# Introduction to GWAS Genotyping

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### Genotyping

### - A very brief overview -

#### The first steps – **Biomarkers**



A MOLECULAR APPROACH TO THE STUDY OF GENIC HETEROZYGOSITY IN NATURAL POPULATIONS. I. THE NUMBER OF ALLELES AT DIFFERENT LOCI IN DROSOPHILA PSEUDOOBSCURA<sup>1</sup>

J. L. HUBBY AND R. C. LEWONTIN Department of Zoology, University of Chicago, Chicago, Illinois Received March 30, 1966

<sup>1</sup>The work reported here was supported in part by grants from the National Science Foundation (GB 3013) and the Public Health Service ((06-15206)).





https://academic.oup.com/genetics/article/54/2/577/5988209

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FIGURE 1.—Gel illustrating sample placement and typical results of strain analysis for Eaterise-5. The first and the last samples were derived from the standard reference strain (E-51-09), while positions 2 through 6 were obtained from five individuals of one strain and positions 7 through 11 are from five individuals of a second strain. Positions 2, 3, and 6 contain Eaterase-5-95, position 5 contains Exterase-51-17, and position 4 contains Esterase-5<sup>49</sup>, Esterase-5<sup>1,12</sup>, and a site of activity between them. Positions 7, 8, and 9 contain Esterase-5<sup>1,13</sup> and positions 10 and 11 contain Esterase-5<sup>1,10</sup> and Esterase-5<sup>1,12</sup>. A site of activity midway between the latter two is barely discernible. In all the figures the direction of migration of the protein is down toward the anode.

### From few to many markers – Molecular markers (DNA markers)



- arise from different classes of DNA mutations such as substitution mutations (point mutations), rearrangements (insertions or deletions) or errors in replication of tandemly repeated DNA
- are usually located in non-coding regions of DNA
- are virtually unlimited in number and are not affected by environmental factors and/or the developmental stage of the plant/animal/human
- RFLP, AFLP, RAPD, SSR (microsatellites), SNP, CNV, InDel ...

### From few to many markers – Molecular markers (DNA markers)



*Euphytica* (2005) 142: 169–196 DOI: 10.1007/s10681-005-1681-5

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# An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts

#### B.C.Y. Collard<sup>1,4,\*</sup>, M.Z.Z. Jahufer<sup>2</sup>, J.B. Brouwer<sup>3</sup> & E.C.K. Pang<sup>1</sup>

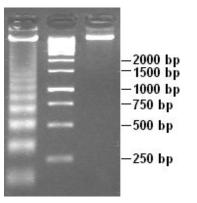
<sup>1</sup>Department of Biotechnology and Environmental Biology, RMIT University, P.O. Box 71, Bundoora, Victoria 3083, Australia; <sup>2</sup>AgResearch Ltd., Grasslands Research Centre, Tennent Drive, Private Bag 11008, Palmerston North, New Zealand; <sup>3</sup>P.O. Box 910, Horsham, Victoria, Australia 3402; <sup>4</sup>Present address: Plant Breeding, Genetics and Biotechnology Division, International Rice Research Institute (IRRI), DAPO Box 7777, Metro Manila, Philippines; (\*author for correspondence: e-mail: bcycollard@hotmail.com)

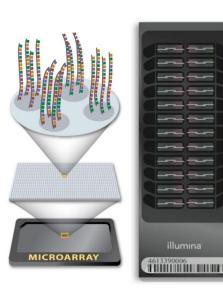
Received 11 July 2004; accepted 2 February 2005

Genotyping Systems

Marker gel

(a few markers)





SNP array

(100s -1,000,000s )



(1,000,000s +)

 $\rightarrow$ (GBS) $\rightarrow$  Genome sequencer





### SNP array genotyping

GENOMIC DNA (200 ng)

DAY 2

3 Fragment Amplified DNA

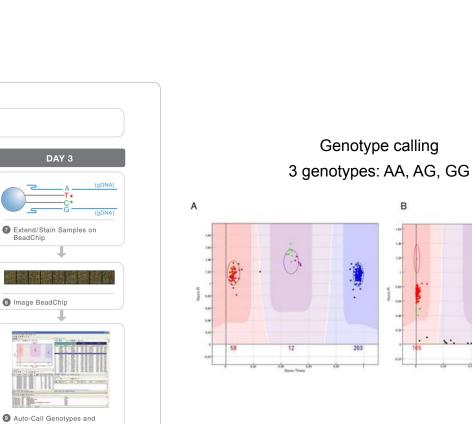
Precipitate & Resuspend

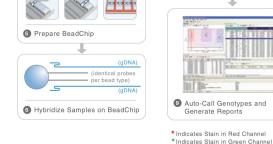
Figure 1: Infinium Assay Protocol

DAY 1

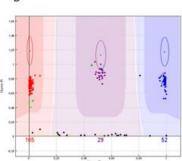
1 Make Amplified DNA

Incubate Amplified DNA



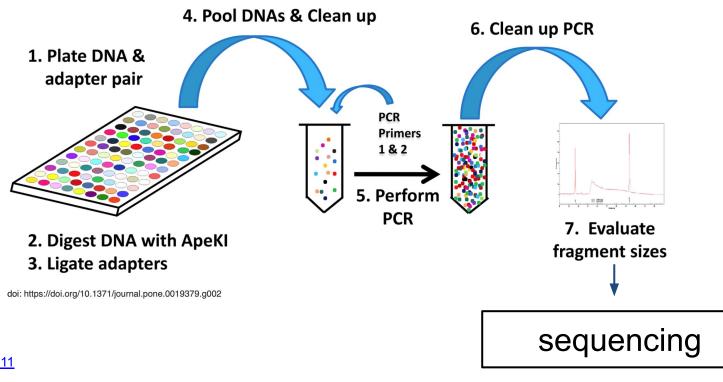


BeadChip





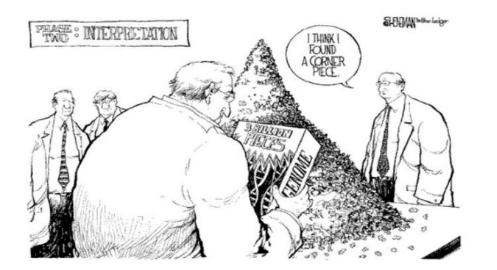
Reduced representation sequencing – Genotyping-by-Sequencing (GBS)



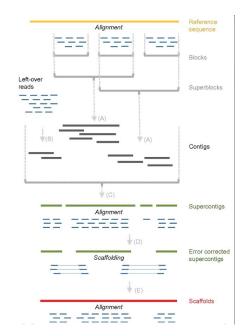
Elshire et al. 2011

### The Next Generation Sequencing Revolution



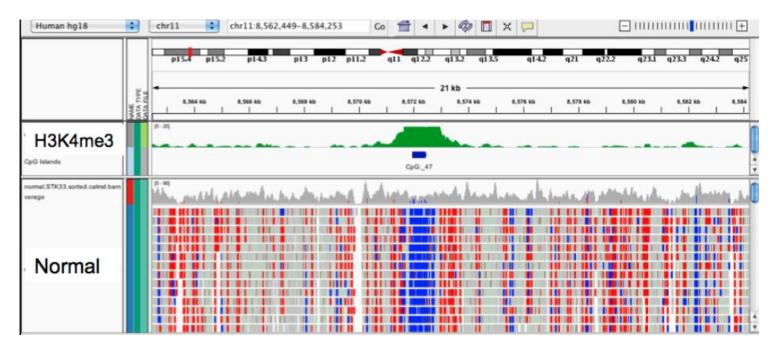


#### Hmmm...now the data is there....so what now?



Assembly!

### The Next Generation Sequencing Revolution



Millions of polymorphisms in the genome sequences...

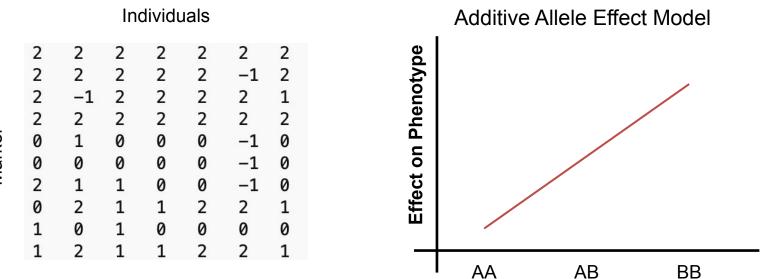
https://link.springer.com/chapter/10.1007/10\_2017\_46

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## The diploid genotype matrix – "additive" effect modeling

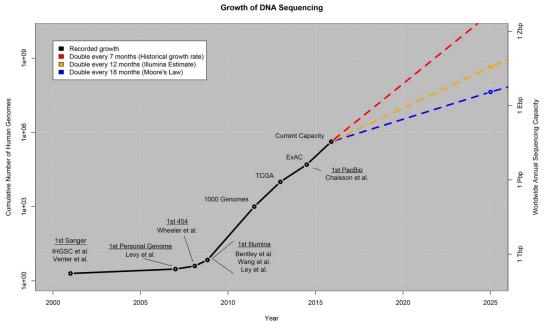


0

Marker



## Big data: astronomical or genomical?



- new technologies e.g. Nanopore long-reads sequencing
- single-cell sequencing
- tons of sequencing/genotyping projects (plants, animals, humans)
- metagenomics
- "four-headed beast":
  - i) data acquisition: 1 ZB/year (10<sup>21</sup>)
  - ii) data storage: 2-40 EB/year (10<sup>18</sup>)
  - iii) <u>data distribution</u>: few massive, many small data exchanges
  - iv) <u>data analysis</u>: highly heterogeneous and intensive

Stephens et al. 2015. Big data: astronomical or genomical?. PLoS biology, 13(7), p.e1002195.

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## \$1 genome?



- emerging/new technologies
- new companies
- streamlined (more efficient) processes
  (e.g. innovative chemistry)
- \$100 genome: not yet there, but promised by several companies
- \$1 genome? we are headed towards that!

on the brink of the next revolution in sequencing?

- Pennisi, E. "\$100 genome? New DNA sequencers could be a 'game changer' for biology, medicine." Washington, DC: Science;
  2022. doi: 10.1126/science.add5060
- Pollie, Robert. "Genomic sequencing costs set to head down again." Engineering 23 (2023): 3-6.