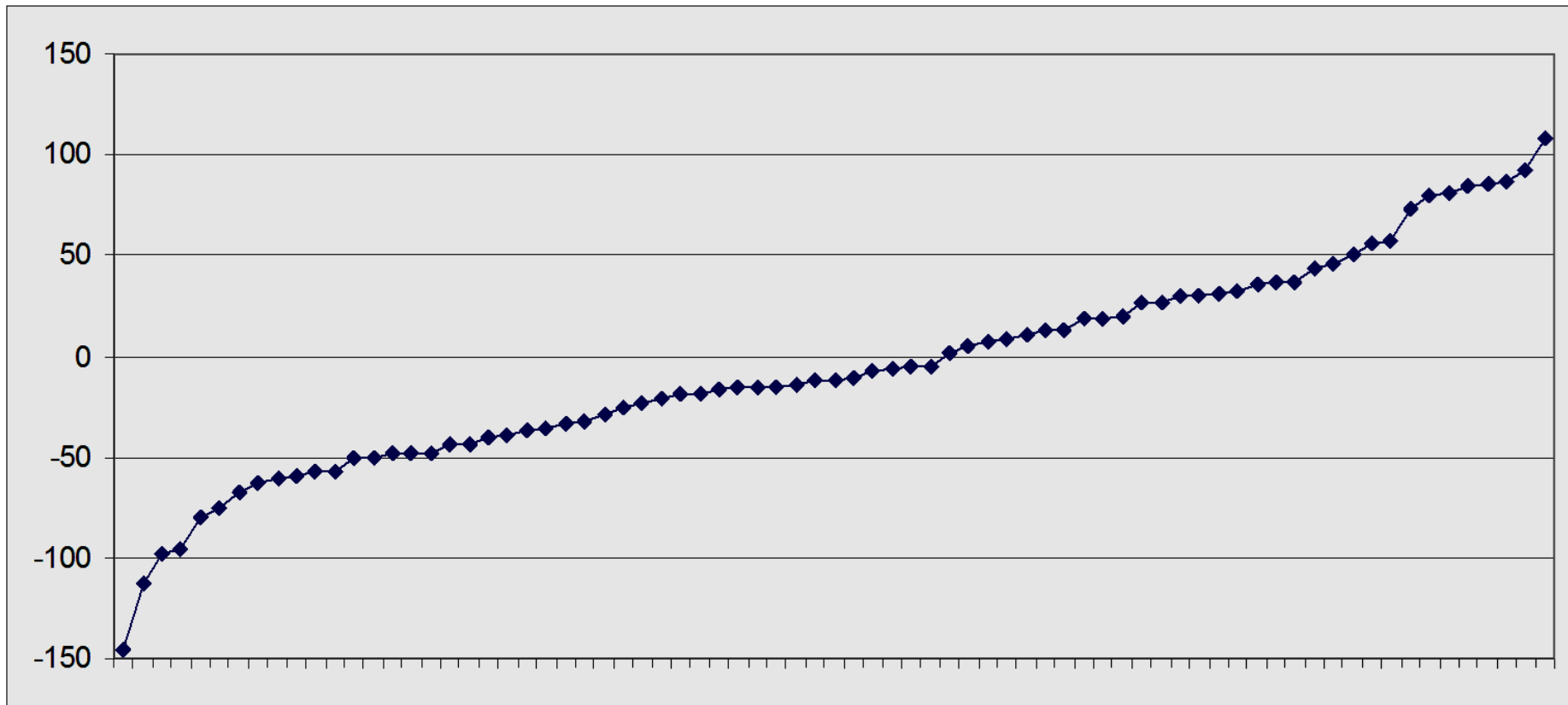Percentage of **daughters** of dams that are genotyped

Percentage of **sons** of dams that are genotyped

NM$ of daughters of dams <u>with</u> records
versus
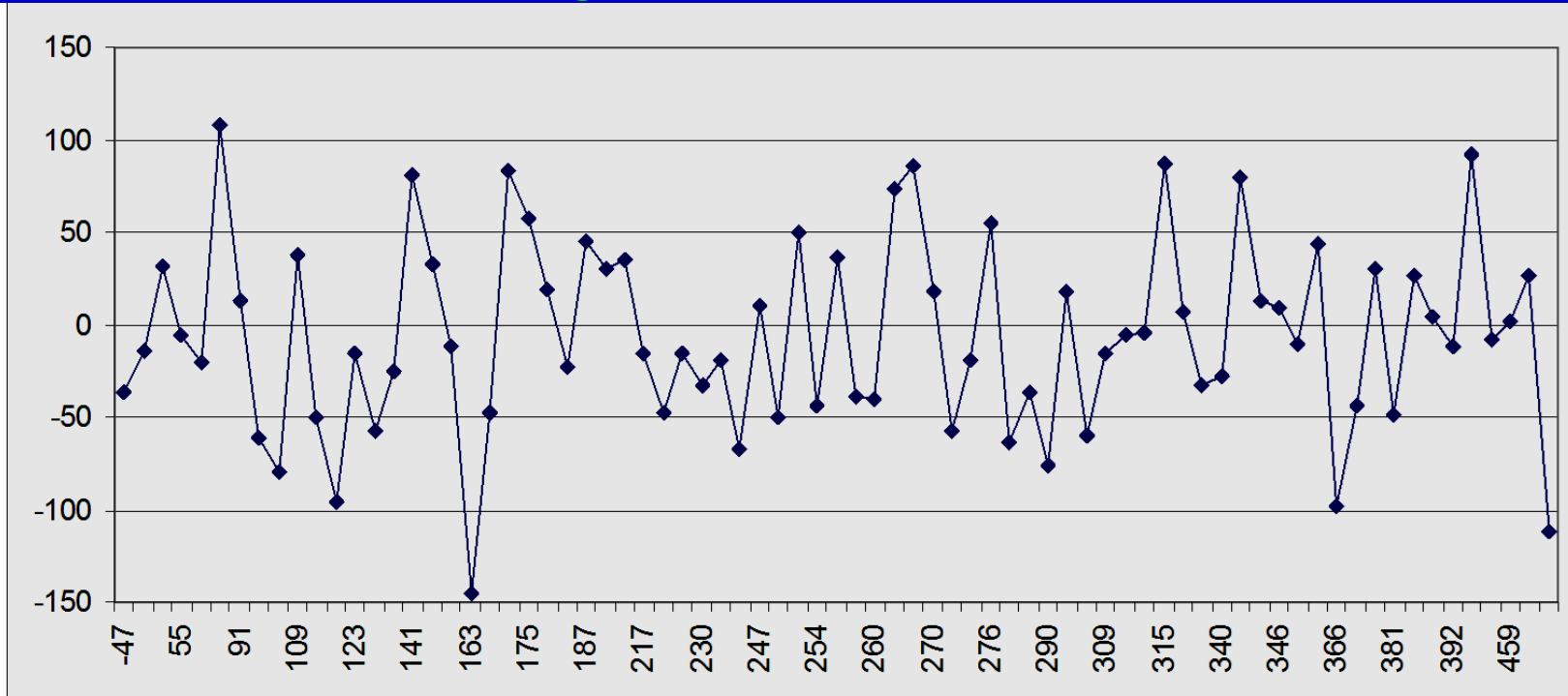# NM$ of daughters of dams <u>without</u> records

Differences between groups is evenly distributed

No relationship between a "favorable" genomic test leading to a lactation record
(for either high or low families)

Difference in Genetic Merit between daughters **with** a record vs. daughters **without** a record

NM$ of daughters with a lactation

No evidence of genomic pre-selection

Potential bias for dams with highly selected sons
Some of this bias is removed by deregression
Large number of daughters dilute bias

Future Bias – Dams of Young Bulls

- Dams with ≥ 1 sampled son born 2008 to 2013

- Son selection differential = $\sum$(GPTA – PA) / # of sons sampled

- Dam's bias = 2 * sons' selection differential * (DE from sampled sons) / (total conventional DE)
  - DE = daughter equivalents or EDC

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An extreme **2013**
6 sons selected out of 29

An extreme **2014**
5 sons selected out of 20

For illustration only

August 2013: 404

Example Dam
HOUSA000065597532

- 29 sons genotyped, 6 selected, each will provide 5.4 DE
- Son selection differential for milk = $\sum$(GPTA − PA) / 6 = 583 pounds
- 30 daughters, each provide 1.5 DE
- 8.3 DE from PA, 7.8 from records
- Dam's future bias = 2 * 583 * 6 * 5.4 / [8.3 + 7.8 + 6 * 5.4 + 30 * 1.5] = 404

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December 2014: 275

Example Dam
HOUSA000062496855

- 20 sons genotyped, 5 selected, each will provide 5.4 DE
- Son selection differential for milk = $\sum$(GPTA − PA) / 5 = 418 pounds
- 26 daughters, each provide 1.5 DE
- 8.3 DE from PA, 7.8 from records
- Dam's future bias = 2 * 418 * 5 * 5.4 / [8.3 + 7.8 + 5 * 5.4 + 26 * 1.5] = 275

Interbull technical workshop, Germany, February 2015 (5)   Paul VanRaden

Illustration of potential bias from genomic tested sons
Bull dams of current top young bulls

August 2013

December 2014

Expected Future Bias – Bull Dams

Trait	Mean	SD	Min	Max	Mean	SD	Min	Max
NM$	29	33	-124	156	24	29	-95	145
Protein	1	3	-10	14	1	3	-9	12
PL	.3	.5	-1.7	2.0	.3	.5	-1.5	2.2
DPR	.1	.2	-.9	.9	.1	.3	-1.3	1.2
SCS	-.01	.04	-.22	.14	-.01	.04	-.17	.13

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Conclusions

- Opportunity for genomic pre-selection continues to grow.

- Our estimates of genomic pre-selection are an approximation: many relatives, mates of ancestors, and contemporaries impact a genetic evaluation.

- To date, there is little evidence to support that genomic pre-selection is a major source of bias.

- This research will help us evaluate the benefits of better genetic evaluations when they are implemented.

Acknowledgements