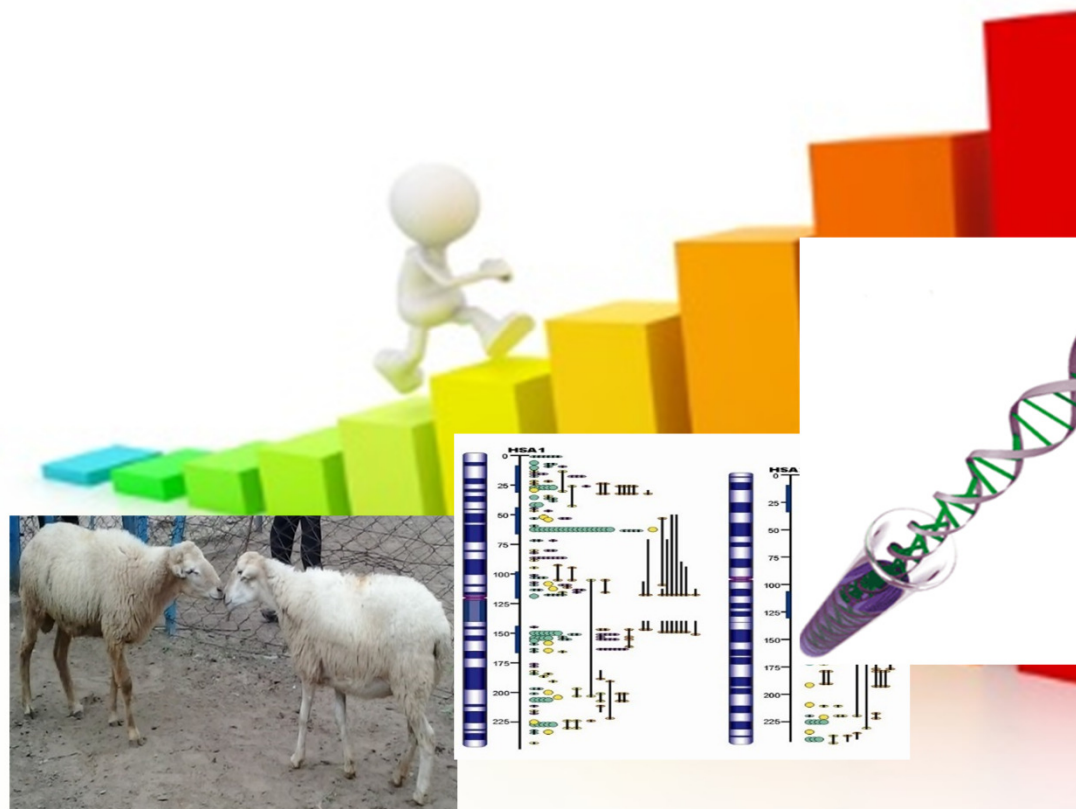


**Economic selection in animal  
breeding- A promising  
strategy for faster genetic  
improvement in livestock**

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# Conventional selection

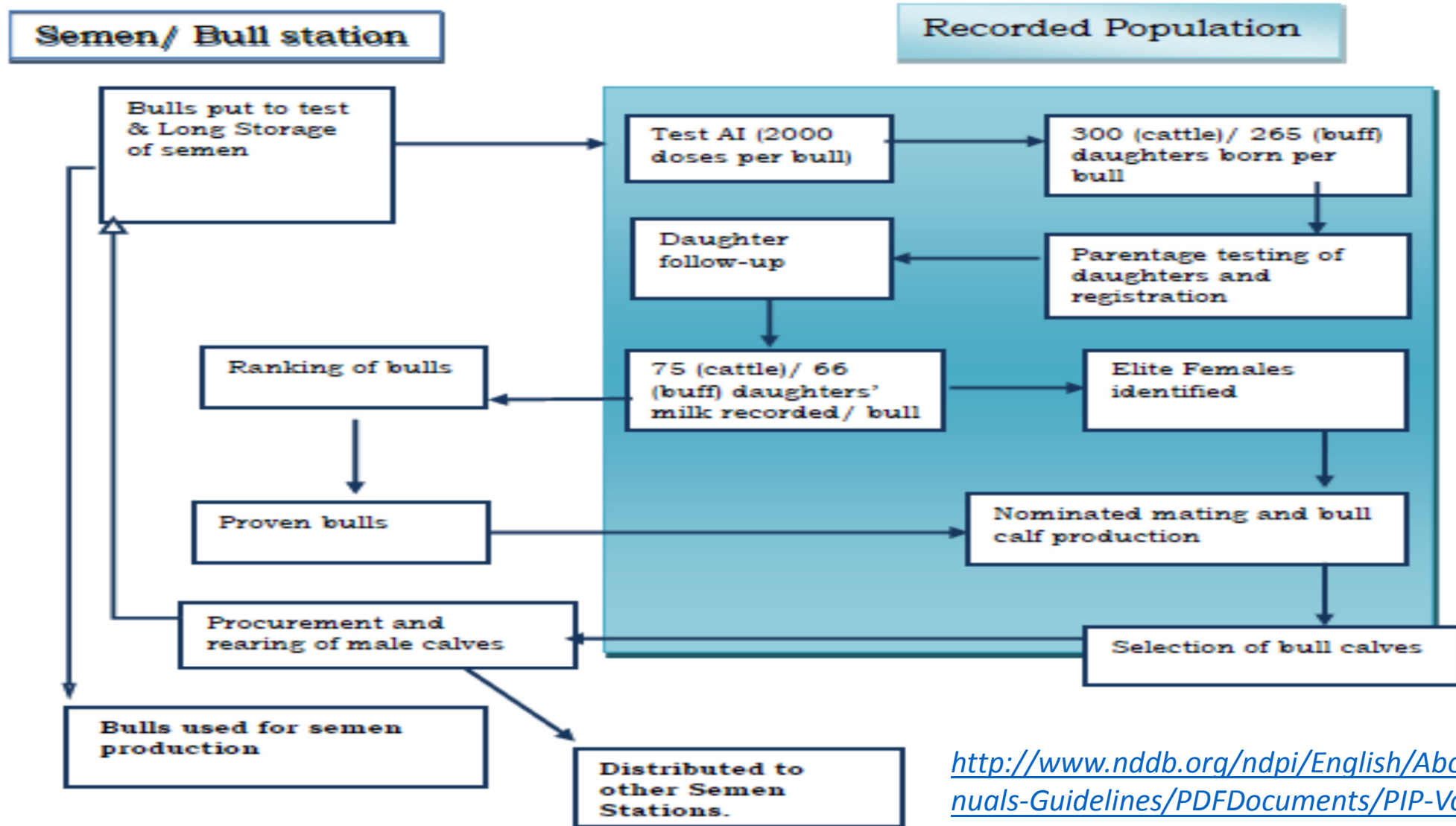
- Based on individual records, pedigree or progeny performance or family performance.



SI=WT9 +1DMY90



# Progeny testing –Bulls evaluated on the basis of daughters performance



<http://www.nddb.org/ndpi/English/About-us/Manuals-Guidelines/PDFDocuments/PIP-Vol-1-Manual-on-Progeny-Testing.pdf>

# History of Genomics

- 1911-The gene map of *Drosophila* by Alfred Sturtevant.
- 1930s-Molecular Biology begins.
- 1965-Margaret Dayhoff's Atlas of Protein Sequences
- 1970-Sequencing techniques by Fredirick Sanger
- Three disciplines Genetics, Molecular biology and Bioinformatics converged in 1980s and 1990s -Genomics

# QTL Analysis

❖ In the 1990s starts QTL analysis in in farm animals

Species	Number of QTIs
Cattle	11543
Chicken	4337
Horse	345
Pig	11610
Sheep	789
Rainbow Trout QTL	127

<http://www.animalgenome.org/cgi-bin/QTldb/index>

# Marker Assisted Selection (MAS)

- 1-Detect one or several QTLs
- 2-Fine mapping
- 3-Find the gene responsible
- 4-Introgression

# Limitations of MAS

**1-**The effect of individual Quantitative trait loci (QTL) on polygenic traits, such as milk yield, are likely to be small

**2-**Number of QTL required is quite large to sufficiently explain the genetic variation in these traits



# Genomic Breeding

In 1990 Human Genome project started and in 2003 human genome was published. This was followed by sequencing of farm animal genomes

Species	Year
Dog (Canis Familiaris)	2003
Chicken (Gallus Gallus)	2004
Cat (Felis sylvestris)	2006
Sheep (Ovis Aries)	2008
Cattle (Bos taurus)	2009
Horse (Equus caballus)	2009
Pig (Sus Scrofa)	2009



- Sequencing revolutionised development of large panels of SNPs in domestic animals
- Genomic Selection was actually first introduced by Haley and Visscher at Armidale WCGALP in 1998
- But the methodology for Genomic Selection was first presented by Meuwissen *et. al.* in 2001

# Genomic Breeding

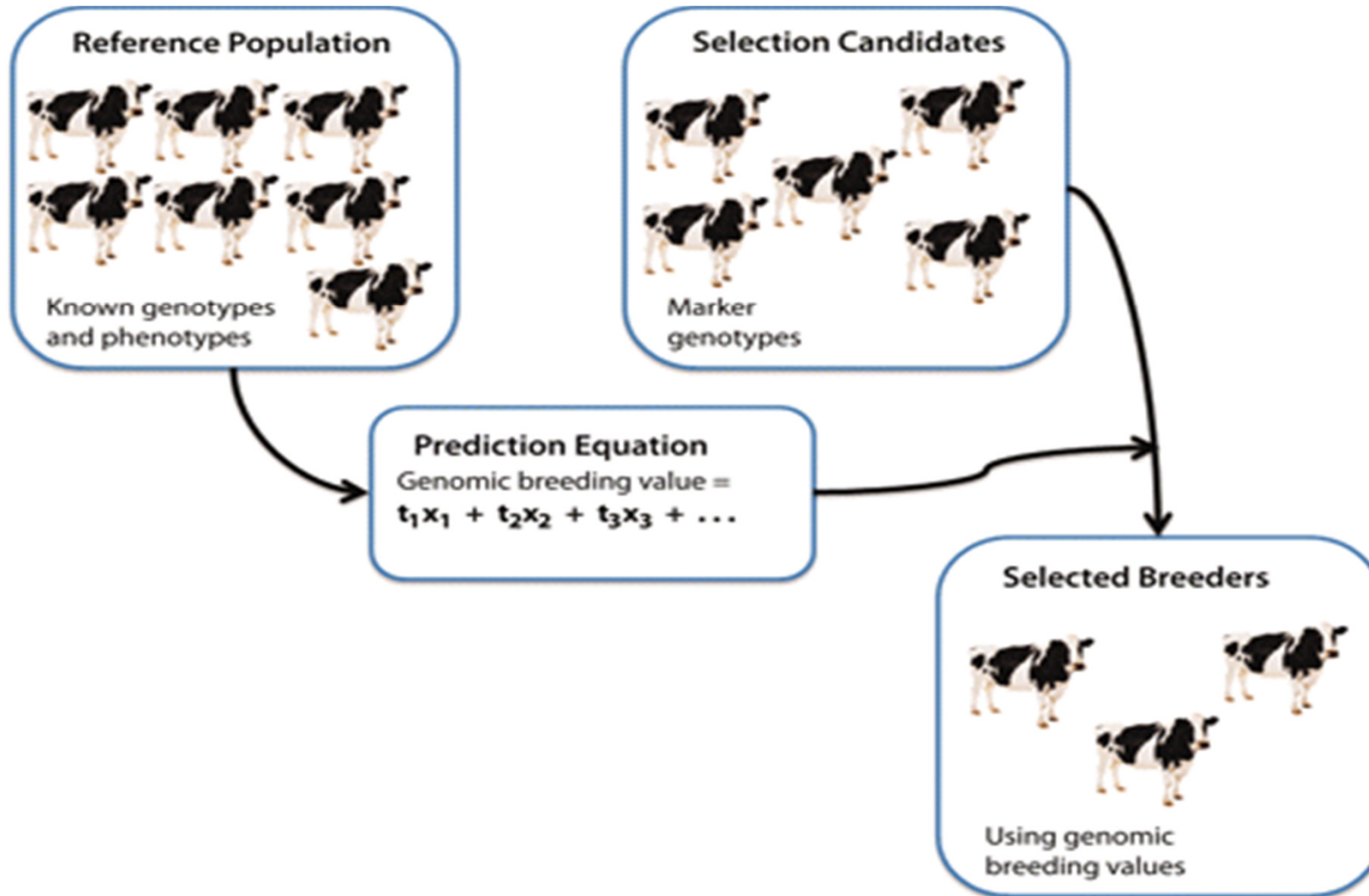
Genomic Selection is defined as a technology for increasing the accuracy with which the genetic merit of young potential breeding animals can be determined". Wickham *et al.* ,2012

## **Two step process:**

Estimate the effects of markers in a reference (training) populations (phenotyped and genotyped)

This information utilized to predict the breeding value of candidates to selection in a testing (evaluation) population (genotyped)

# Methodology



Eggen, 201

## Differences with MAS

- MAS concentrates on few QTLs having association with marker
- Genomic selection uses a genome-wide panel of dense marker

# Advantages

Animals at an early age because breeding values can be predicted with an accuracy of 0.8 for selection candidates at birth

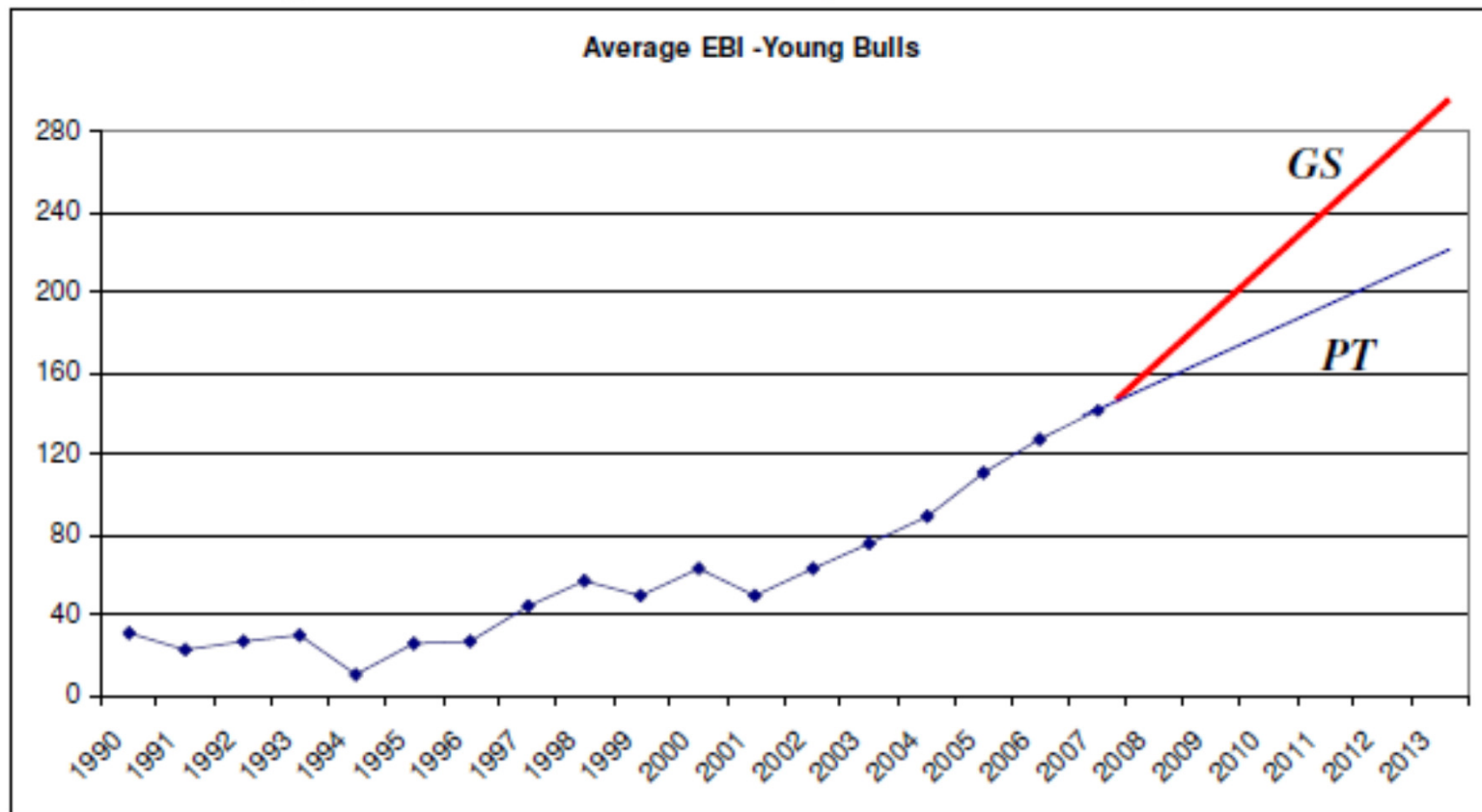
## *Current scenario*

Year -	Year 0	Year 1	Year 2	Year 3	Year 4	Year 5
♂ Cows Contract Mated	Bull Calves Bought	100 Bulls enter € IRELAND	Daughters born	Daughters mated	Daughter calves/mil k recorded	Bulls chosen for AI (10- 20)

## *Genomic Selection scenario*

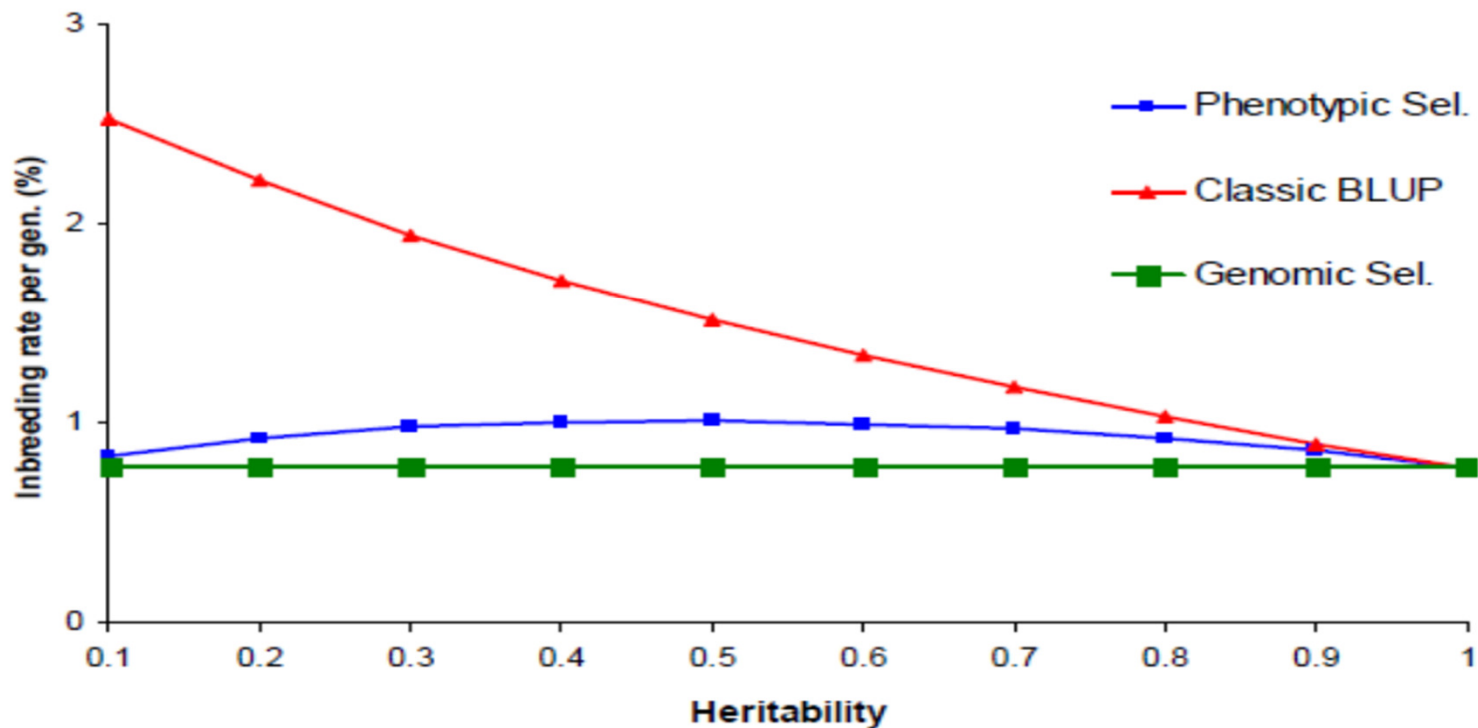
Year -	Year 0	Year 1	Year 2	Year 3	Year 4	Year 5
♂ Cows Contract Mated	'000s Bulls selected on GS	100 (or less) Bulls enter € IRELAND	Bulls chosen for AI	3 Years Advanced Gain		

# Higher rate of gain as compared to Progeny testing



# Lower rate of Inbreeding per generation

## Inbreeding rates of methods





## **Genomic selection for future uses:**

-Mitigation of effects of climatic change-select for lower GHG (green-house gas) emissions in species: "Eco friendly cattle"(Hayes *et. al.* , 2013)

## **Genomic selection is especially useful for**

- Traits with low heritability(fitness traits)
- Traits difficult/expensive to measure(like wool quality in sheep)
- Disease susceptibility/resistance traits
- Traits that take a lifetime to measure(longevity)

# High-density SNP Chips available for

- Cattle
- Sheep
- Goat
- Pigs
- Horses
- Dogs
- Chicken
- Salmon
- Human

# Countries following Genomic Selection

- USA & Canada (In Collaboration)
- New Zealand
- Netherlands
- Australia
- Denmark & Sweden
- Brazil

# Limitations

- Genotyping requires sufficiently large set of animals for accurate marker estimates
- For Low heritable traits more records are needed
- Between breed accuracy low-High Density chip
- Marker estimates must be estimated in population where they have to be used

Thank you