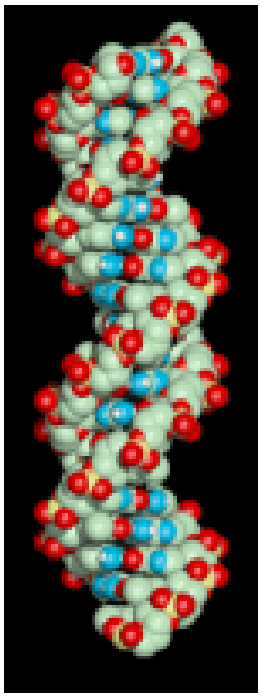
Introduction to Animal Breeding & Genomics

Sinead McParland

Teagasc, Moorepark, Ireland

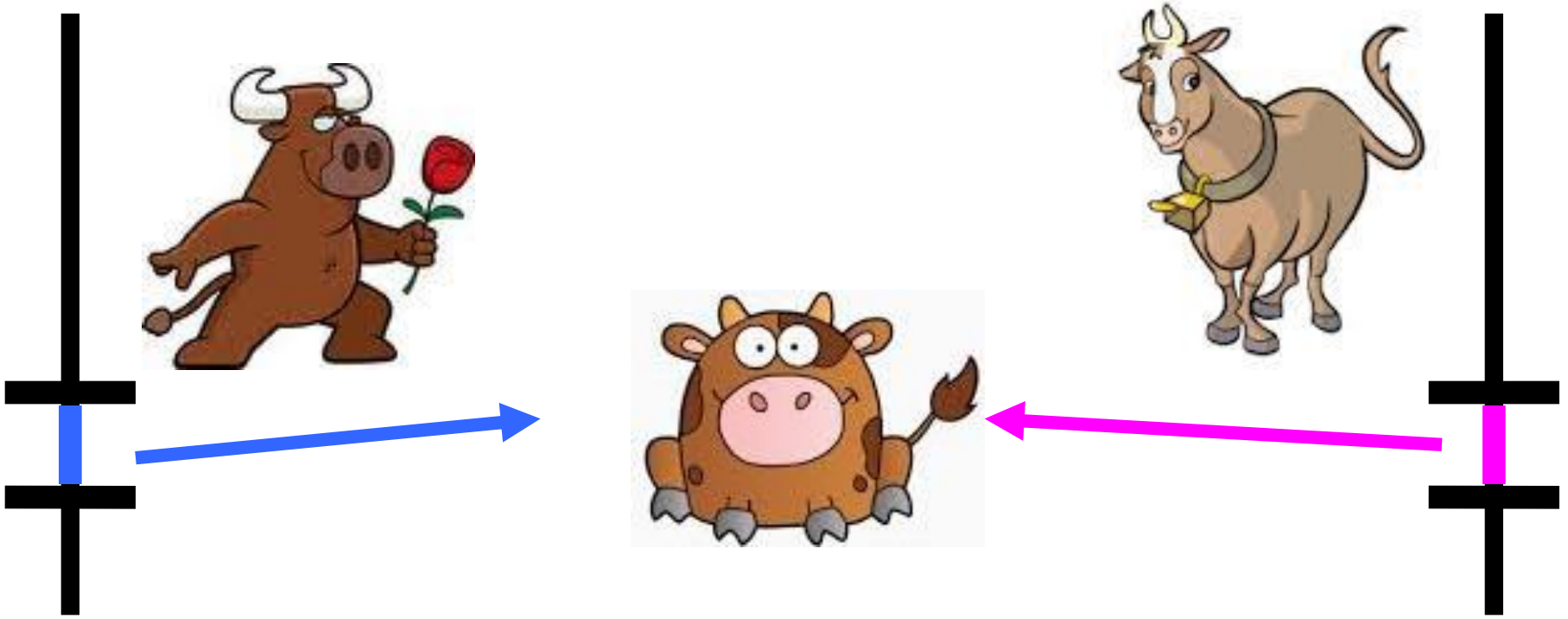
Sinead.McParland@teagasc.ie

Overview



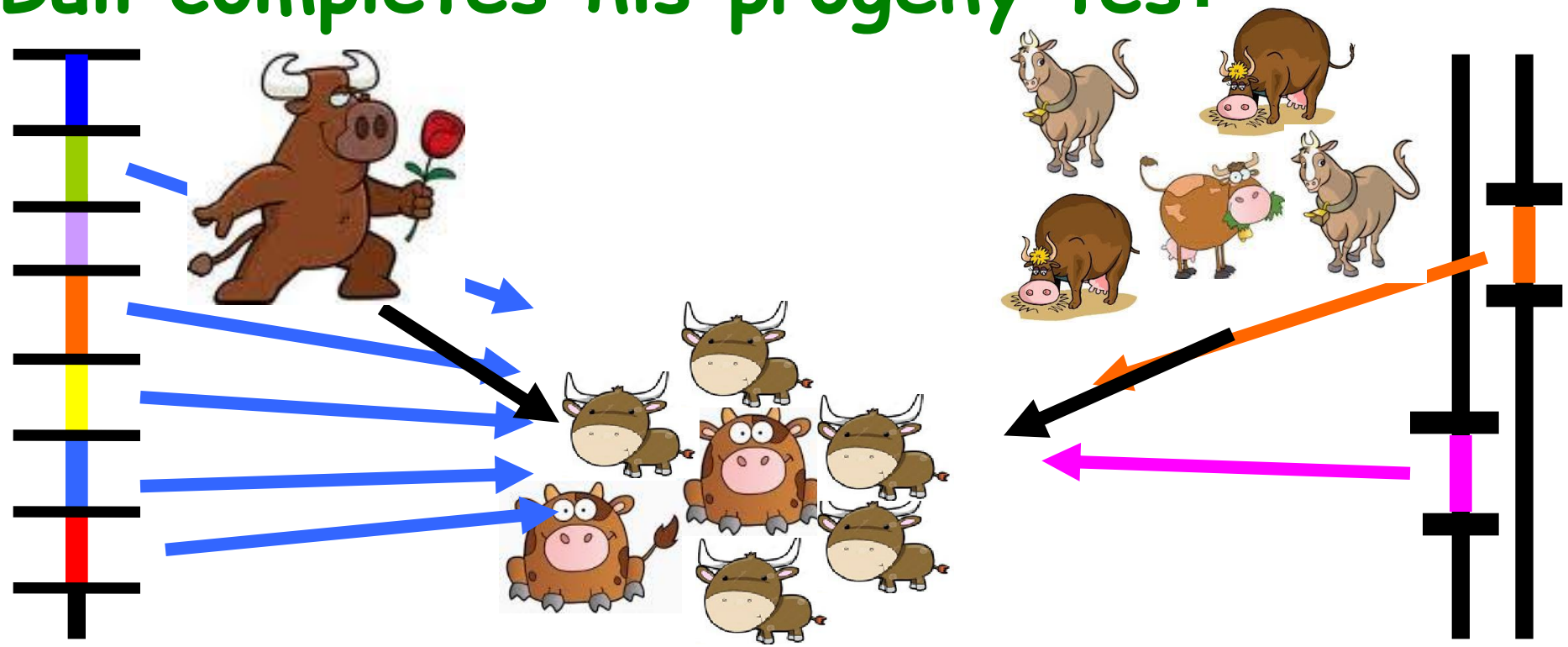
- Changes to traditional animal breeding
- Using DNA in animal breeding
- What is a SNP?!
- De-mystify genomic selection!!

Traditional Animal Breeding



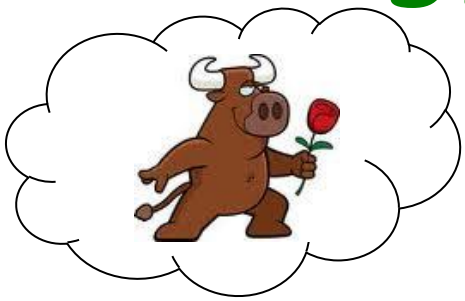
- Calf has weaning weight of 250 kg
- Bull reliability 25%

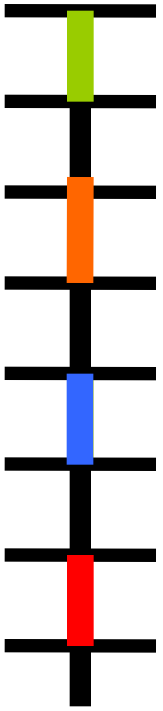
Bull completes his progeny test



- Bull has 100 calves on the ground
- More of his DNA expressed in the population
- Bull reliability increases to ~80%

Using technology of today





- At birth we know about parts of the calf DNA
- Calf BV reliability increases to ~ 58%
  - Equivalent to 54 daughters milking

DNA - From the tip of your nose to the tops of your toes!!

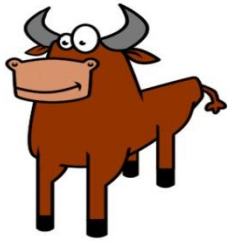
DNA is the same in every cell of your body and doesn't change throughout your life

How do we use this DNA information?

What is a SNP?

- 99.9% of human DNA is identical – most of the differences are in the form of SNPs

… ACGTACGTCAATGACTTTTACGTAT…



… ACGTACGACAATGACTTTTACGTAT…

- Single Nucleotide ~~Polymorphism~~ Change

How do SNPs relate to performance?

- The cattle genome has ~ 3 billion nucleotides
- Scientists have discovered ~ 40 million SNPs

- At a SNP locus different variants are present
  - Different variants have different associations with performance

SNP effect on performance

SNP	Var	Carcass Fat	Wean Wt
1	A	+5	-0.6
1	G	+20	-0.4
2	A	12.3	-0.6
2	T	-14.46	+20.2
⋮	⋮	⋮	⋮
n	A	+25	+5.2

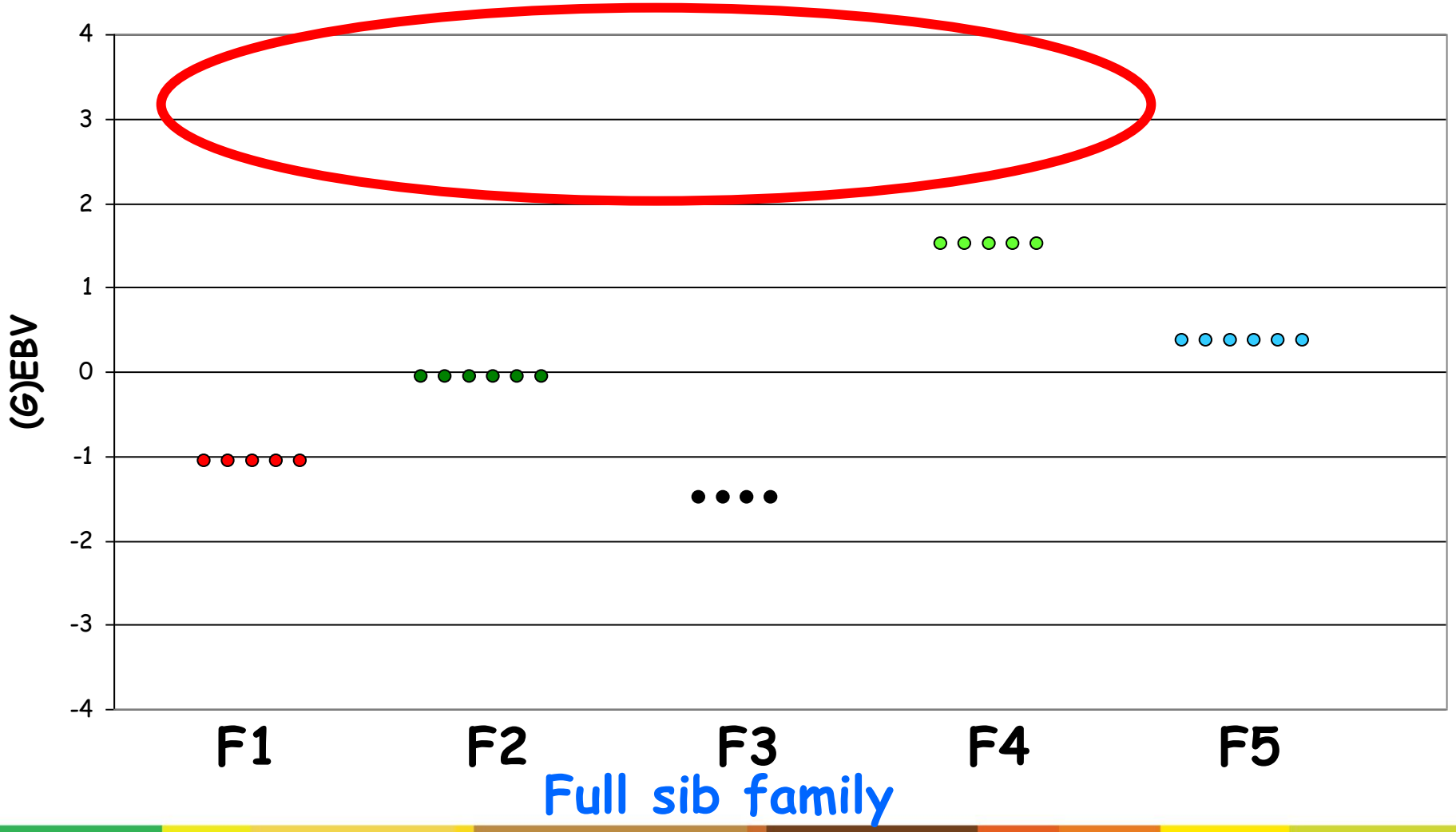
Genomic selection

- Increase accuracy of selection at a younger age

- Traditionally used parental information
  - Progeny = ½ mother + ½ father DNA
  - Progeny = average of mother & father BVs
  - Assumed full sibs were identical

- Available SNP information can be used to supplement the traditional approach
  - See difference in full-sibs at birth

Indentifying Mendelian sampling term



Why not 100% accurate?

- Phenotypes / performance are typically affected by more than one gene
  - Up to 80% of human stature attributable to genetics – no major gene found to date
- Genes may influence more than one phenotype / performance
- Genes interact with one another
- Genes interact with the environment

Cost of sequencing has decreased

But we don't need to know about EVERY piece of DNA in the body

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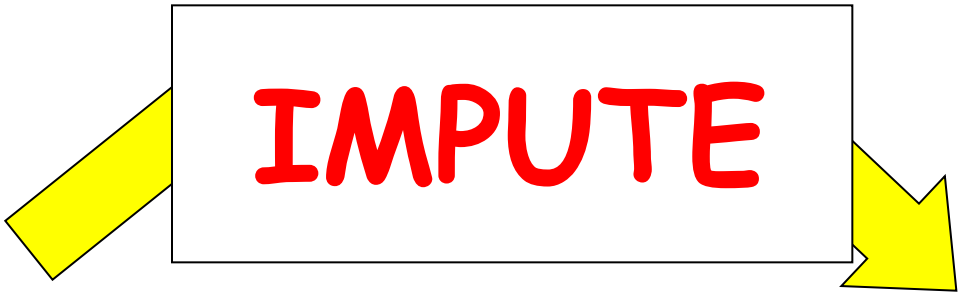
Applied Biosciences (2004)
$15,000,000

Illumina (2011)
$15,000

Different SNP platforms (levels of DNA information) available

54,609 SNPs

50k chip



15,000 SNPs

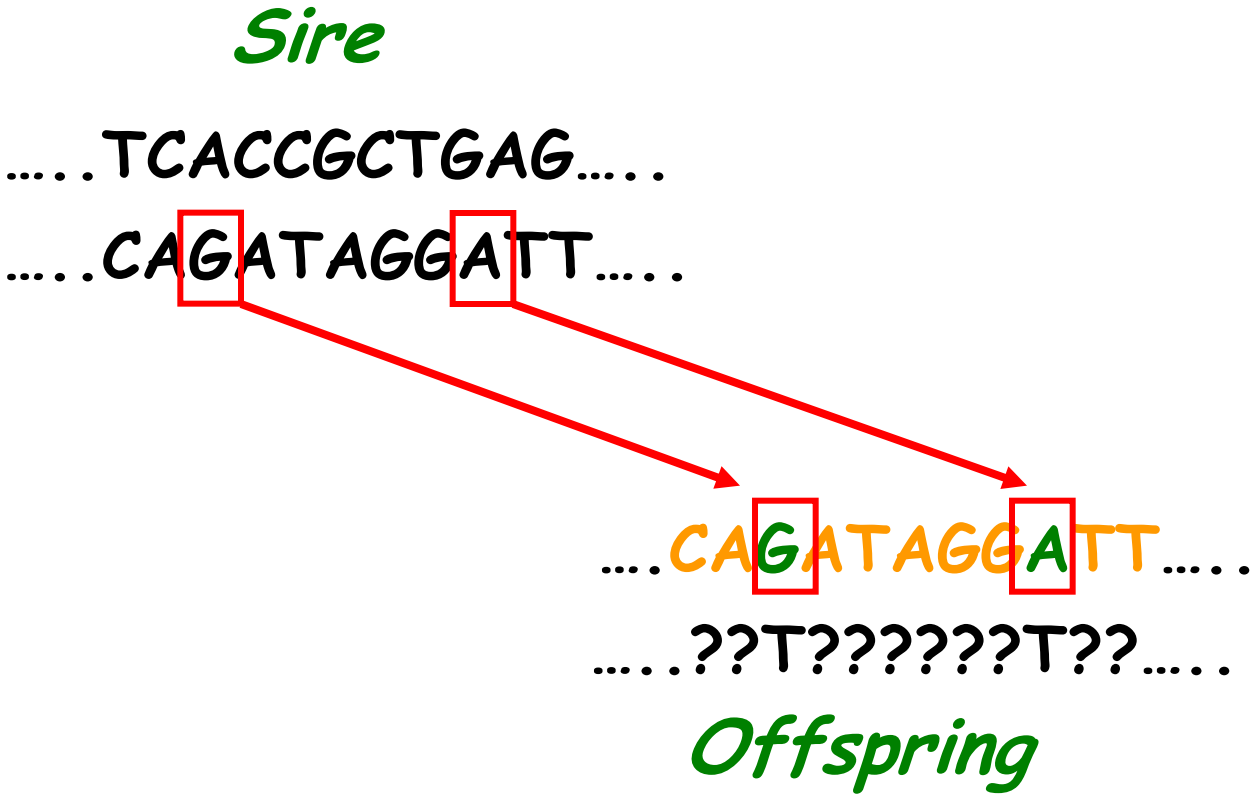
IBD

777,962 SNPs

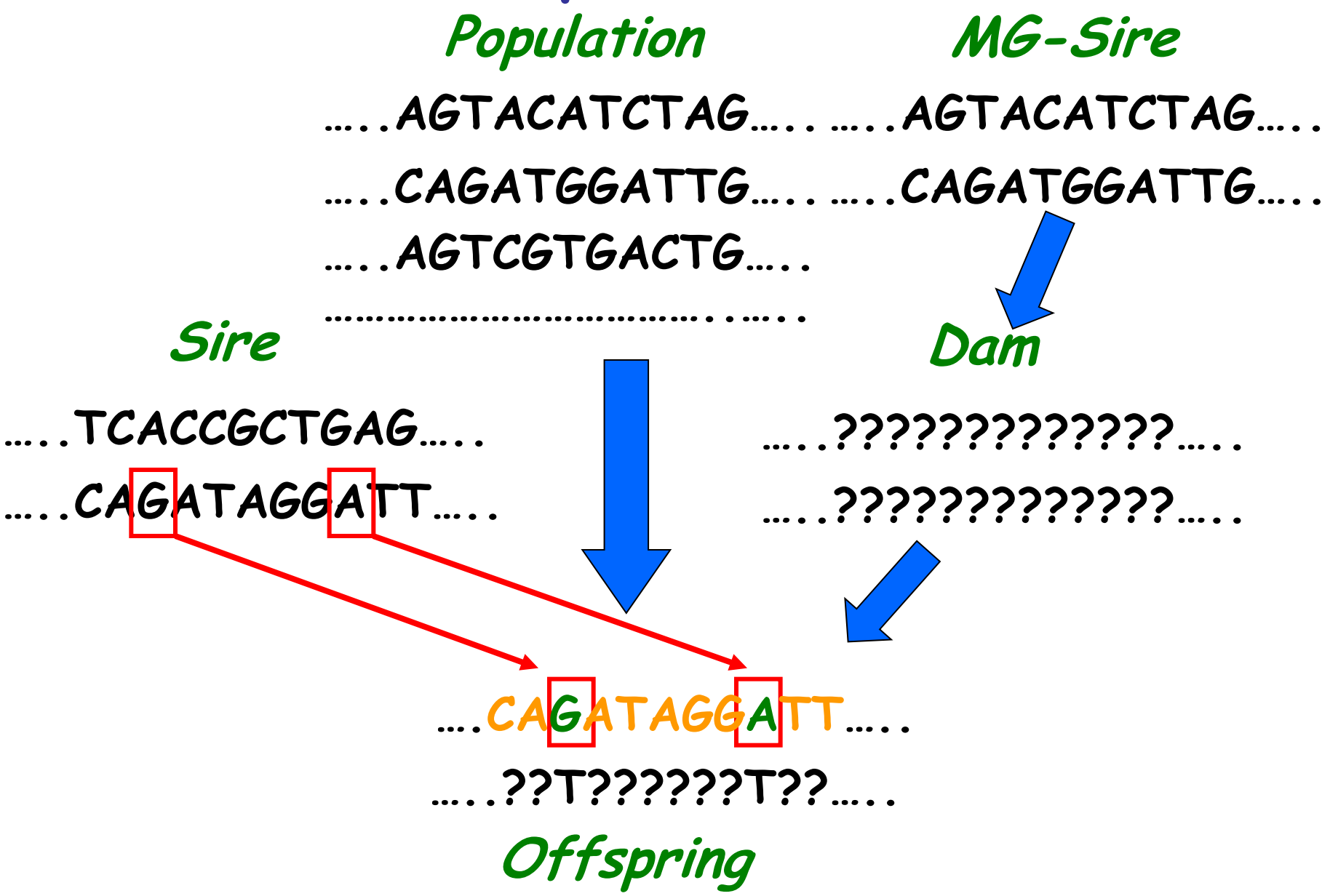
High Density chip

Imputation

Imputation



Imputation


Population
MG-Sire
…..AGTACATCTAG…..
…..CAGATGGATTG…..
…..AGTCGTGACTG…..
……
…..AGTACATCTAG…..
…..CAGATGGATTG…..
Sire
Dam
…..TCACCGCTGAG…..
…..CAGATAGGATT…..
…..???????????…..
…..???????????…..
….CAGATAGGATT…..
…..??T?????T??…..
Offspring

Imputation

Population *MG-Sire*

…..AGTACATCTAG….. …..AGTACATCTAG…..

…..T

…..C

Accuracy in dairy populations

Sire is known – 99%

No sire or MGS – 98%

….CAGATAGGATT…..

….AGTACATCTAG…..

Offspring

Parentage

Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

…..??G?????A??….

…..??T??????T??…..

Offspring

Parentage

Database

Sire 1 …..TCGGGCTGTG…..

Sire 2 …..CAGATAGGATT…..

Sire 3 …..TCACCGCTGAG…..

Sire 4 …..CAAATAGGCTT…..

Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

…..??A?????C??….

…..??T?????T??…..

Offspring

Parentage

Database

Sire 1 TCCCCCTCTC...

T.....

.....

.....

80% of parentage errors corrected using this method

....CAAATAGGCTT.....

.....??T??????T??.....

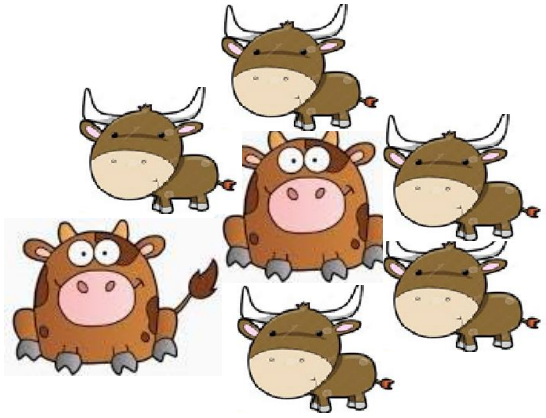
Offspring

Additional advantage of the IDB

- Screening of
  - Deleterious recessive disorders
  - Congenital disorders
  - Major genes

Deleterious recessive genetic disorders

AB



AB

Has CVM

AA

AB

BB

No CVM

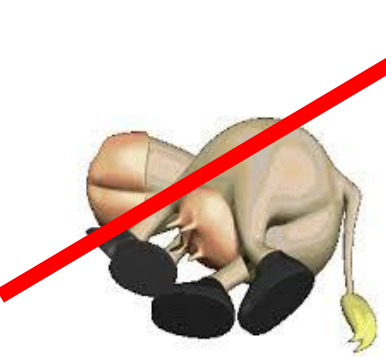
Carries CVM

- Non-CVM allele (B) expressed whenever present
- CVM Allele is recessive "hidden" when with non-CVM

Screen for CVM through genotyping

AB

BB



AA

BB No CVM

AB Carries CVM

- Customised chip will identify "carriers" of genetic recessive disorders
- Choose NOT to mate 2 carriers of CVM

To Conclude

- Differences seen between individuals of a species are mostly due to SNPs
- We can relate SNP variants to performance
  - Genomic selection
- Customised chip developed for Ireland for beef & dairy animals
- SNP information can also be used to predict parentage accurately & identify disorders

Thank you
for your attention