



# Is genomic selection increasing the diversity of bulls available to dairy producers?

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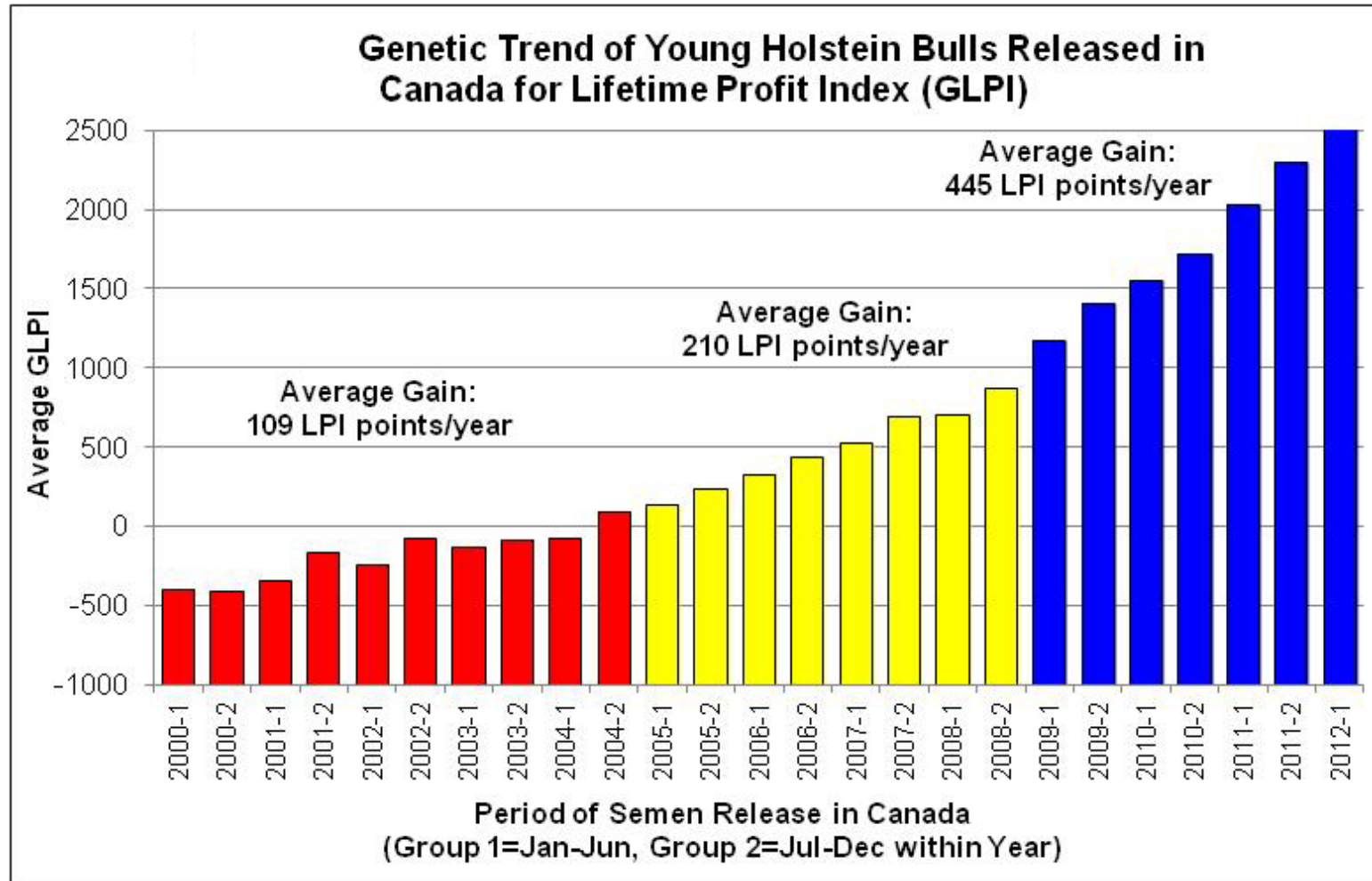


# Introduction

- ❖ **The application of genomics to dairy cattle improvement became a reality in 2009**
  - **when a handful of countries published the first official genomic evaluations for Holsteins**
- ❖ **The fast adoption rate of this new technology stemmed from its potential to significantly increase rates of genetic progress for traits contributing to dairy cattle profitability**

# Impact of Genomics

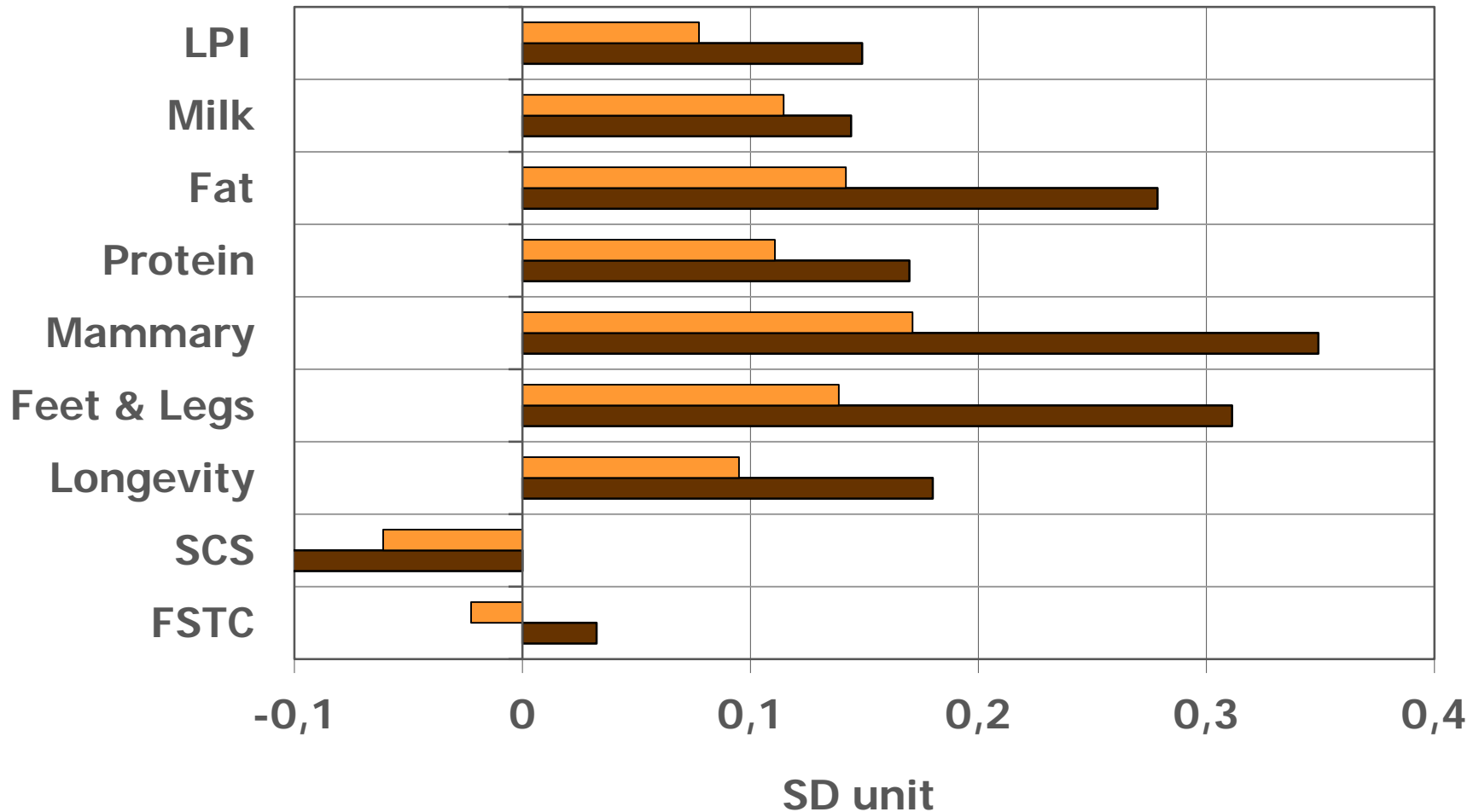
## *Increase in genetic gain – males*



# Impact of Genomics

## *Increase in genetic gain – females*

2006-09 2010-13



# New opportunity with Genomics

- ❖ With traditional evaluations, same families to breed next generation of bulls
- ❖ With genomics, opportunity to identify previously ignored families to generate future bulls
  - General belief that genomics would bring a wider portfolio of bulls to dairy producers

# Objective

- ❖ **The objective of this investigation was to verify if indeed a larger pool of bulls has been available for selection by producers**

# Analysis I

- ❖ **Interbull pedigrees of bulls born between 2001 and 2010 were analyzed**
  - **countries that participated to the G-MACE test run of March 2013**
- ❖ **Country of birth was determined based on country of registration**
- ❖ **Analyses performed**
  - **by year (2001, 2004, 2007 and 2010)**
  - **by geographical area (Global, North America, main European dairy countries, other countries)**

# Geographical Labels

## ❖ North America

- Canada and United States

## ❖ Europe

- France, Germany, Great Britain, Italy, the Netherlands and DFS (Denmark, Finland, Sweden)

## ❖ Other countries

- Australia, Japan, Poland, Spain and Switzerland

## ❖ Global

- All of the above

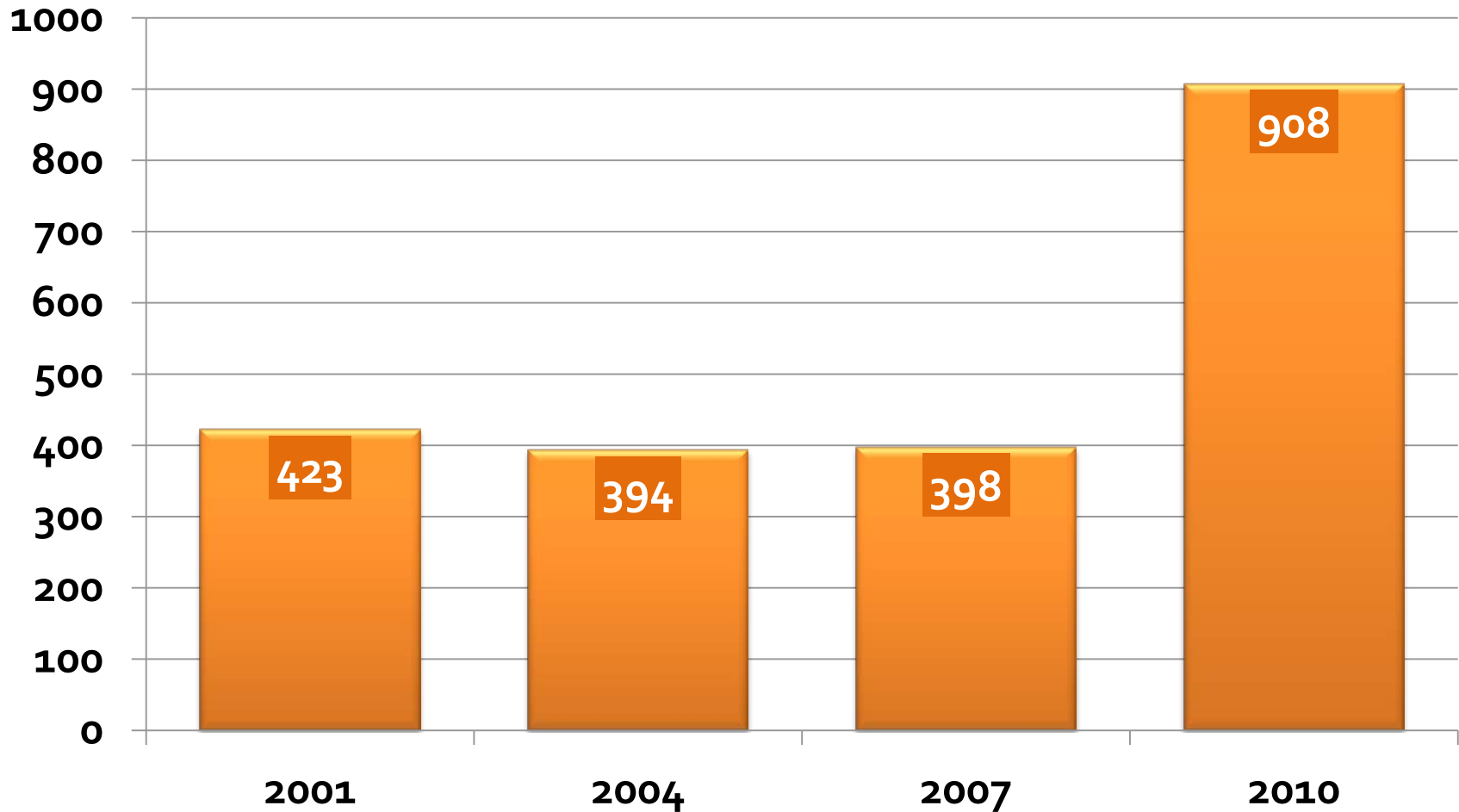


# Analysis II

- ❖ **Additionally, a comparison was performed for North American bulls born in 2010**
  - pre-screened bulls vs. those that entered AI
- ❖ **This additional analysis done for NA only since this information was available for US and Canada**
- ❖ **Co-ancestry among bulls in the same birth year and across birth years was also investigated**
  - For North American and for Global Interbull pedigree
  - Using CFC (Sargolzaei et al., 2006)

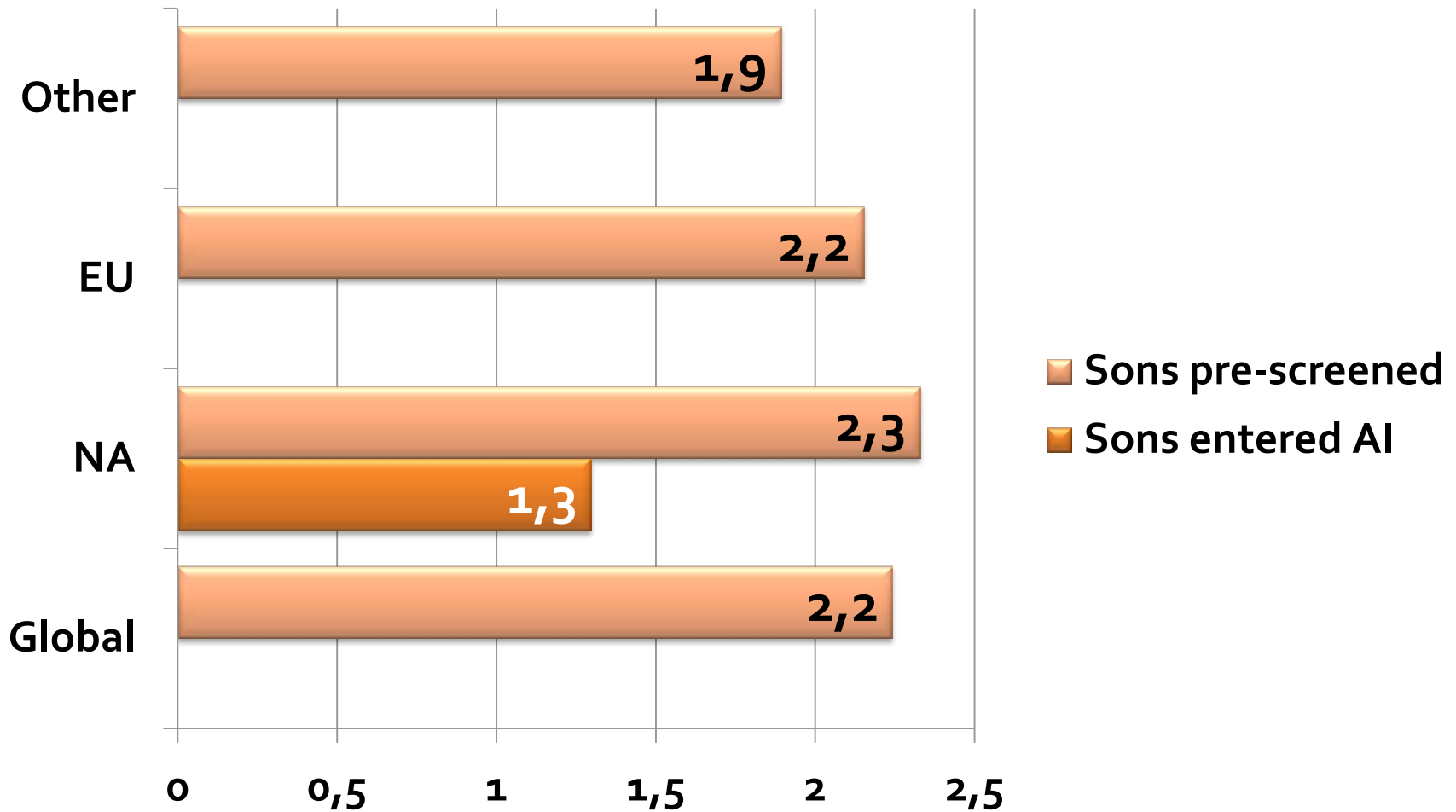
# No. of sires of sons *Before and after genomics*

Global



# No. of sires of sons

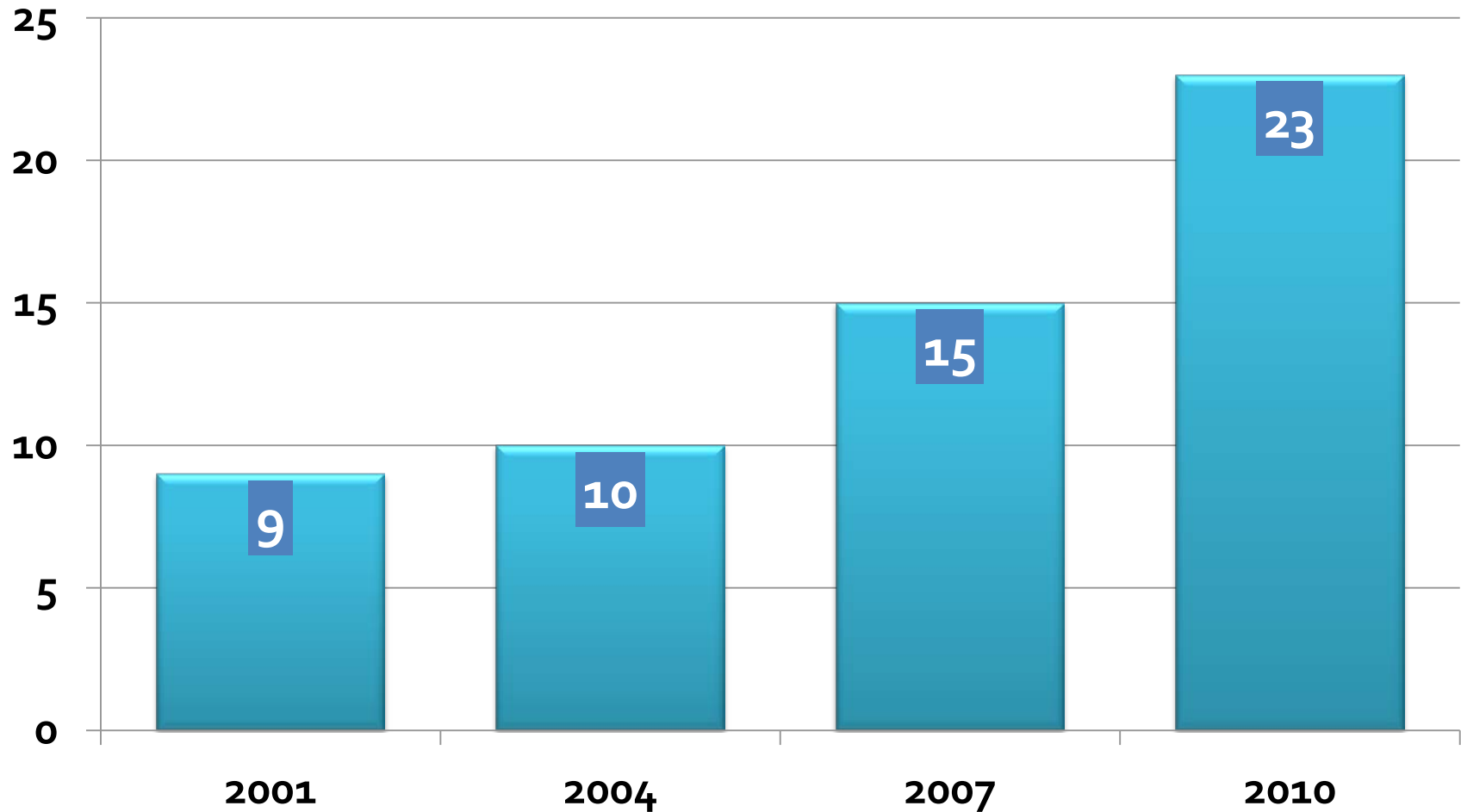
## *Ratio for 2010 over 2001-2007*



# No. of sires with 50% of sons

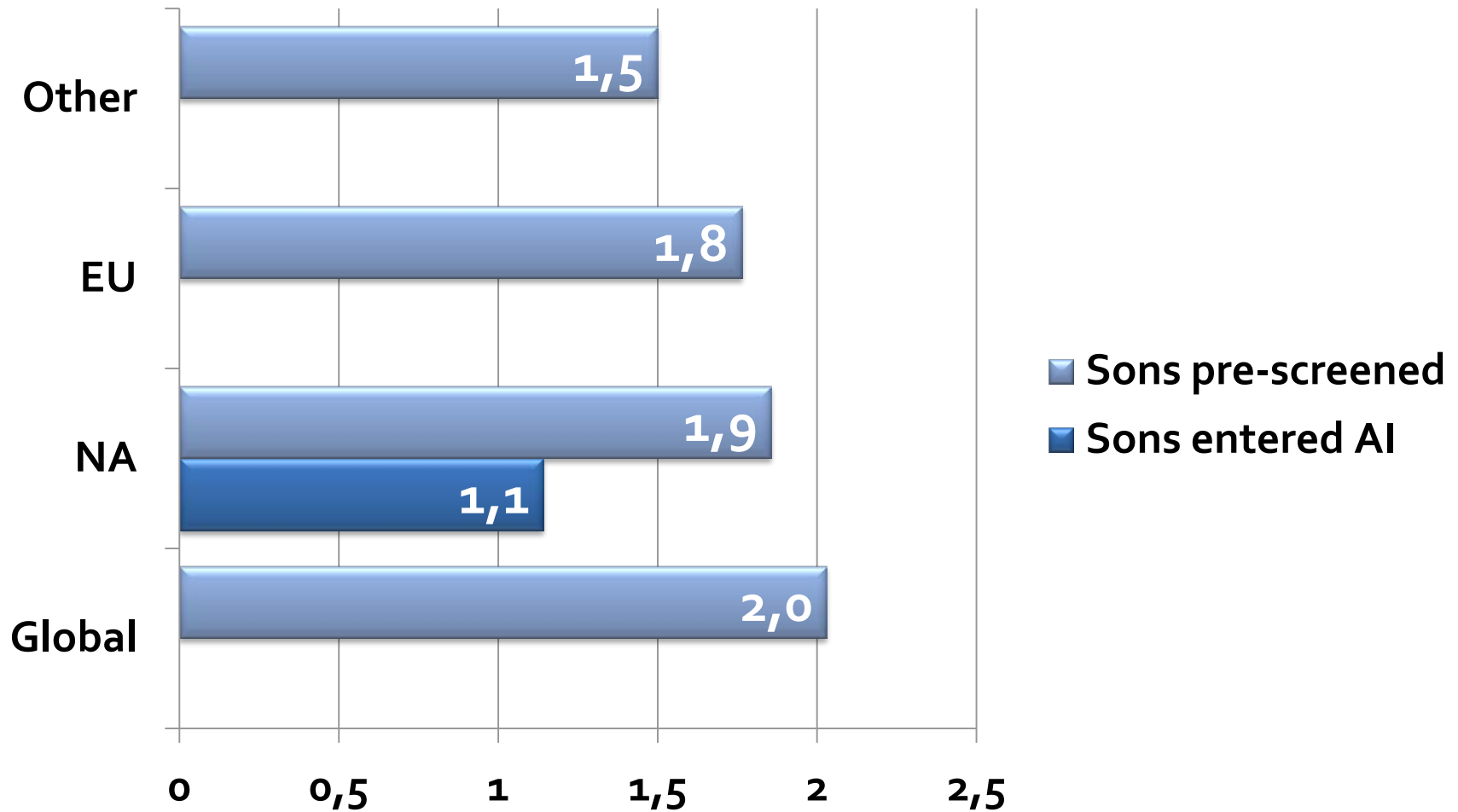
## *Before and after genomics*

Global



# No. of sires with 50% of sons

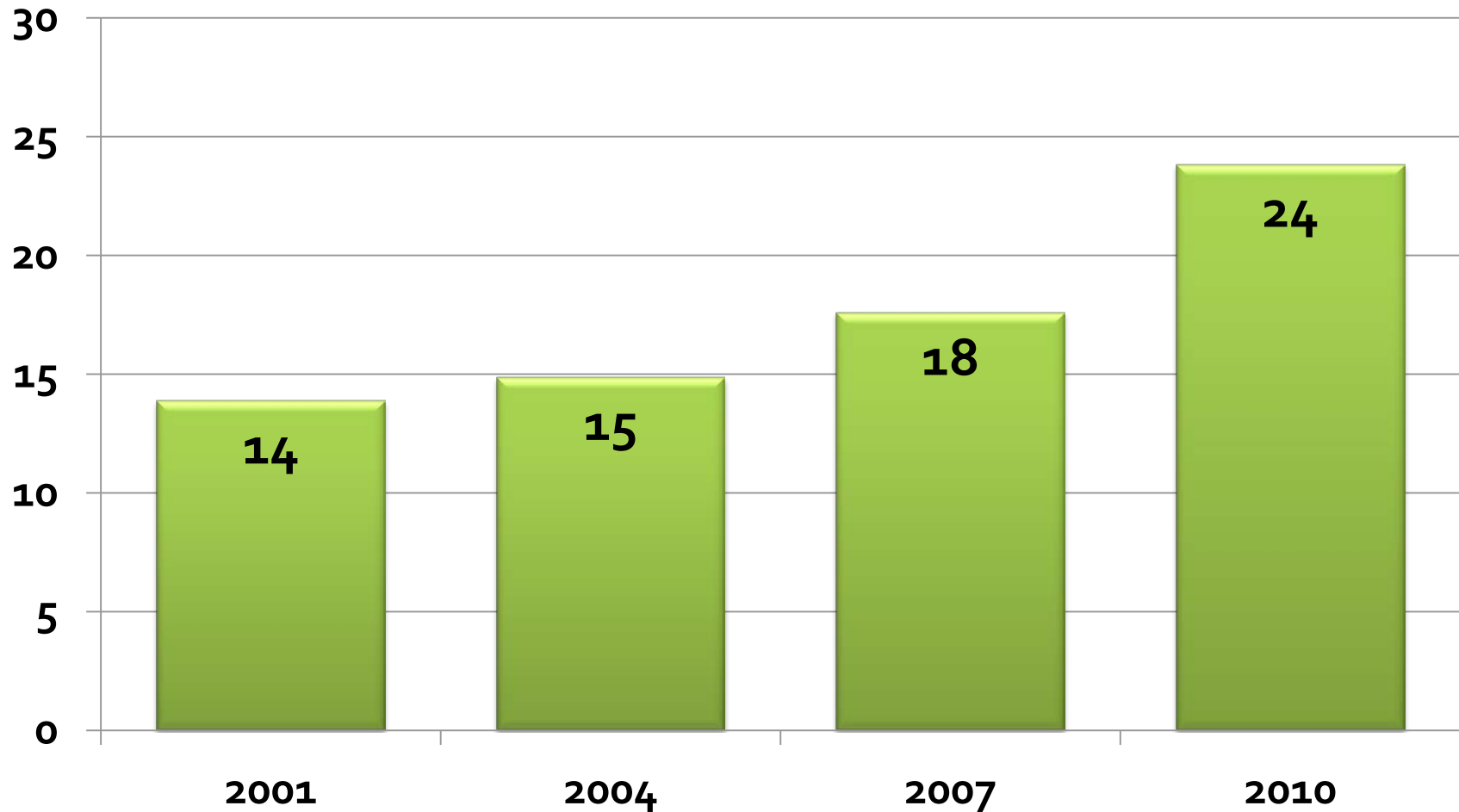
## *Ratio before over after genomics*



# No. of sons per sire

## *Before and after genomics*

Global



# No. of sons per sire

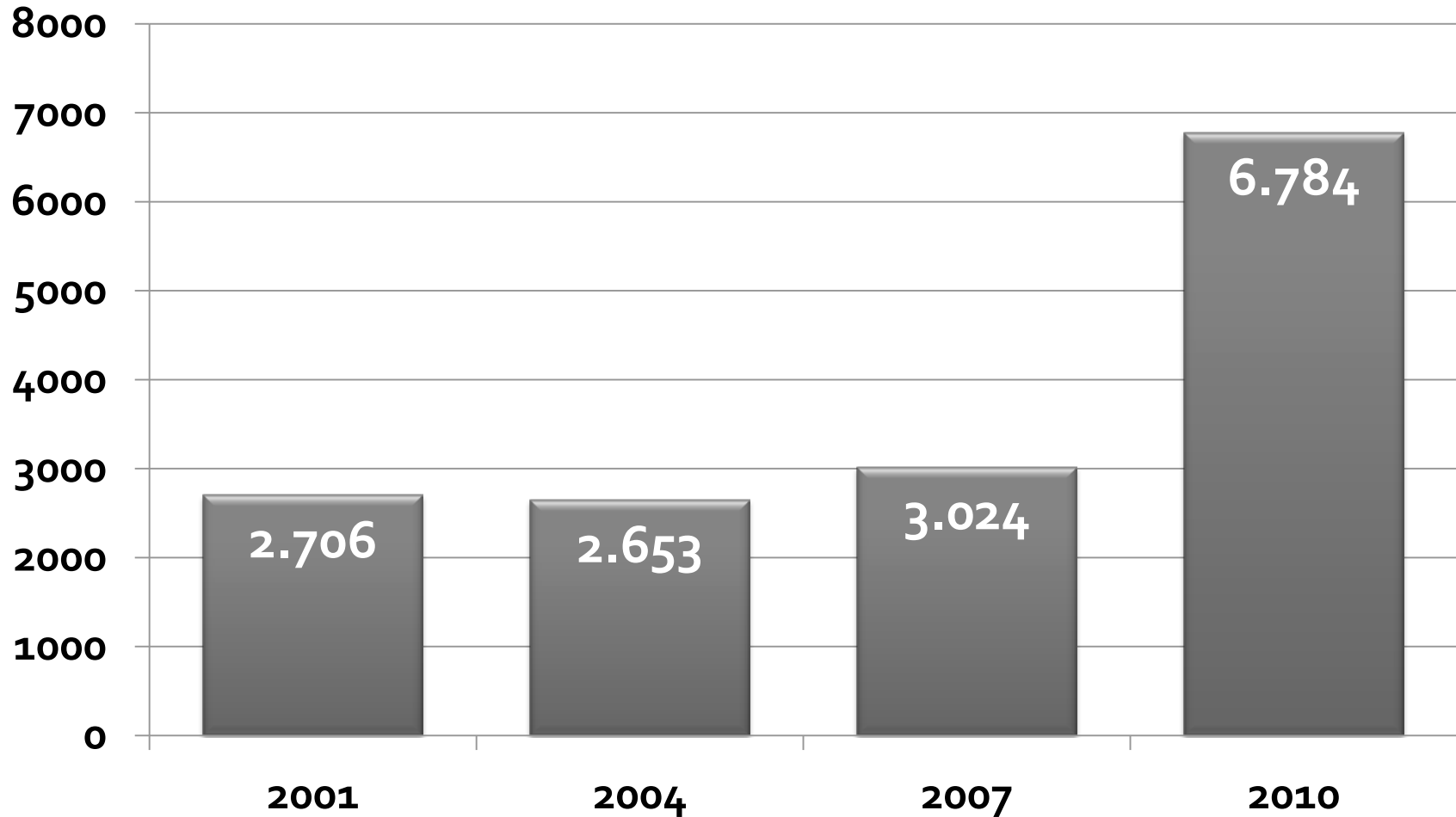
## *Ratio for 2010 over 2001-2007*



# No. of sires-MGS

## *Before and after genomics*

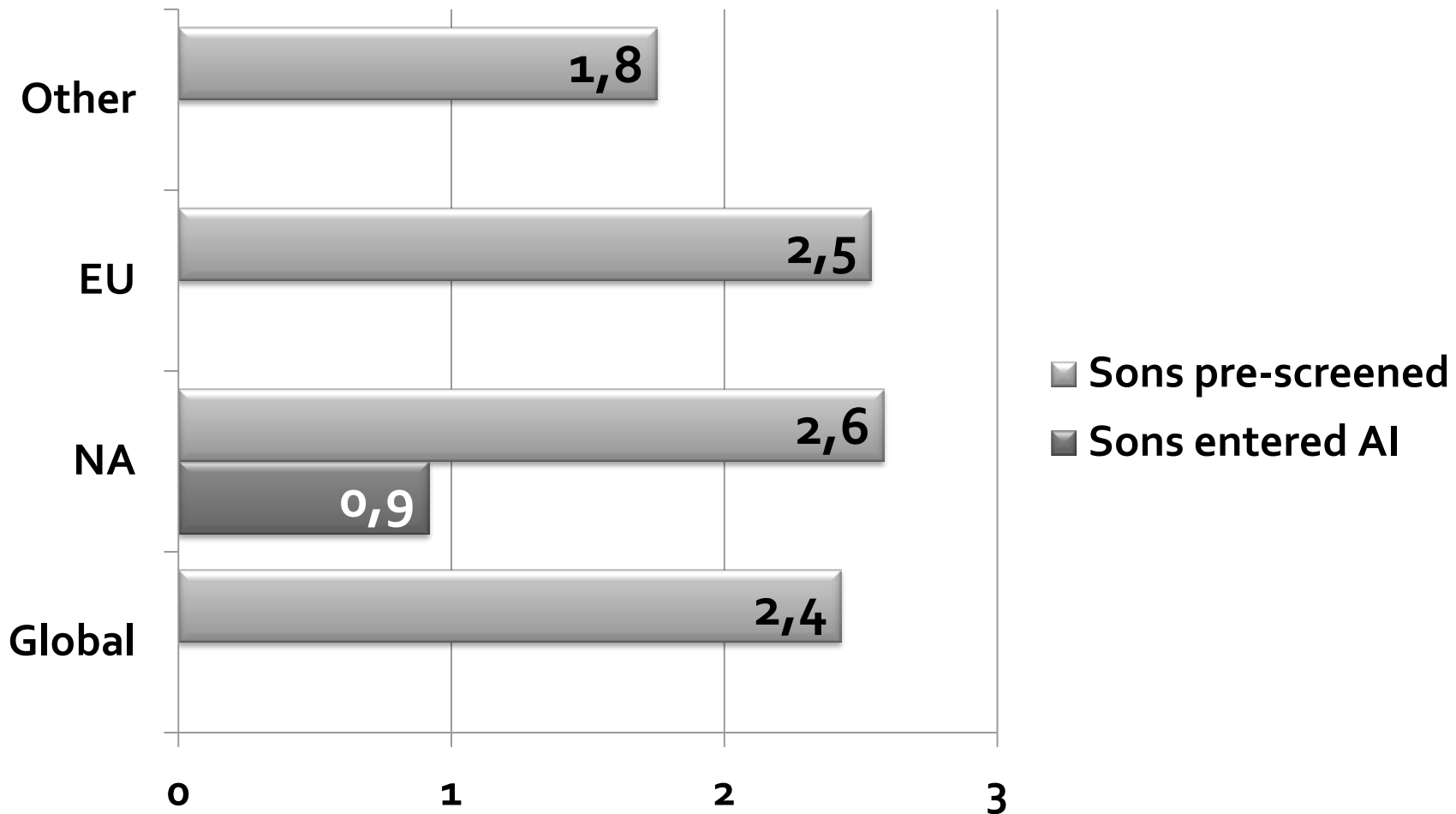
### Global





# No. of sire-MGS

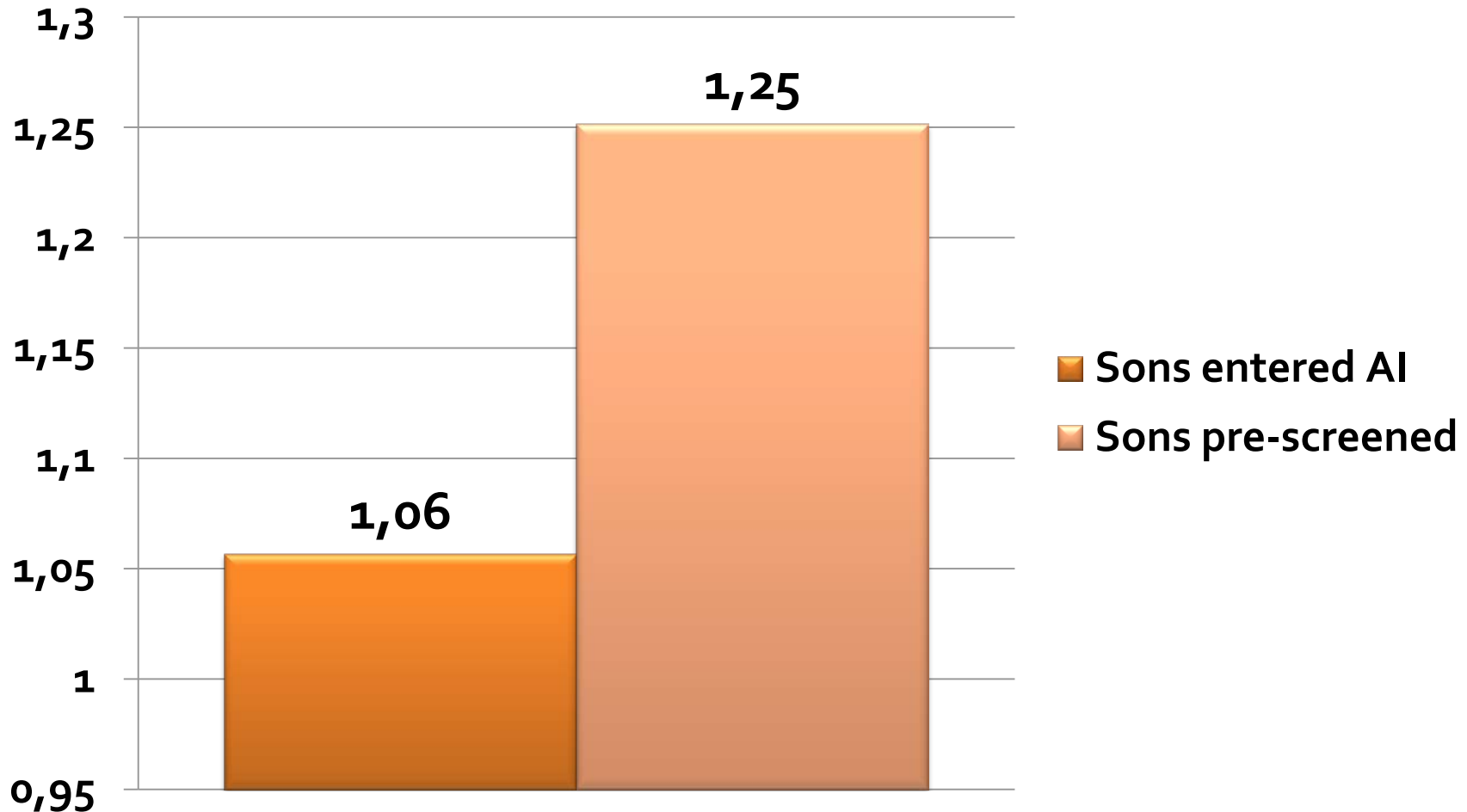
## *Ratio for 2010 over 2001-2007*



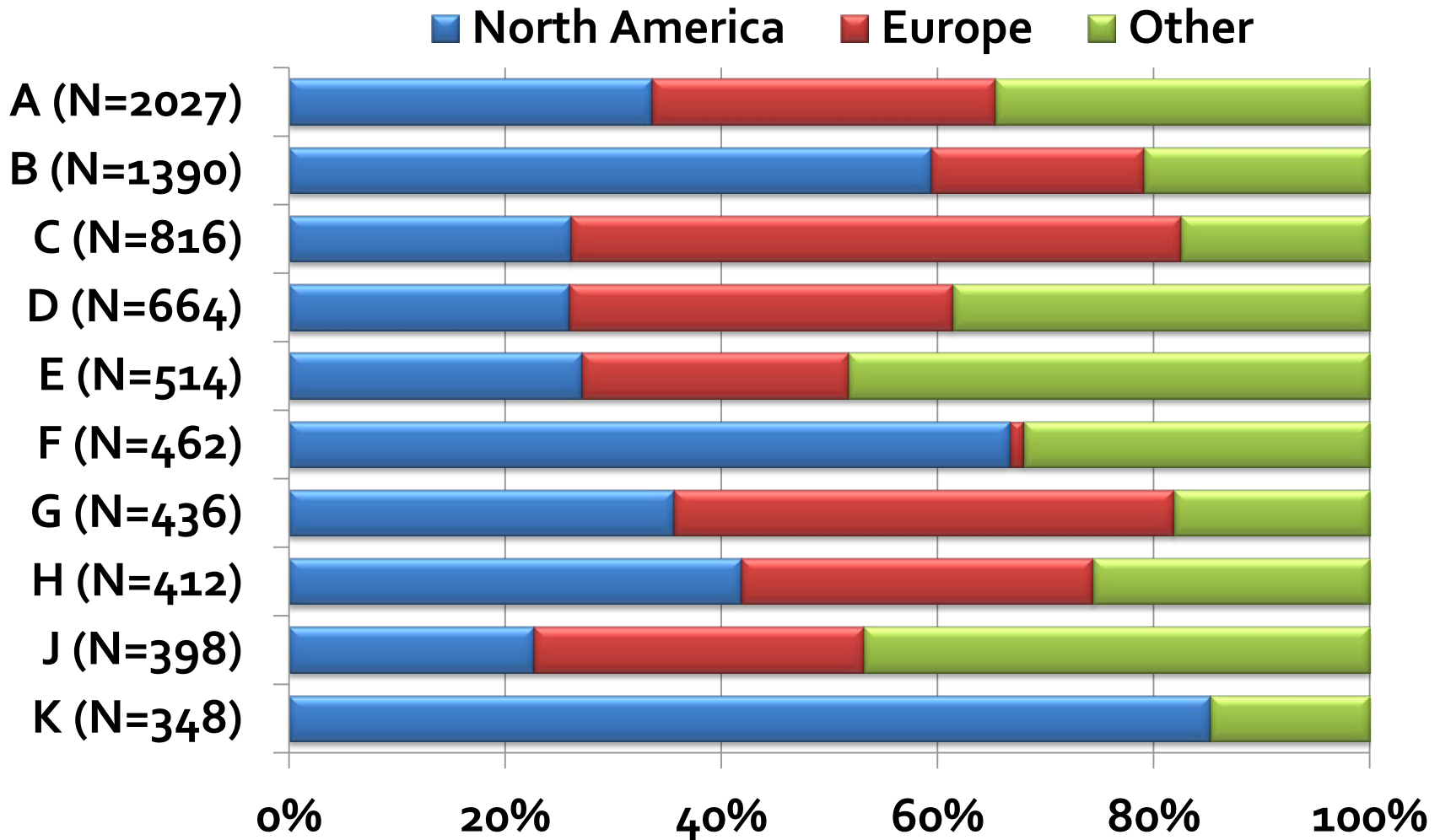
# No. of full-sibs

## *Ratio for 2010 over 2001–2007*

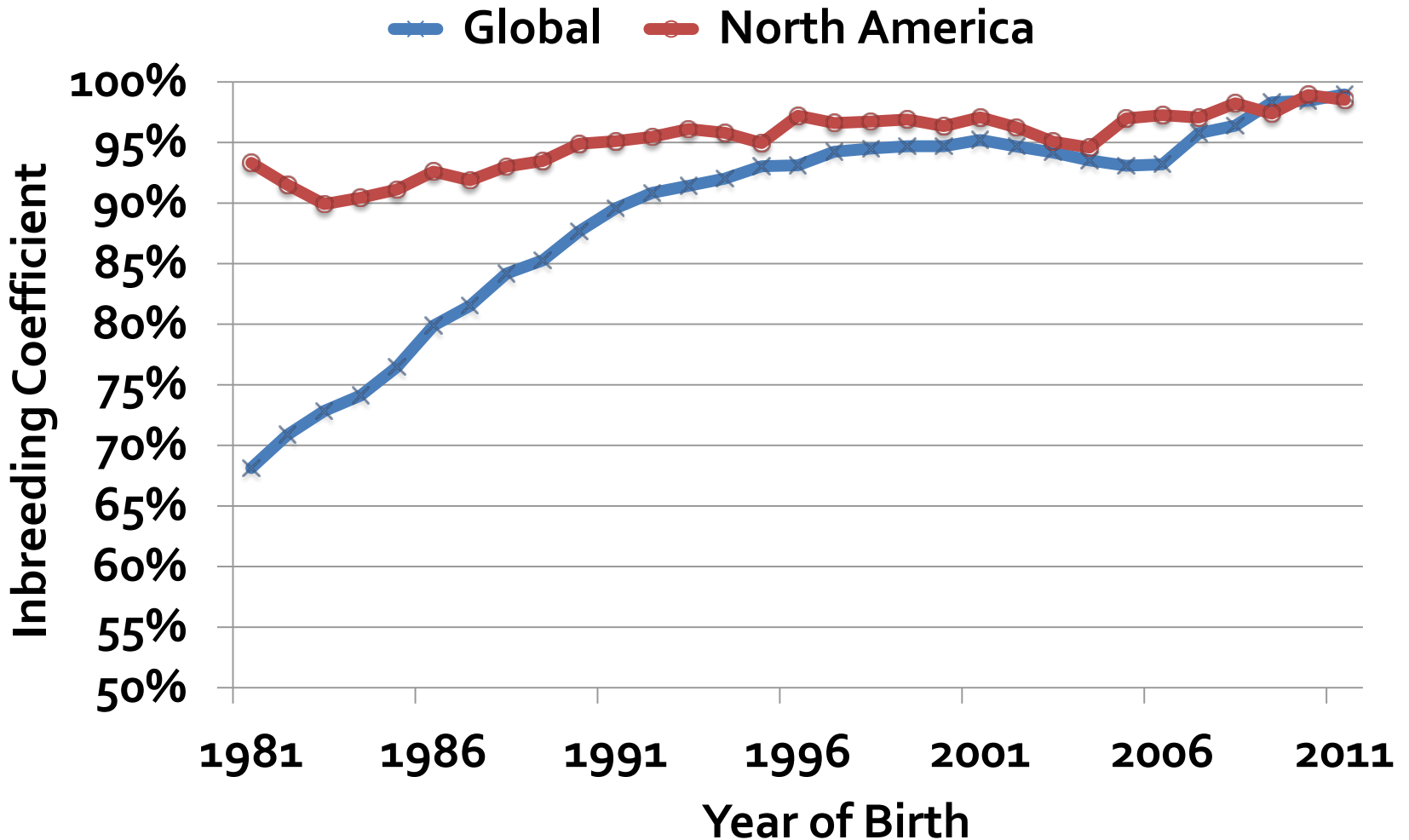
North America



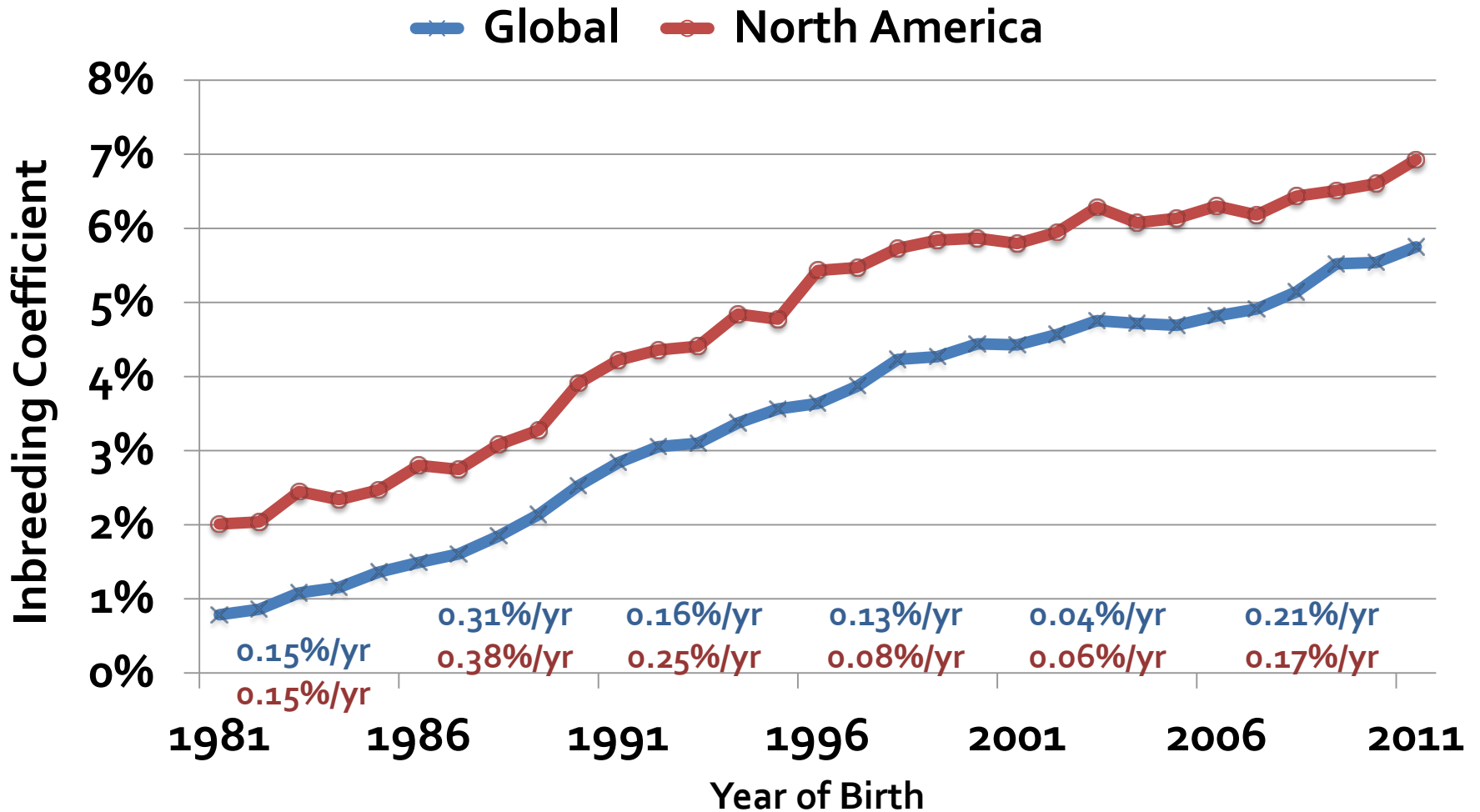
# Top 10 sires of sons in 2010



# Average Pedigree Completeness Index

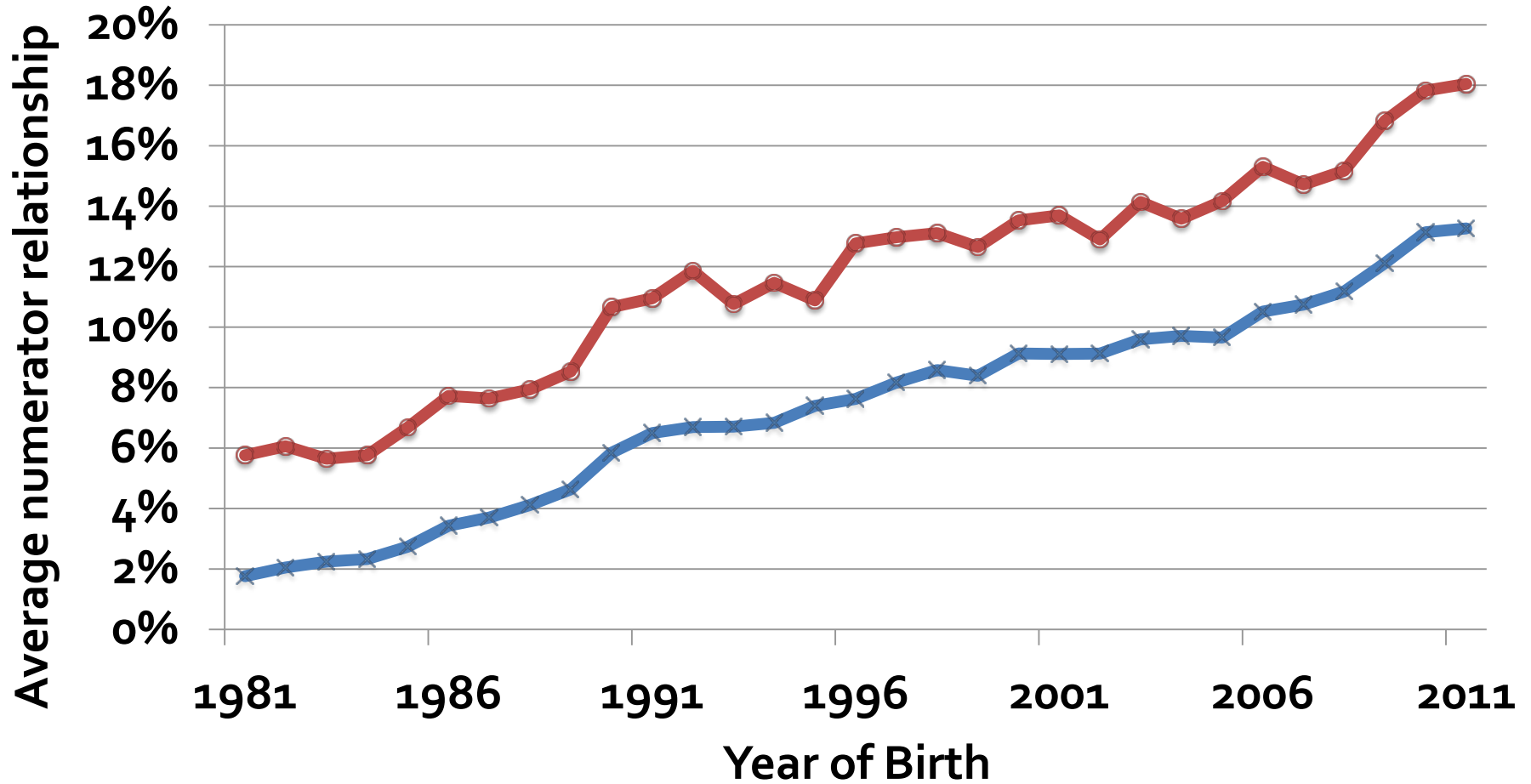


# Average Inbreeding

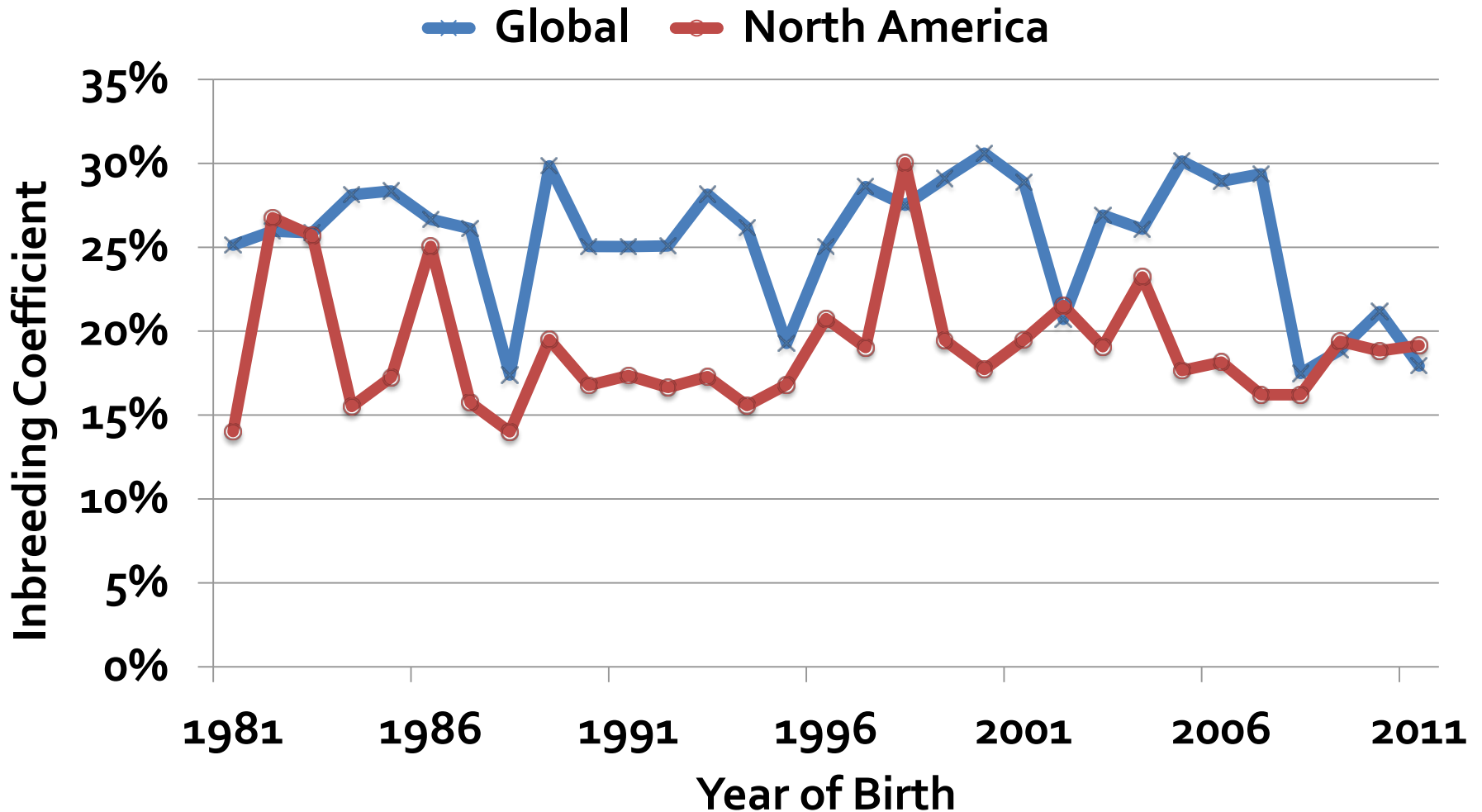


# Average Numerator Relationship

Global North America



# Maximum Inbreeding



# Top 20 Sires of Sons since 1986

1	TO-MAR BLACKSTAR-ET	2998
2	S-W-D VALIANT	2387
3	LONG-LANGS OMAN OMAN-ET	2334
4	ENSENADA TABOO PLANET-ET	2231
5	ROTHROCK TRADITION LEADMAN	2191
6	PICSTON SHOTTLE	1982
7	A RONNYBROOK PRELUDE ET	1735
8	WALKWAY CHIEF MARK	1689
9	BRAEDALE GOLDWYN	1612
10	ENGLAND-AMMON MILLION-ET	1599
11	CHARLESDALE SUPERSTITION-ET	1592
12	ROUND OAK RAG APPLE ELEVATION	1476
13	HANOVERHILL STARBUCK	1442
14	SINGING-BROOK N-B MASCOT-ET	1408
15	EMERALD-ACR-SAT-BAXTER	1302
16	WHITTIER-FARMS NED BOY	1247
17	MADAWASKA AEROSTAR	1245
18	MAIZEFIELD BELLWOOD-ET	1148
19	BIS-MAY TRADITION CLEITUS	1129
20	KED OUTSIDE JEEVES-ET	1108



# Challenges

- ❖ Large use of some prominent bulls as sires of sons, at least until 2010, despite increasing use of young bulls as sires of sons
- ❖ Inbreeding rate is again increasing at a faster rate
- ❖ Portfolio of bulls offered to farmers have not increased significantly in terms of family diversity
- ❖ With faster generation interval, no time for natural selection to counter balance negative effects of inbreeding

# Opportunities

- ❖ AI organizations are trying to find new bloodlines
- ❖ With shorter generation interval, sires of sons not used for too long
- ❖ Turnover of top bulls is much faster than before
- ❖ Maximum inbreeding levels have decreased due to effective mating plans to generate new generation of elite animals

# Conclusions

- ❖ AI organizations are pre-screening a very large number of young bulls through genotyping
  - the size of the genetic pool that serves to identify the next generation of elite bulls has more than doubled
- ❖ However, the results from genomic evaluations tend to favor a limited number of sire and maternal grand-sire families
  - bulls that enter AI service are drawn from a genetic pool that until today has only increased slightly compared to the years before genomics

# Conclusions

- ❖ The use of young genotyped bulls as service sires by producers and as sires of sons by AI companies has increased greatly from 2010 to 2012
- ❖ This might change the over-all picture substantially
- ❖ Despite this, it remains important to closely monitor the situation
- ❖ The use of optimum selection (OS) strategies or the discounting of economic indices based on expected future relationships would be worth investigating

# 10<sup>th</sup> World Congress on Genetics Applied to Livestock Production

Vancouver, BC, Canada  
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