The FUN side of Breeding & Genetics: from genotypes to phenotypes

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Nov/2016

UGA

Disclaimer

There is NO fun in breeding and genetics…

…this title was just to trick YOU…

…otherwise nobody would come

Would you come if

- Methods to approximate reliabilities in single-step GBLUP when more genotypes are available

```
PROGRAM fun

implicit none
integer :: Npic, Nform

write (*,*) "Enter the number of Pictures"
read(*,*) Npic

write(*,*) "Enter the number of Formulas"
read(*,*) Nform


  if (Npic > Nform) then
    write(*,*) "Animal Breeding and Genetics is FUN"
  else
    write(*,*) "There is NO FUN in Animal Breeding and Genetics"
  end if

END PROGRAM fun
```

Misunderstanding AB & G

Most of the people don’t really understand

what AB & G is

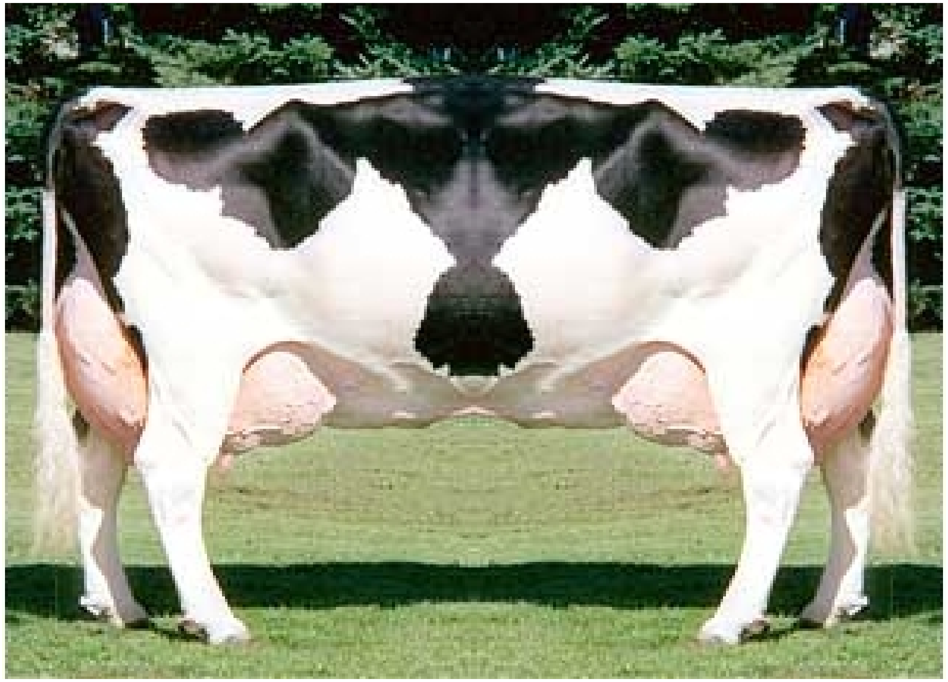
Misunderstanding AB & G

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'Z_1} & \mathbf{X'Z_2} & \mathbf{X'W} \\ \mathbf{Z_1'X} & \mathbf{Z_1'Z_1+A^{-1}}\alpha_{11} & \mathbf{Z_1'Z_2+A^{-1}}\alpha_{12} & \mathbf{Z_1'W} \\ \mathbf{Z_2'X} & \mathbf{Z_2'Z_1+A^{-1}}\alpha_{21} & \mathbf{Z_2'Z_2+A^{-1}}\alpha_{22} & \mathbf{Z_2'W} \\ \mathbf{W'X} & \mathbf{W'Z_1} & \mathbf{W'Z_2} & \mathbf{W'W+I}\lambda \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{m} \\ \hat{p} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z_1'y} \\ \mathbf{Z_2'y} \\ \mathbf{W'y} \end{bmatrix}$$

Misunderstanding AB & G

Maddox Dairy, CA http://menzelphoto.photoshelter.com/image/I00001E2Pn04gL4c

Misunderstanding AB & G



Understanding AB & G

www.agriland.ie

www.angus.org

Understanding B & G

Heritability for human height

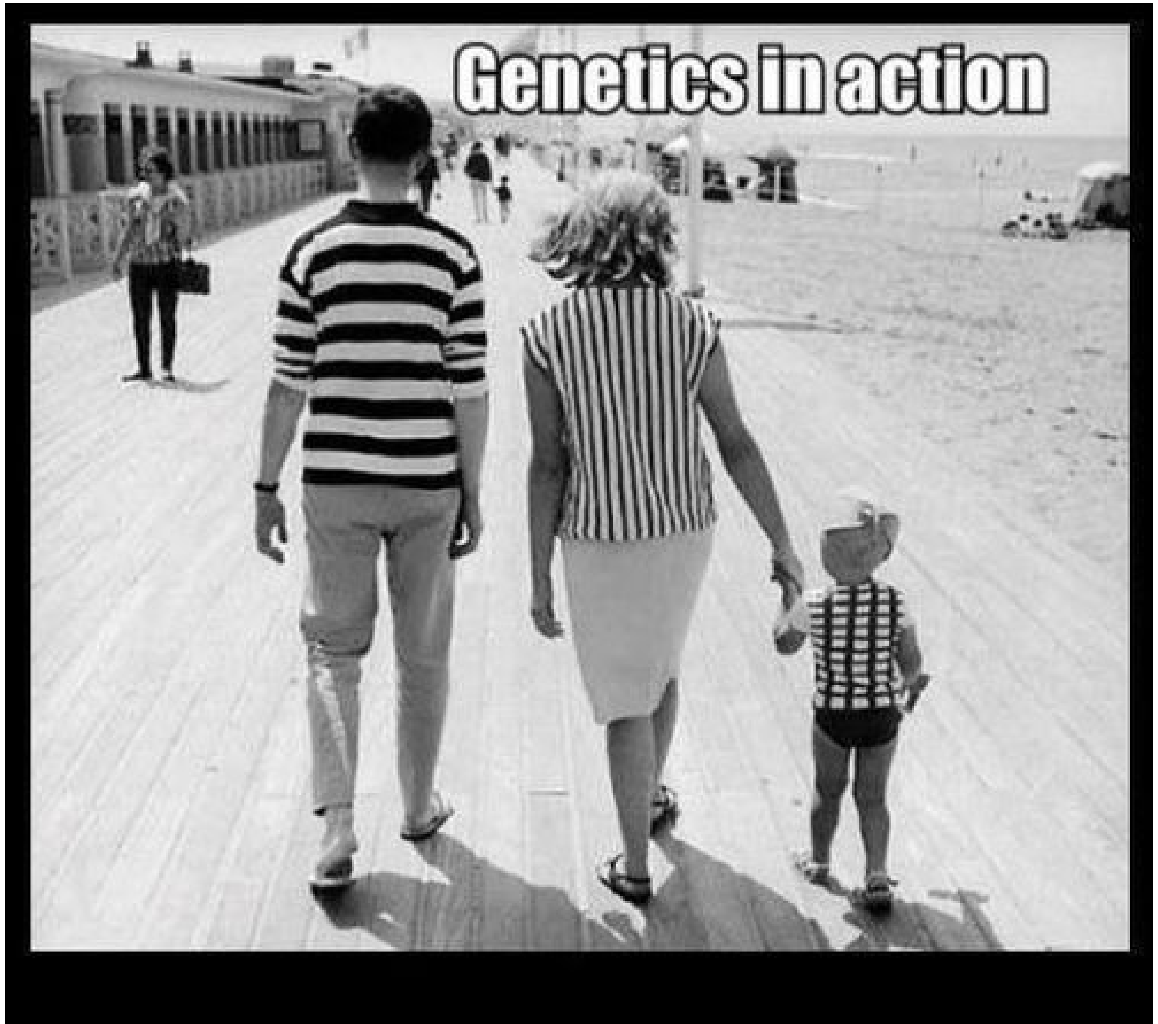
$h^2 = 0.80$

$$h^2 = \frac{\textit{Genetic Variance}}{\textit{Phenotypic Variance}}$$

h^2 $P = G + E$

h^2 $P = G + E$

Understanding B & G



http://imgfave.com/view/6159566

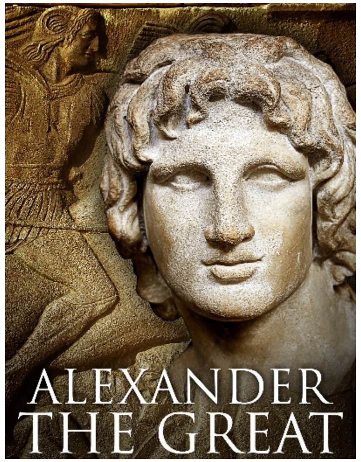
Selection based on phenotypes…

Selecting the best animals BEFORE 1960 – Phenotypic Selection

Jacob in the book of Genesis (2000 BC): Color and strength

https://wwyeshua.wordpress.com/2014/04/10/laban-and-jacob-genesis-3025-chapter-31/

Finest Indian cattle to Macedonia to improve the breed (330 BC)



https://www.youtube.com/watch?v=qdKAooNvA7Y

Selection based on phenotypes…

Selecting the best animals BEFORE 1960 – Phenotypic Selection

#1

#2

http://www.selectsires.com

Phenotypes…

#1

#2

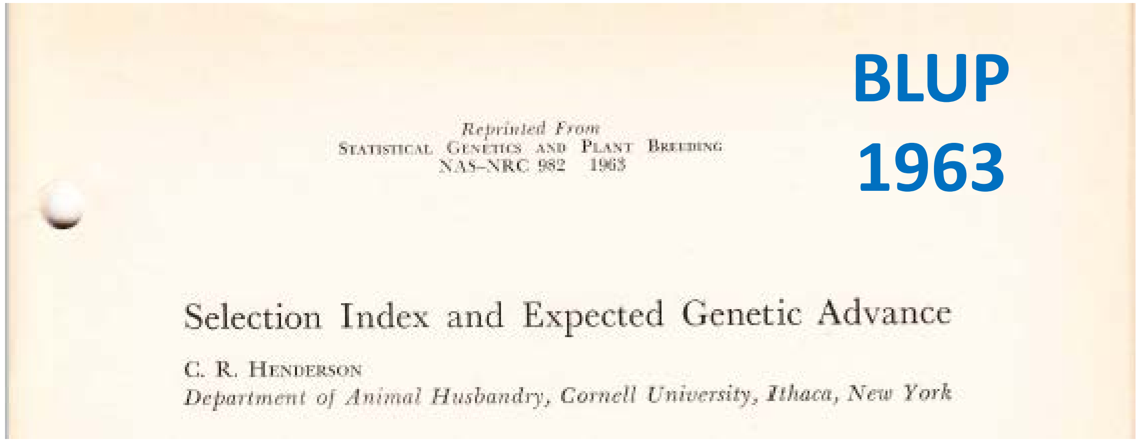
Phenotypes…

Selection: phenotypes + pedigree

Selecting the best animals AFTER 1960

P = G + E

inherited


Reprinted From
STATISTICAL GENETICS AND PLANT BREEDING
NAS–NRC 982 1963

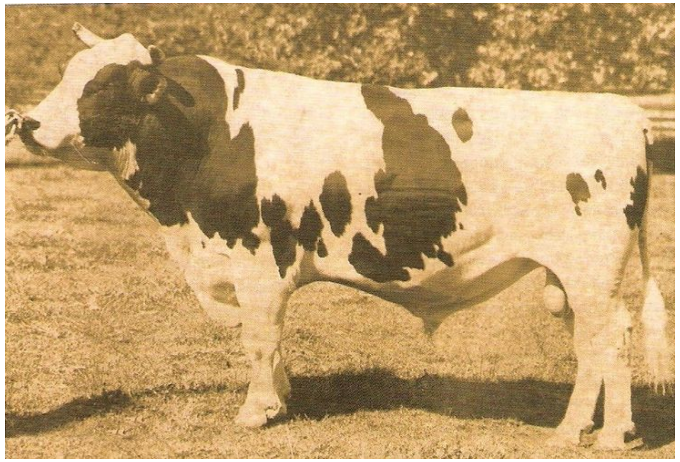
Selection Index and Expected Genetic Advance

C. R. HENDERSON
Department of Animal Husbandry, Cornell University, Ithaca, New York

BLUP
1963

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\lambda \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Selection: phenotypes + pedigree



Pawnee Farm Arlinda Chief

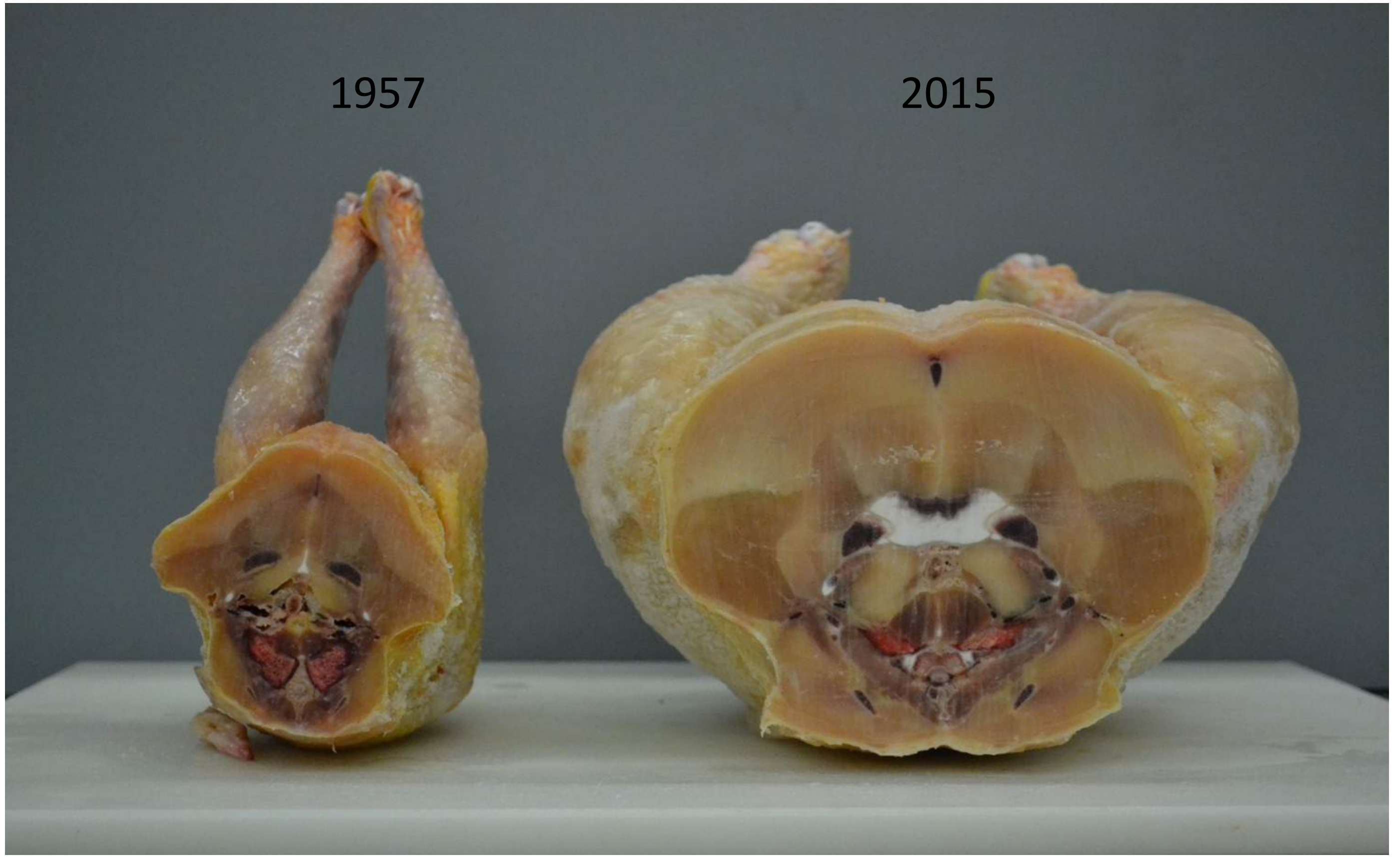
16k daughters

500k grand-daughters

2M great grand-daughters

14% of all Holstein genetics

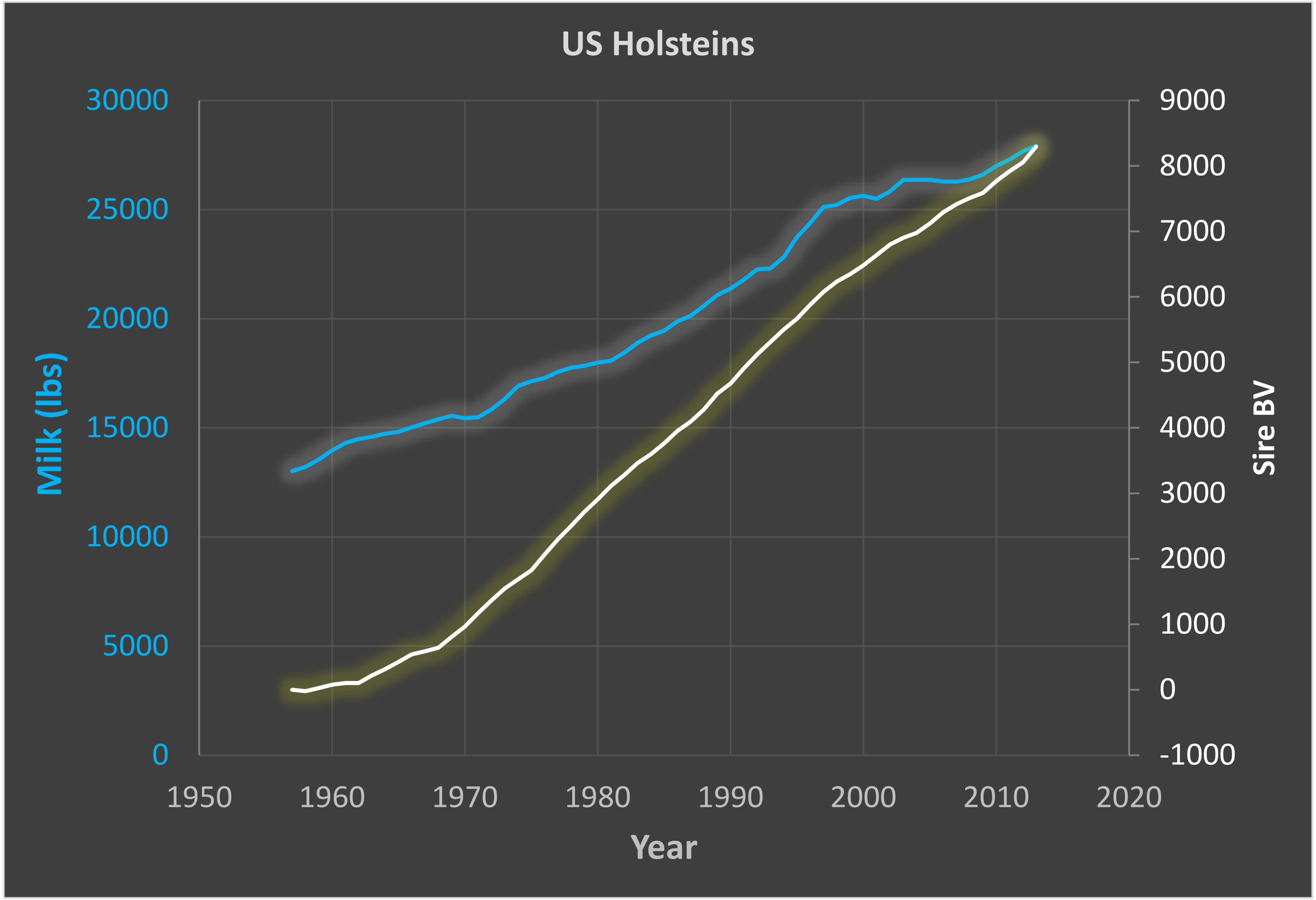
Selection: phenotypes + pedigree



Courtesy of Dr. Nick Dale, Poultry Science, UGA

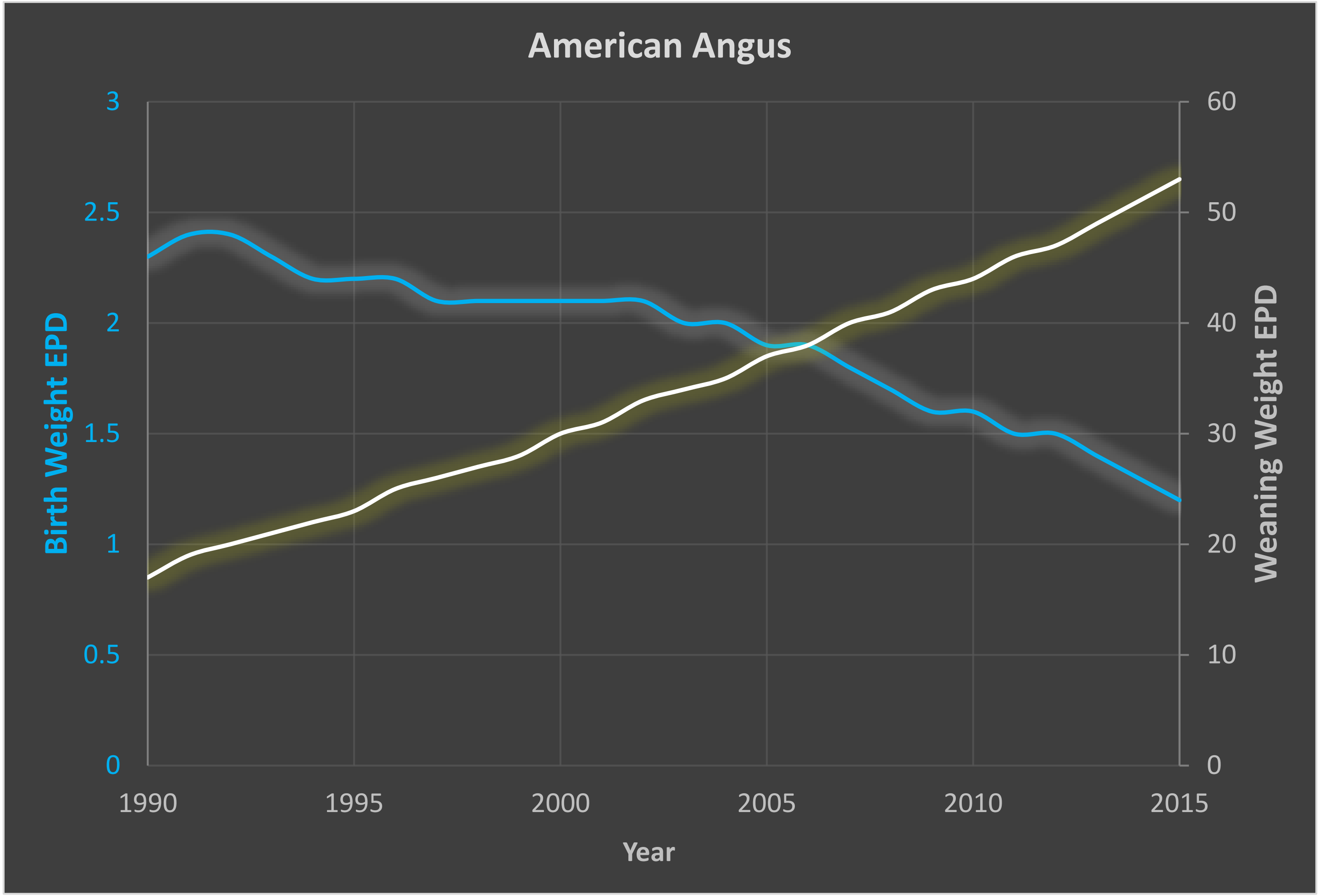
Selection: phenotypes + pedigree

- Production
  - 1957 = 13,000 lbs
  - 2015 = 27,000 lbs
  - 1942 = 25M cows
  - 2015 = 16M cows
- Efficiency
  - 23% of feed intake
  - 35% of water intake



(Adapted from http://aipl.arsusda.gov/eval/summary/trend.cfm)

Selection: phenotypes + pedigree



Selection: phenotypes + pedigree

Feed = 836 lbs

mkt weight = 220 lbs

FCR = 3.8

1972

Feed = 715 lbs

mkt weight = 275 lbs

FCR = 2.6

2007

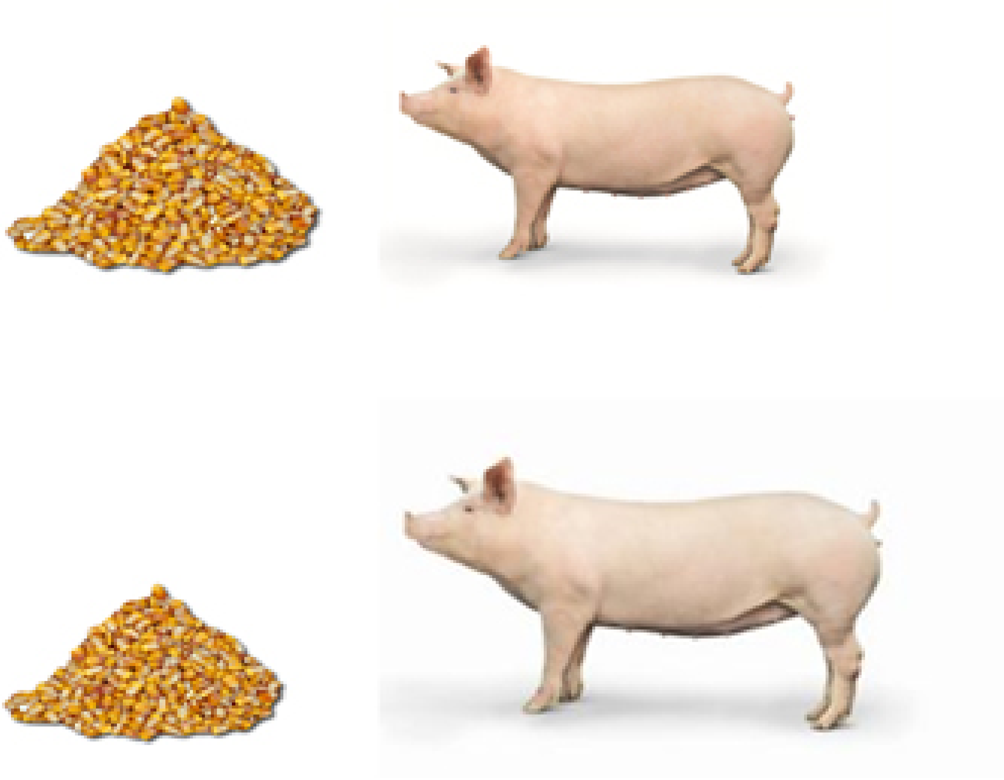
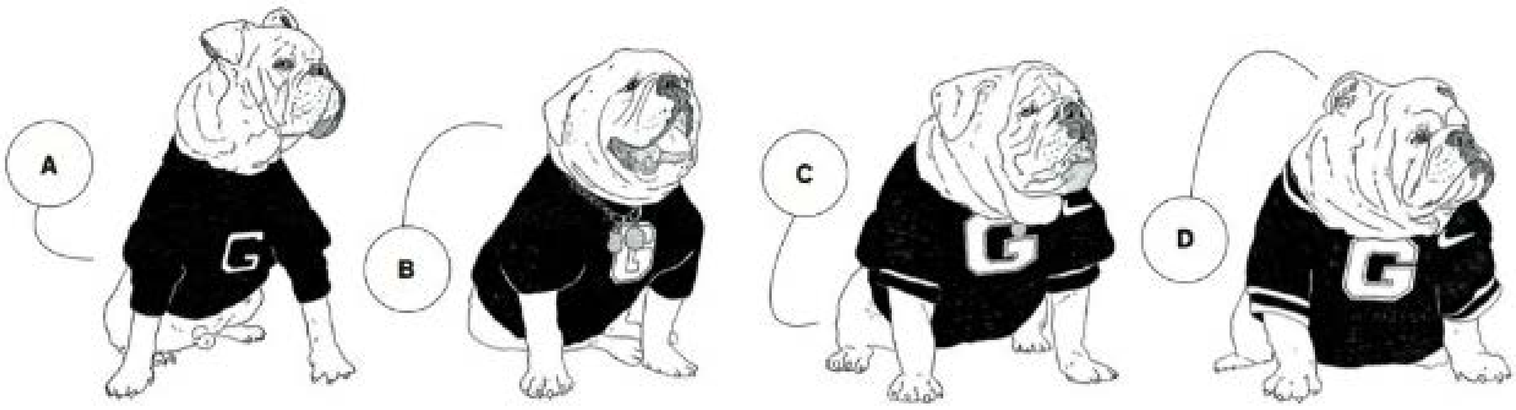


Figure 2. **Improvements in feed conversion ratio.** Feed requirements moved from 836 lbs to produce a 220 market hog in 1972 to 715 lbs of feed in 2007 to produce a 275 lb market hog. (Adapted from Graham Plastow, 2012)

Selection: Game day

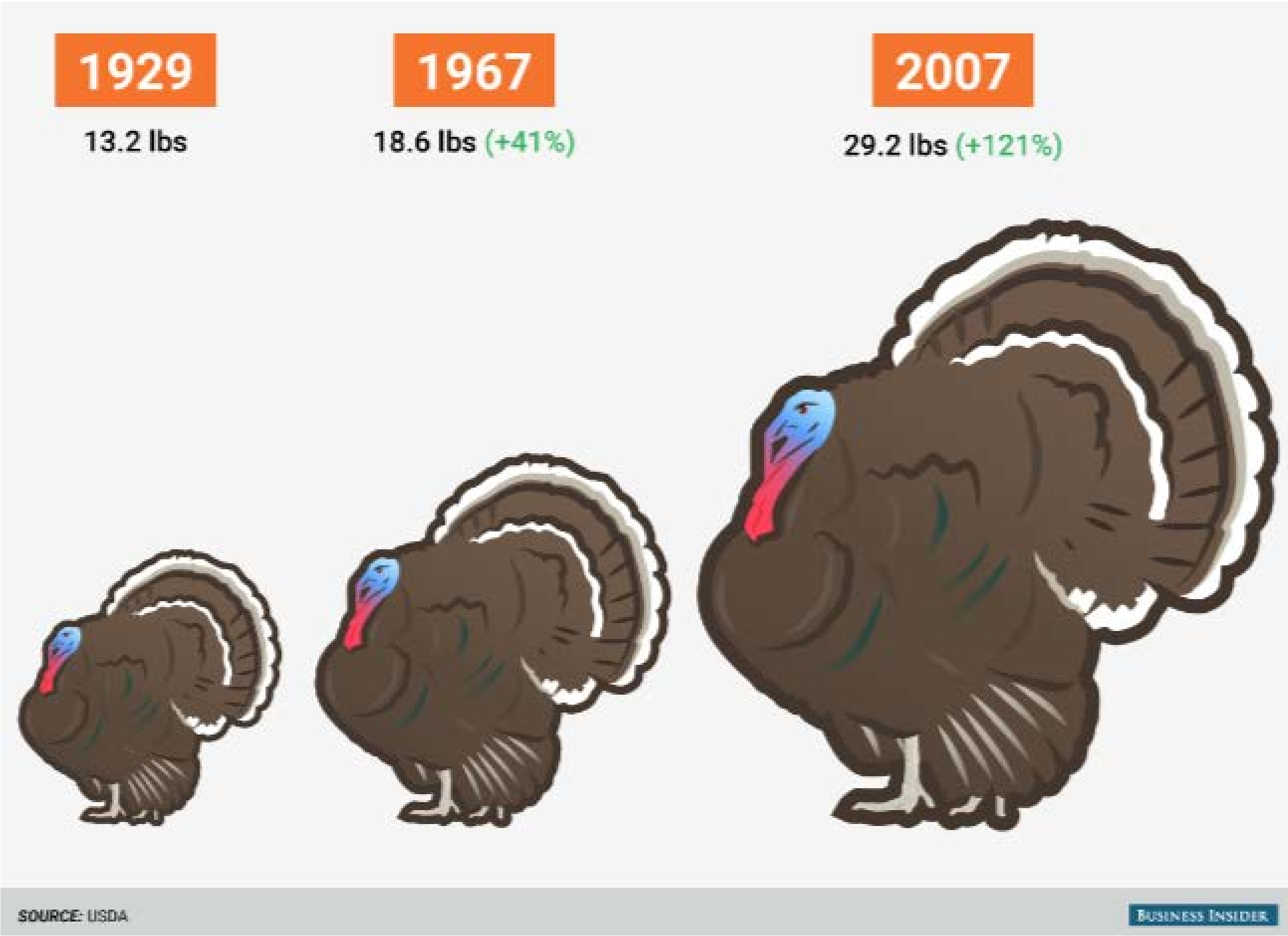


A) Uga I, 1956-66. B) Uga III, 1972-81. C) Uga V, 1990-99. D) Uga VIII, 2010-11. Illustration by Agnese Bicocchi.

http://www.nytimes.com/2011/11/27/magazine/can-the-bulldog-be-saved.html?_r=2&ref=magazine&pagewanted=all&

- No details about selective breeding
- “male-preference genealogy and legitimate birth”

Selection: Thanksgiving



http://www.businessinsider.com

AI

Selection: the urban legend… Chester

The New York Times

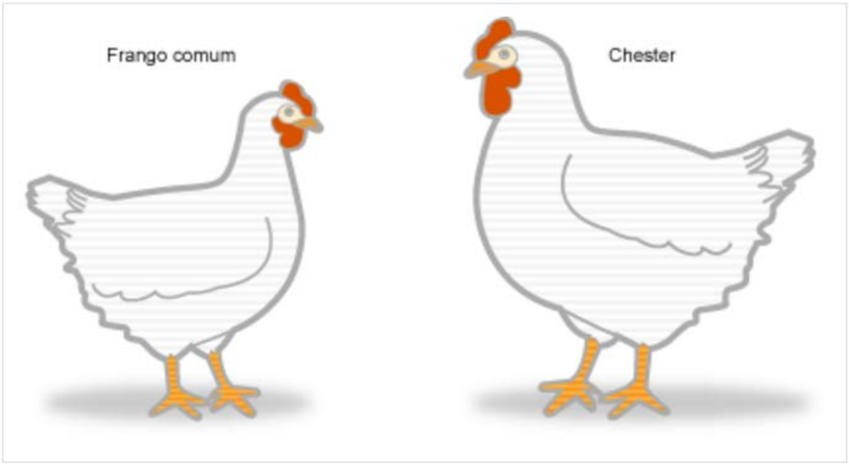
Brazil's Mythical 'Super-Chicken': What, Exactly, Is a Chester?

Perdigão team developed a "super-chicken" that was about 70 percent breast and thigh by weight, compared with 45 percent for typical chickens

"The Chester is just a chicken," BRF says, "in the same way that Pelé is just a soccer player."

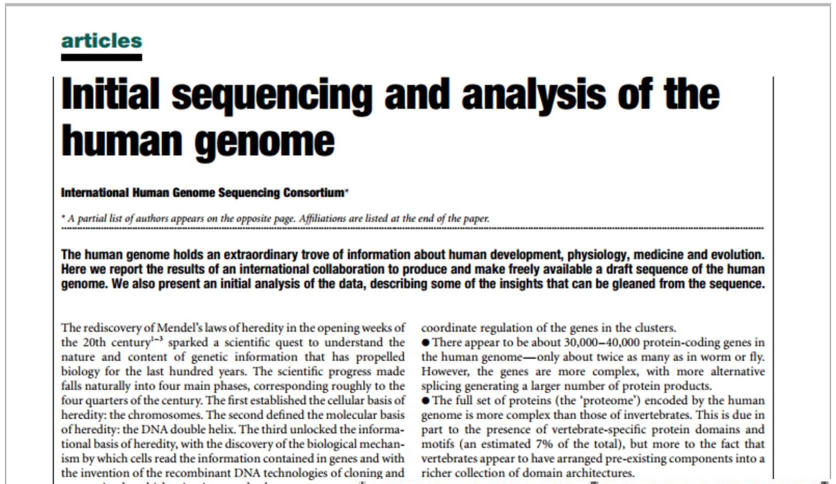
Illustration by Antonio de Luca; Photo by Chepko Danil Vitalevich/shutterstock

http://www.perdigao.com.br



http://ciencia.hsw.uol.com.br/chester.htm

2001: Genotypes as an extra help



articles

Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium*

* A partial list of authors appears on the opposite page. Affiliations are listed at the end of the paper.

The human genome holds an extraordinary trove of information about human development, physiology, medicine and evolution. Here we report the results of an international collaboration to produce and make freely available a draft sequence of the human genome. We also present an initial analysis of the data, describing some of the insights that can be gleaned from the sequence.

The rediscovery of Mendel's laws of heredity in the opening weeks of the 20th century[1–3] sparked a scientific quest to understand the nature and content of genetic information that has propelled biology for the last hundred years. The scientific progress made falls naturally into four main phases, corresponding roughly to the four quarters of the century. The first established the cellular basis of heredity: the chromosomes. The second defined the molecular basis of heredity: the DNA double helix. The third unlocked the informational basis of heredity, with the discovery of the biological mechanism by which cells read the information contained in genes and with the invention of the recombinant DNA technologies of cloning and sequencing by which scientists can do the same.

The last quarter of a century has been marked by a reler to decipher first genes and then entire genomes, spawnir of genomics. The fruits of this work already include th sequences of 599 viruses and viroids, 205 naturally plasmids, 185 organelles, 31 eubacteria, seven arcl fungus, two animals and one plant.

Here we report the results of a collaboration involving from the United States, the United Kingdom, Japa Germany and China to produce a draft sequence of t genome. The draft genome sequence was generated from map covering more than 96% of the euchromatic part of t genome and, together with additional sequence in public it covers about 94% of the human genome. The seq produced over a relatively short period, with coverage r about 10% to more than 90% over roughly fifteen mo sequence data have been made available without restri updated daily throughout the project. The task ahead is to finished sequence, by closing all gaps and resolving all ar Already about one billion bases are in final form and t bringing the vast majority of the sequence to this standa straightforward and should proceed rapidly.

The sequence of the human genome is of interest respects. It is the largest genome to be extensively sequen being 25 times as large as any previously sequenced ge eight times as large as the sum of all such genomes. It vertebrate genome to be extensively sequenced. And, uni the genome of our own species.

Much work remains to be done to produce a comple sequence, but the vast trove of information that ha available through this collaborative effort allows a global p on the human genome. Although the details will cha sequence is finished, many points are already clear.

● The genomic landscape shows marked variation in th tion of a number of features, including genes, tra elements, GC content, CpG islands and recombination gives us important clues about function. For example, opmentally important HOX gene clusters are the most re regions of the human genome, probably reflecting the ver

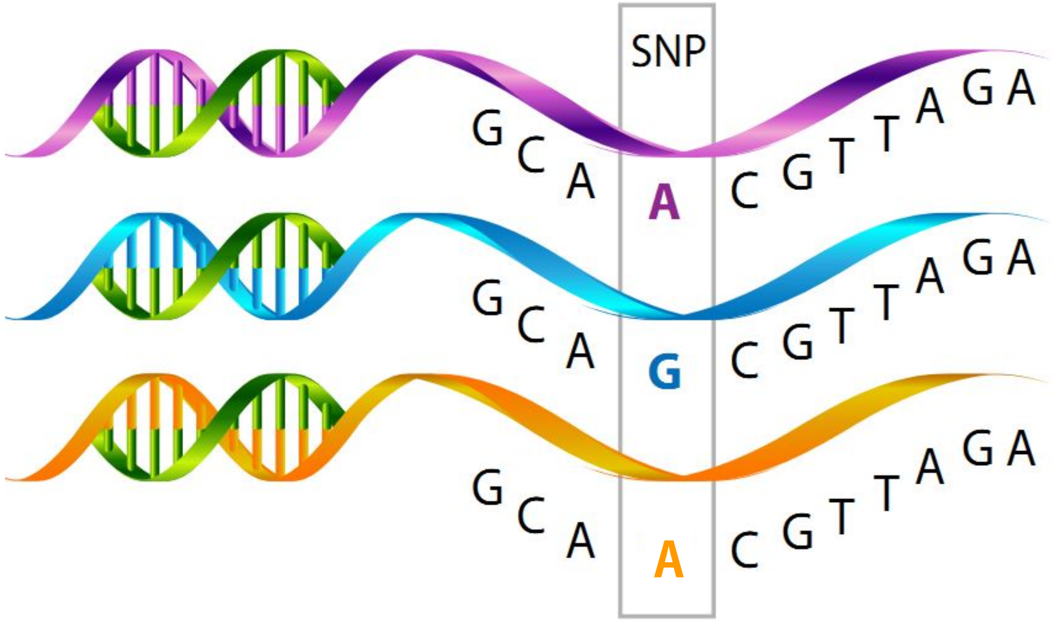
coordinate regulation of the genes in the clusters.

● There appear to be about 30,000–40,000 protein-coding genes in the human genome—only about twice as many as in worm or fly. However, the genes are more complex, with more alternative splicing generating a larger number of protein products.

● The full set of proteins (the 'proteome') encoded by the human genome is more complex than those of invertebrates. This is due in part to the presence of vertebrate-specific protein domains and motifs (an estimated 7% of the total), but more to the fact that vertebrates appear to have arranged pre-existing components into a richer collection of domain architectures.

860

What kind of genomic info?

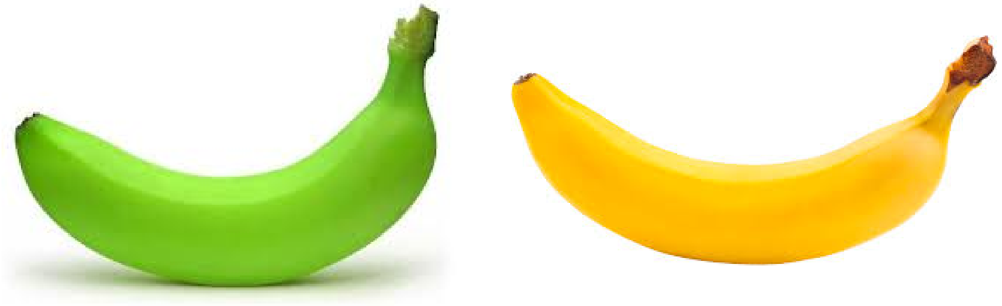


http://neuroendoimmune.files.wordpress.com/2014/03/snp.png

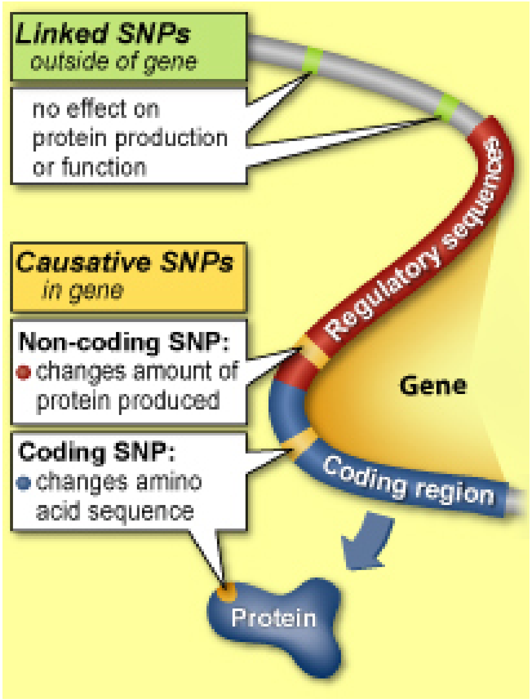
Mutation < 1% < SNP

SNP

- SNP used as markers for genes



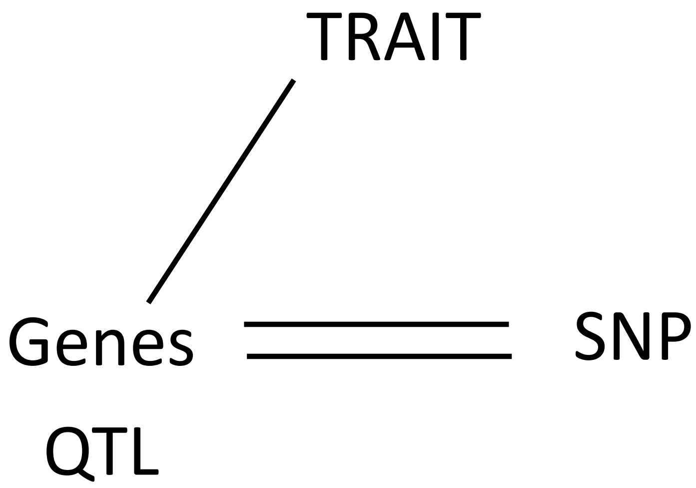
- SNP usually outside genes

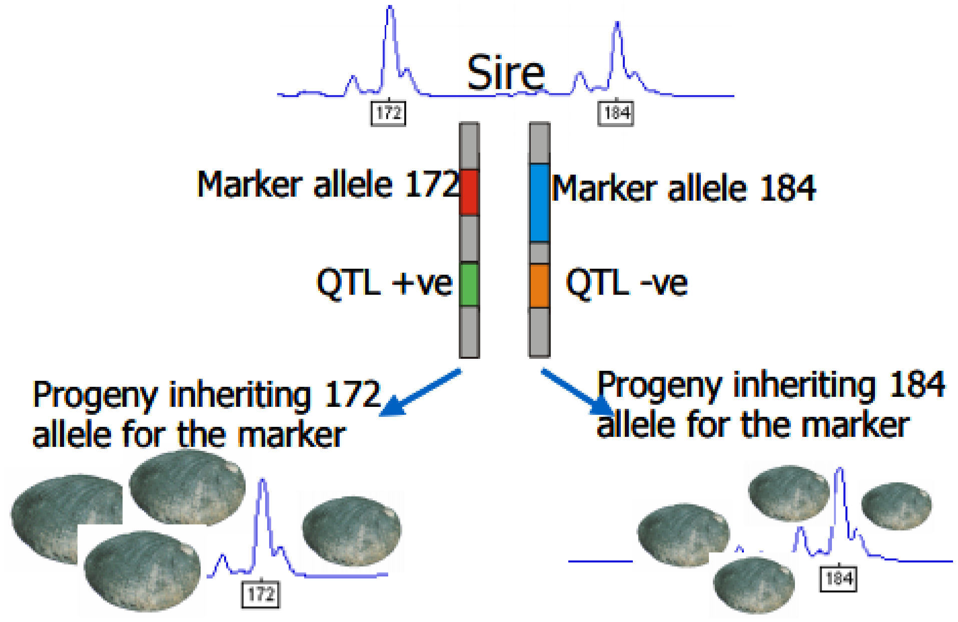


QTL

http://learn.genetics.utah.edu

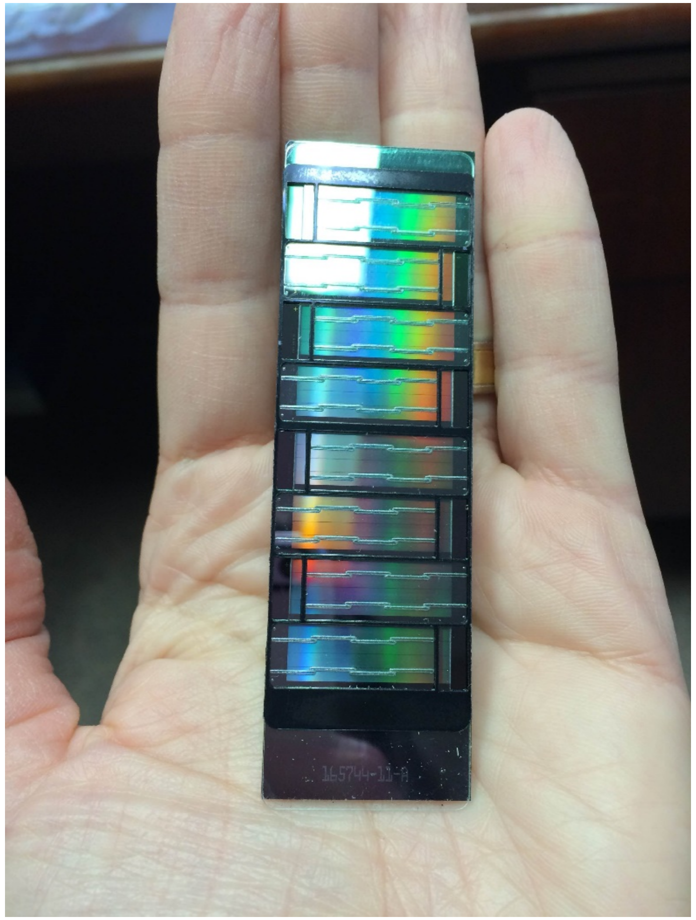
SNP





Adapted from Ben Hayes' course notes: http://snp.toulouse.inra.fr/~alegarra/ben_hayes_course/toulouse_course_notes.pdf

SNP



- Traits of interest are polygenic

- 3k SNP
- 50k SNP
- 777k SNP

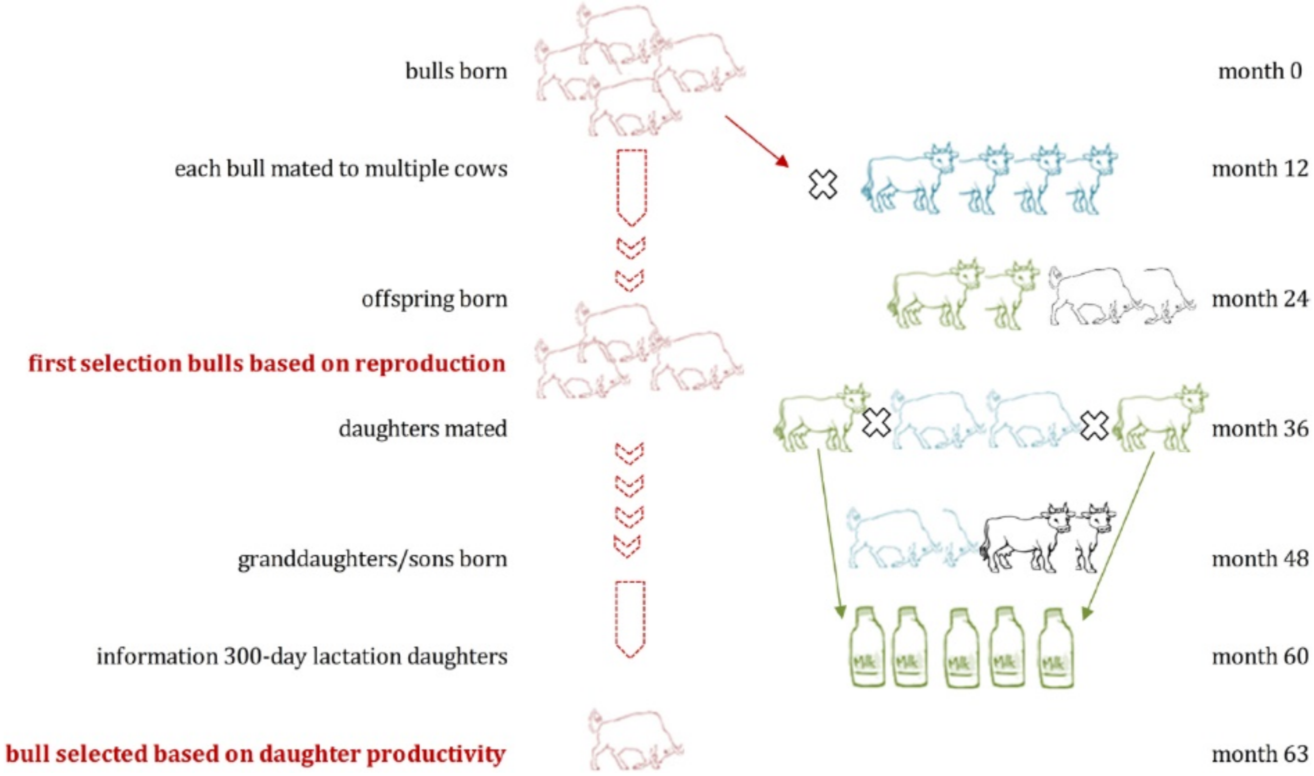
- How can it help us?

Selection: phenotypes + pedigree

Freddy: 2004

http://genex.crinet.com

Jonas & de Koning 2015

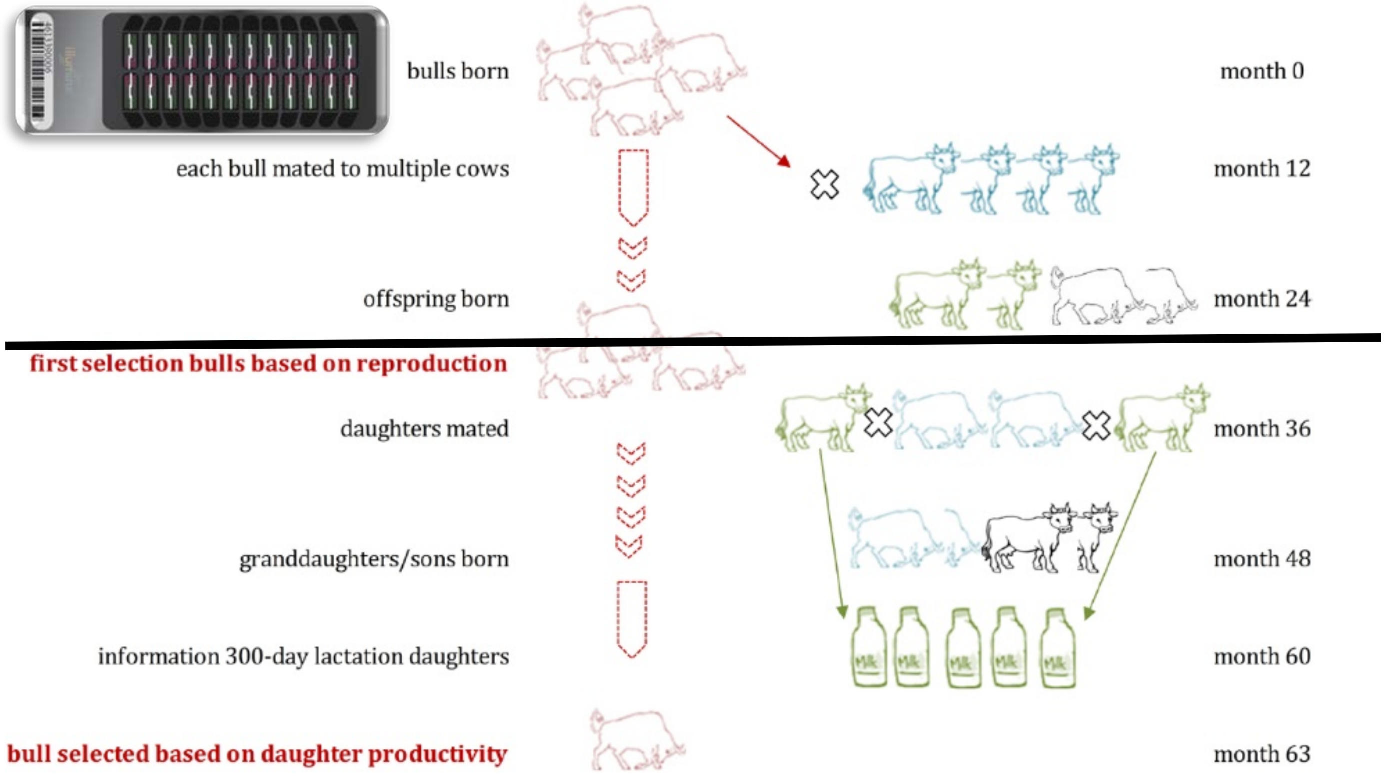


Selection: phenotypes + pedigree + genotype

Freddy: 2004

http://genex.crinet.com

Jonas & de Koning 2015



Selection: phenotypes + pedigree + genotype

Freddy: 2004

http://genex.crinet.com

daughters 2009:
0

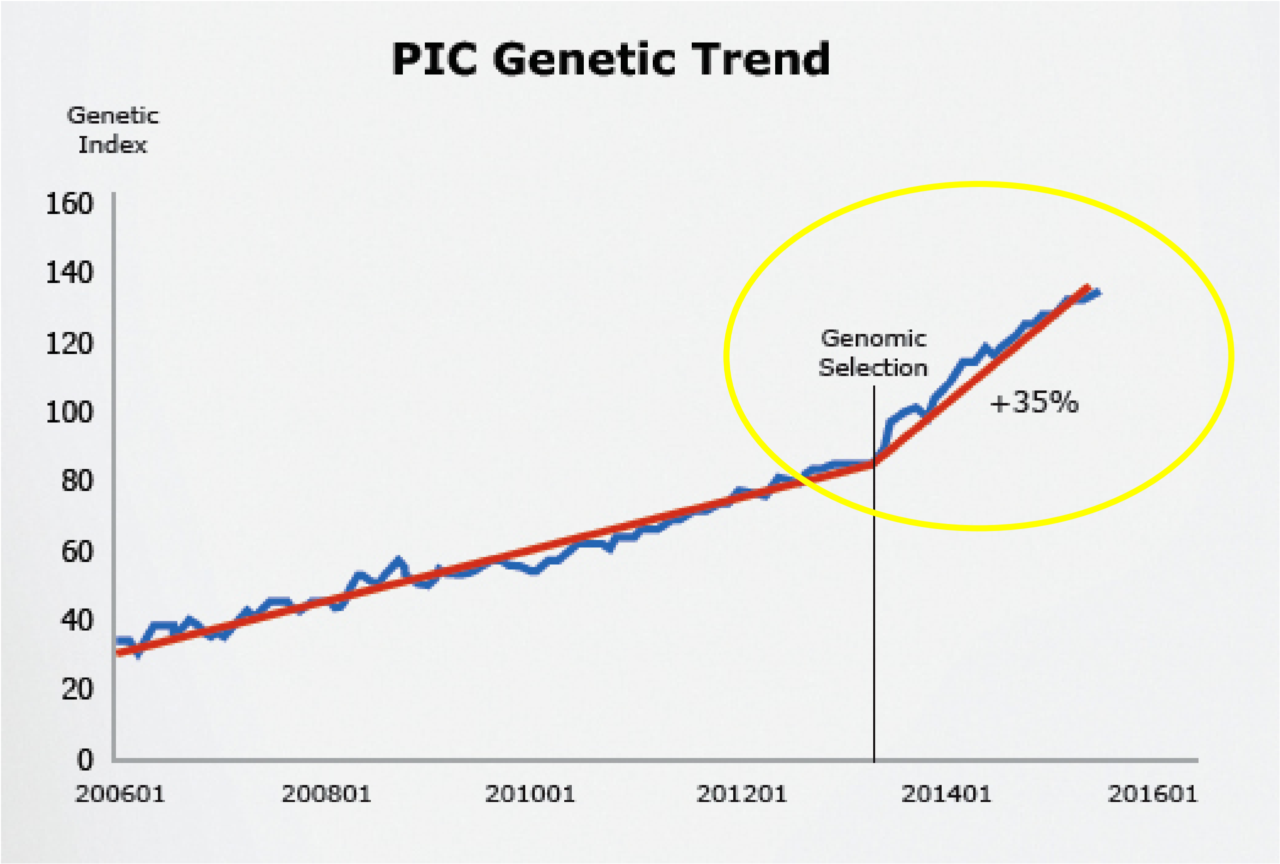
50K SNP + parent information

daughters 2012:
346

Net merit = $792

7 bulls > $700

Selection: phenotypes + pedigree + genotype



http://www.thepigsite.com/swinenews/42116/the-next-step-in-pig-genetic-improvement-sequencing-the-pic-genome/

- Genomic Evaluation/Selection
- All livestock Species

Next : phenotypes + pedigree + sequence data

- 38M SNP

https://mokaspetridish.files.wordpress.com/2012/11/screen-shot-2012-11-18-at-11-21-25-am.png

http://mtc.science/playing-around-with-ngs-step-by-step

Still developing methods

AB & G

https://www.google.com/imghp

Codebreakers

- Statistical methods by AB & G Researchers
- Used in plant breeding and Human genetics

Statistical methods

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'Z_1} & \mathbf{X'Z_2} & \mathbf{X'W} \\ \mathbf{Z_1'X} & \mathbf{Z_1'Z_1+A^{-1}}\alpha_{11} & \mathbf{Z_1'Z_2+A^{-1}}\alpha_{12} & \mathbf{Z_1'W} \\ \mathbf{Z_2'X} & \mathbf{Z_2'Z_1+A^{-1}}\alpha_{21} & \mathbf{Z_2'Z_2+A^{-1}}\alpha_{22} & \mathbf{Z_2'W} \\ \mathbf{W'X} & \mathbf{W'Z_1} & \mathbf{W'Z_2} & \mathbf{W'W+I}\lambda \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{m} \\ \hat{p} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z_1'y} \\ \mathbf{Z_2'y} \\ \mathbf{W'y} \end{bmatrix}$$

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \tau(\alpha\mathbf{G} + \beta\mathbf{A}_{22})^{-1} - \omega\mathbf{A}_{22}^{-1} \end{bmatrix}$$

$$\mathbf{G}^{-1} = \begin{bmatrix} \mathbf{G}_{pp}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{-G}_{pp}^{-1}\mathbf{G}_{py} \\ \mathbf{I} \end{bmatrix} \mathbf{M}_g^{-1} \begin{bmatrix} \mathbf{-G}_{yp}\mathbf{G}_{pp}^{-1} & \mathbf{I} \end{bmatrix}$$

$$m_{g,i} = g_{ii} - \mathbf{G}_{ip}\mathbf{G}_{pp}^{-1}\mathbf{G}_{pi}$$

[THANKS]