

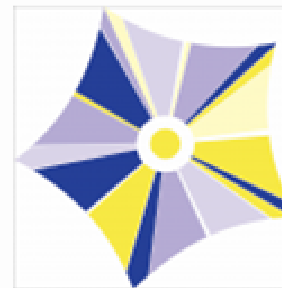
Building on the sequencing of the Potato Genome

Glenn Bryan

Group leader, The James Hutton Institute



The James
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PGSC

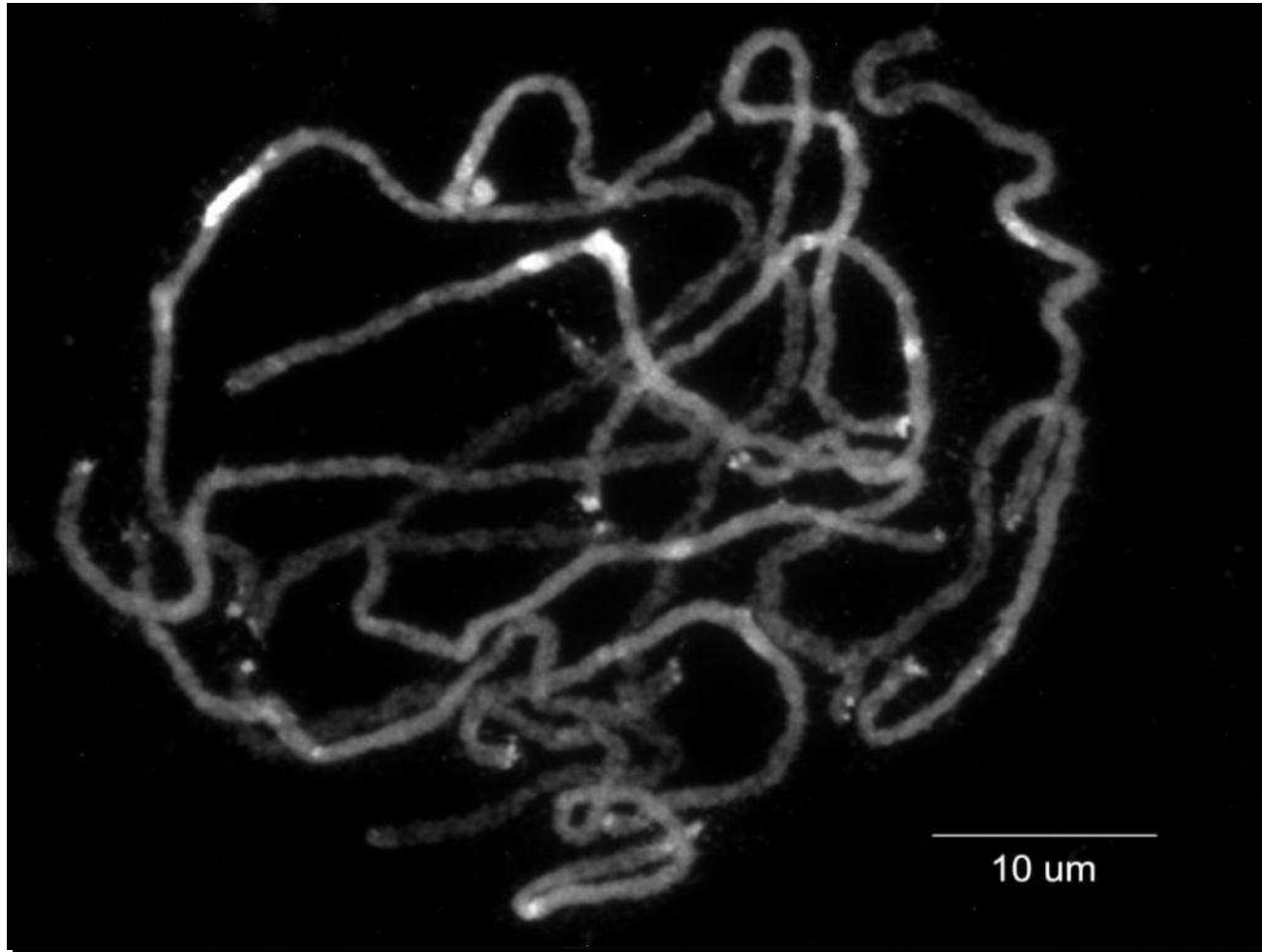
Outline

- What do we mean by 'the Potato Genome'?
- Why sequence potato?
- How the consortium sequenced the potato genome.
- Using the genome sequence.
- Future applications in research and breeding.

What do we mean by the Potato Genome?

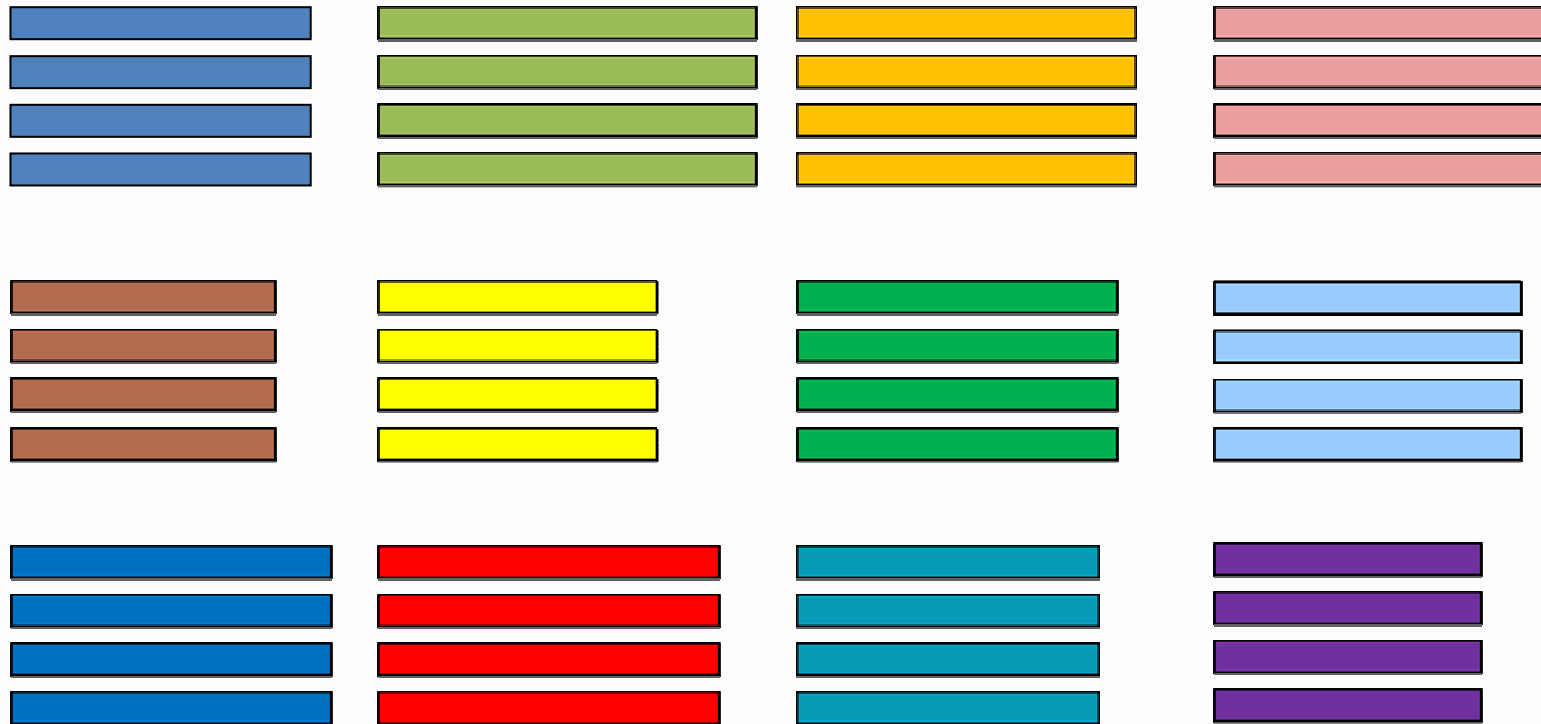
- The genome of any organism is the genetic material (usually DNA).
- The genome is organised into chromosomes.
- Potato varieties have 48 chromosomes in the nucleus of each somatic cell.
- It contains all the information needed for the organism to develop and live (i.e. the genes)
- Total genome size is ~850,000,000 'base pairs' (G, A, T, or C)
- Potato genome is twice the size of the rice genome, and 25% the size of the human genome

The Potato Genome



Hans de Jong, Xiaomin Tang

The genome of potato



- 12 chromosomes, 4 of each in a potato cultivar.
- 'Diploid' potatoes have only 2 of each.

Why sequence potato ?

- Potato genetics is difficult (outbreeding, tetraploidy).
- Potato breeding is slow – 12 years for a new cultivar.
- Potato traits are complex resulting from several genes.
- Crossing two varieties yields a vast number of combinations.
- A genome sequence provides locations of the genes in relation to 'trait' and 'marker' positions.
- It will make genetics and breeding more efficient.

The Potato Genome Sequencing Consortium



PGSC meeting in Carlow, Ireland, June 2009.

The Potato Genome: a tale of two genotypes



DM

RH

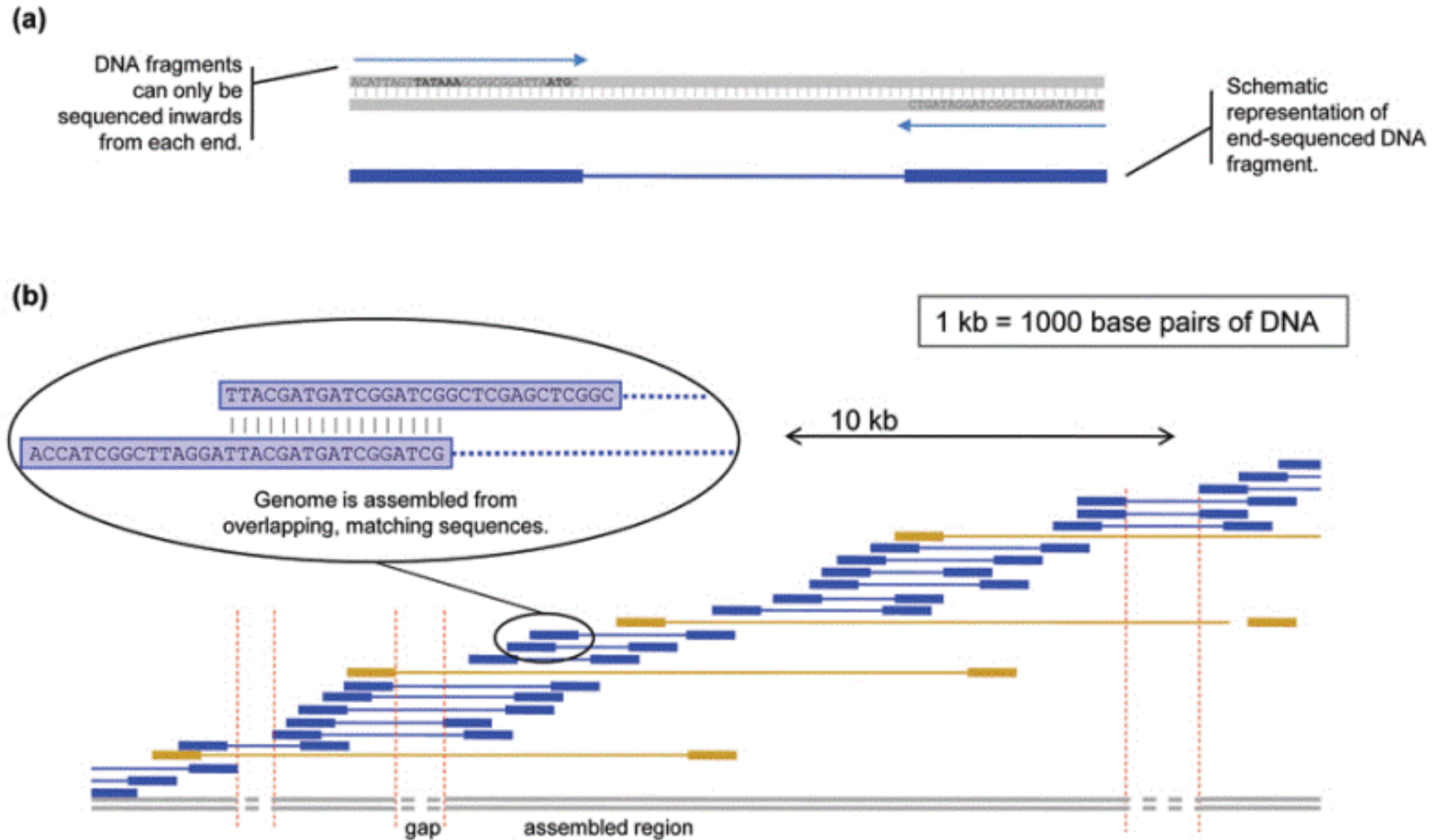
Next Generation Sequencing



Sequencing the genome

- DM sequenced by Whole Genome Shotgun (WGS) approach.
- DNA broken into small fragments and sequenced by NGS methods.
- Genome was sequenced >125 times
- Data were 'assembled' to make larger fragments.
- These longer fragments or 'scaffolds' were analysed to find the genes, a process known as 'annotation'.
- A mapping process was used to reassemble the chromosomes ('pseudomolecules').

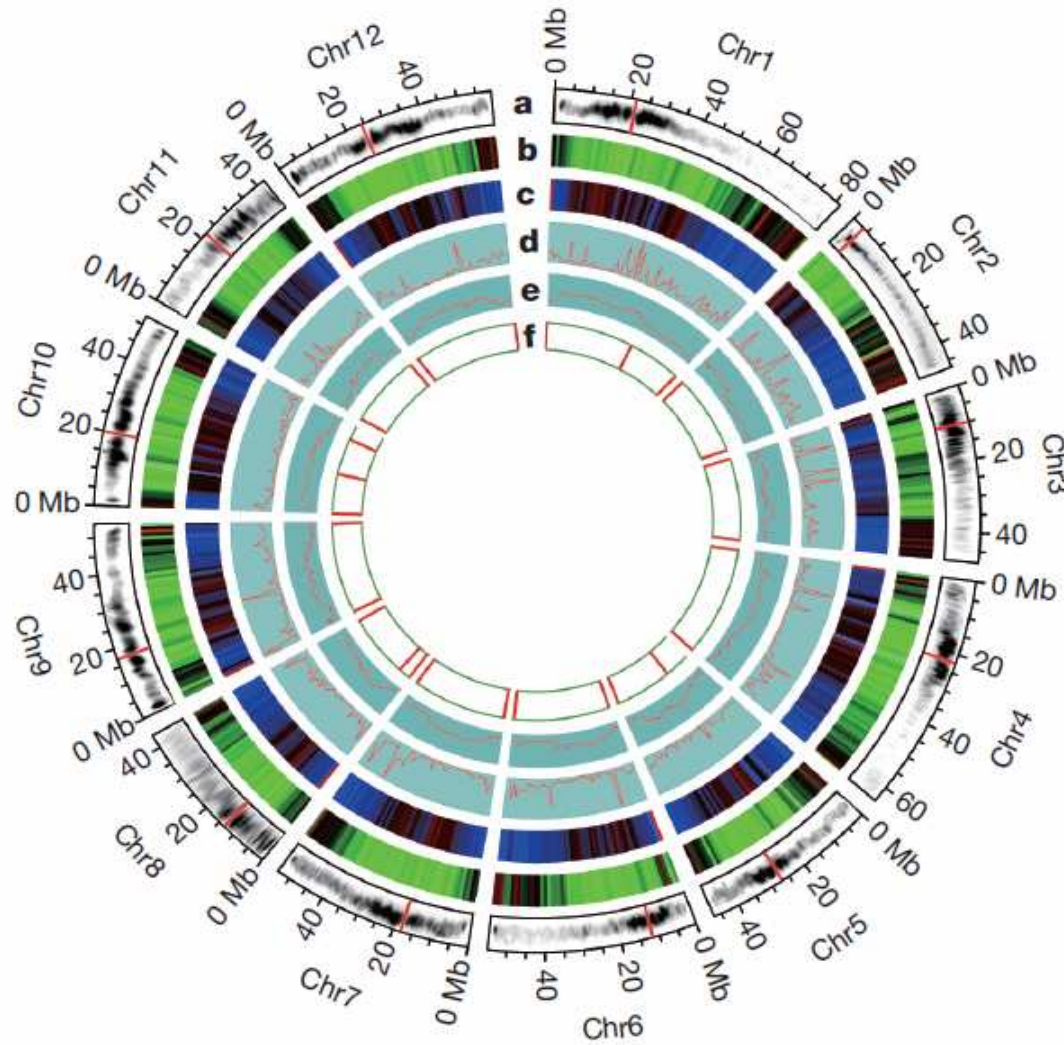
Whole Genome Shotgun sequencing



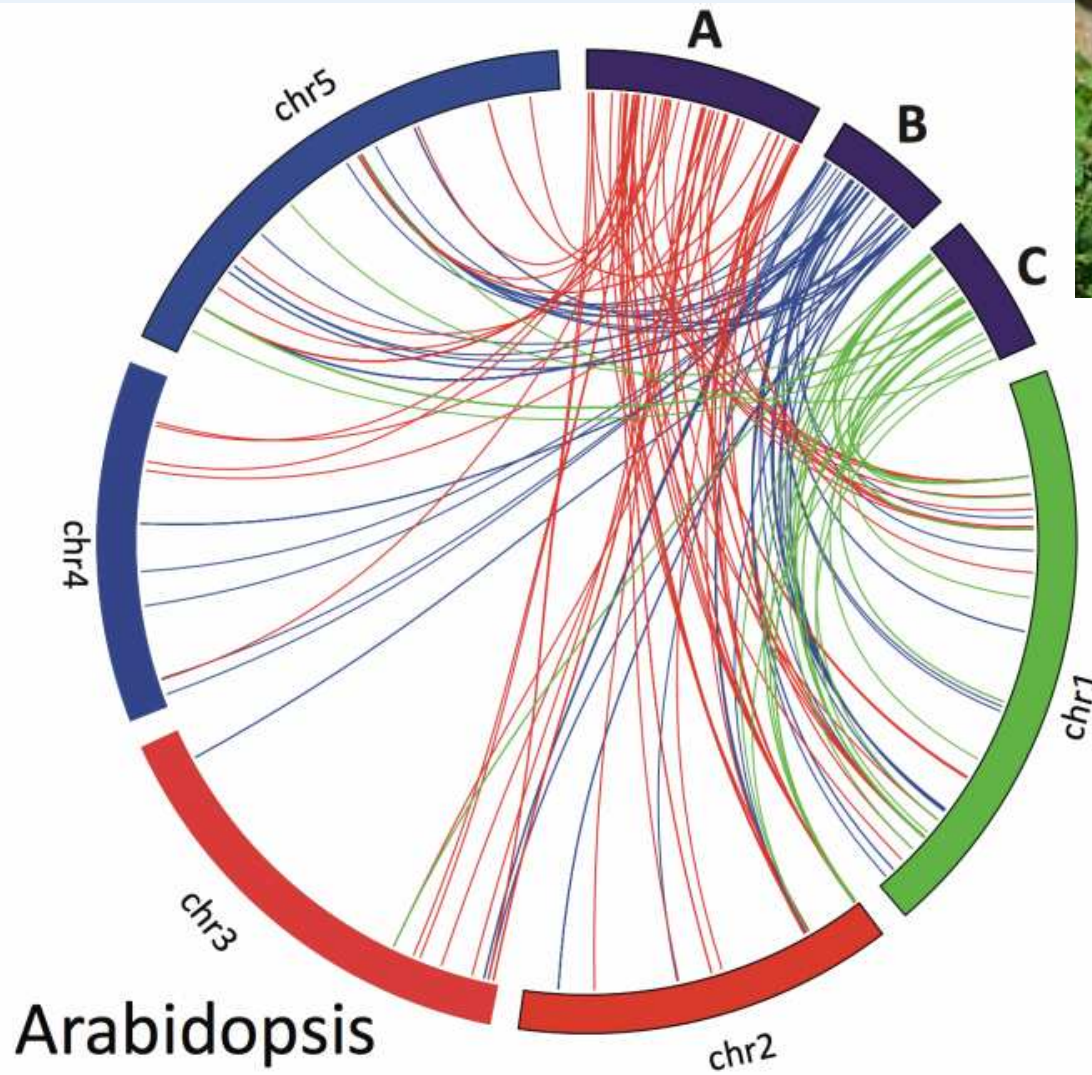
What have we learned?

- Potato genome contains ~39,000 genes, ~65% are expressed.
- The precise location of >95% of genes is known.
- There are roughly the same number of genes on each chromosome.
- Pieces of the genome are duplicated and are very similar to other plants.
- Potato genome has been duplicated millions of years ago.

Genome view of potato



Genome evolution



The Publication

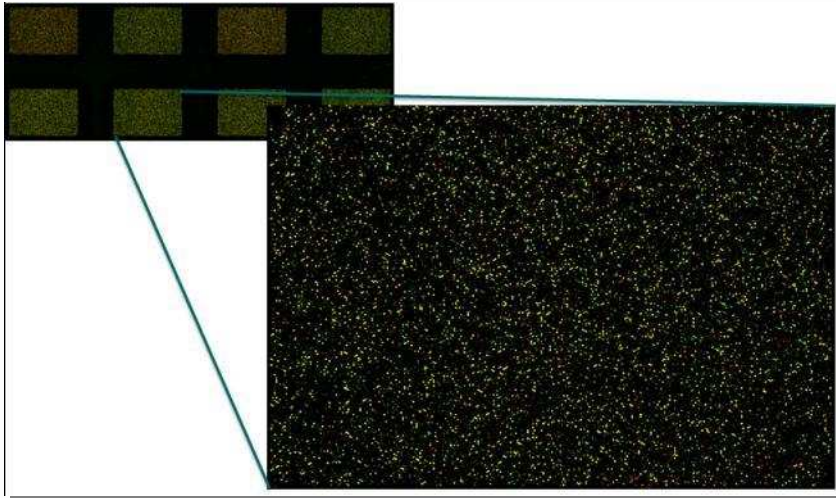


So now what.....?

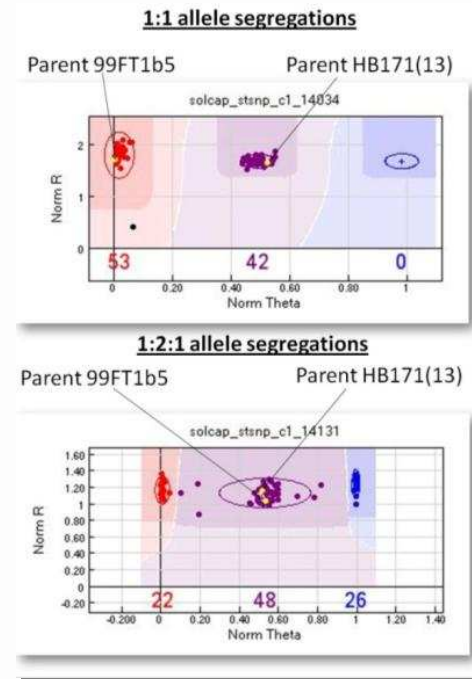


Using the genome – new tools

- New tools for measuring gene expression
- New resources for mapping



New 8 x 55K array
All 39,000 genes

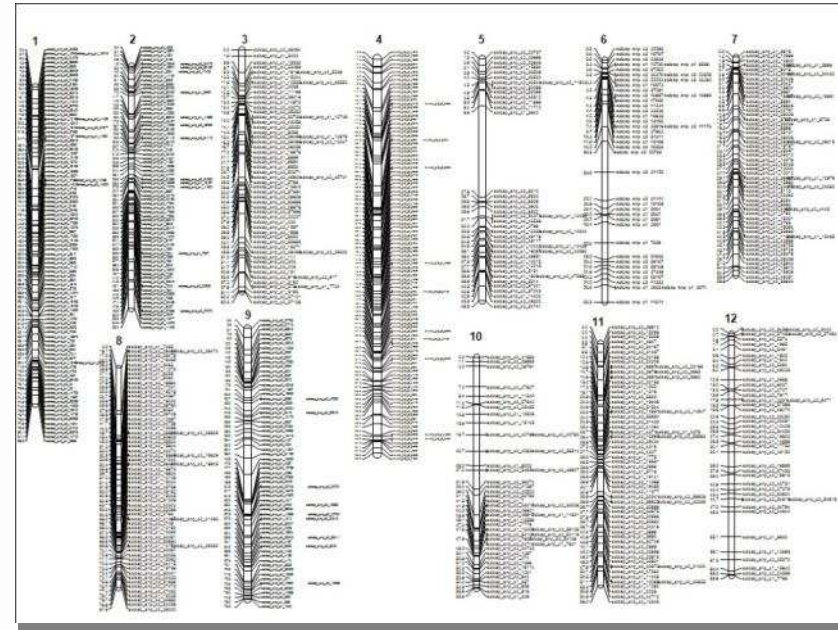


New SNP panel
8300 SNP loci

Trait mapping 'post genome'



Measure traits

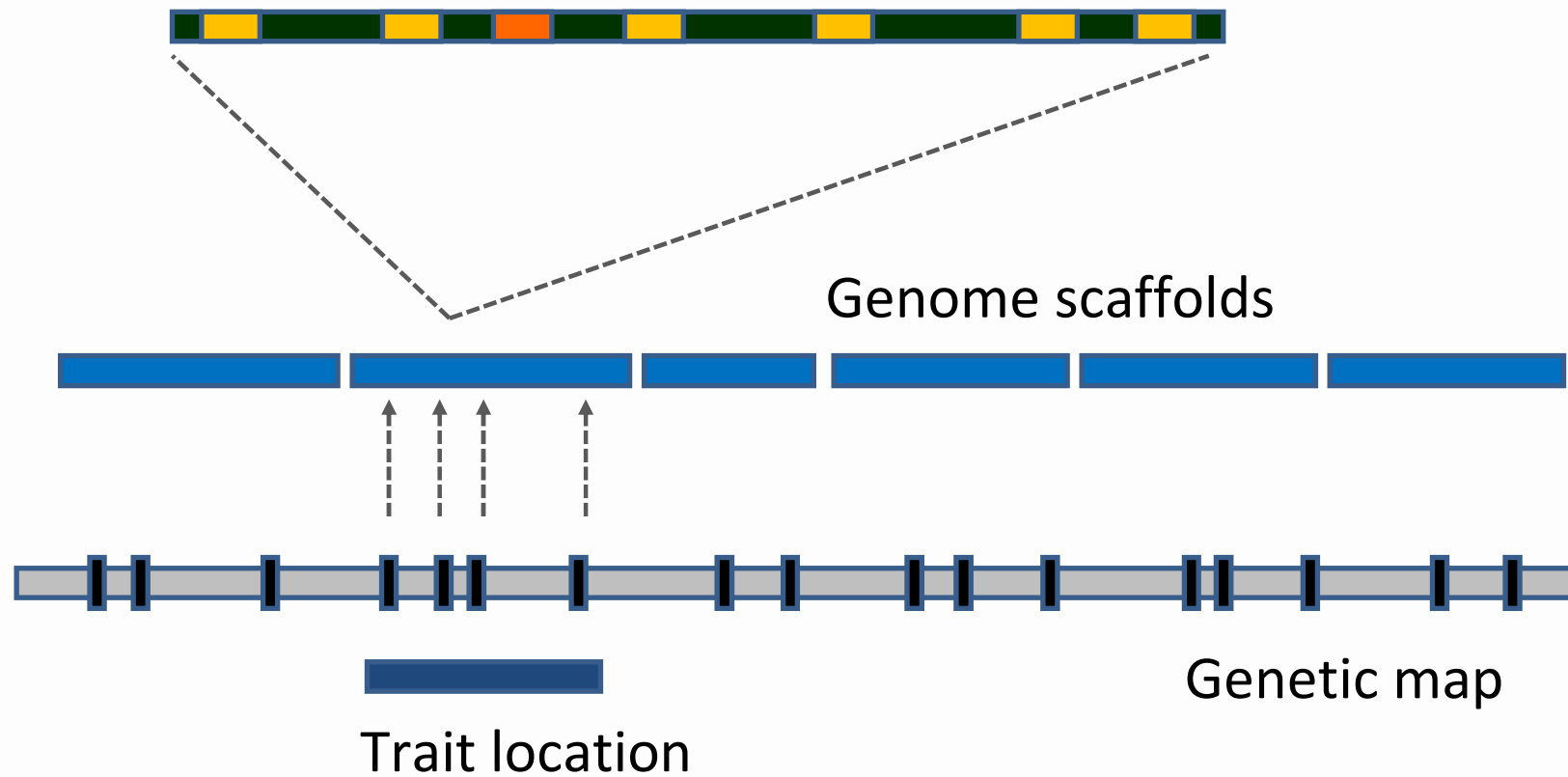


Genetic Maps

Localise
Trait effects

Can we use genome to identify candidate genes for traits?

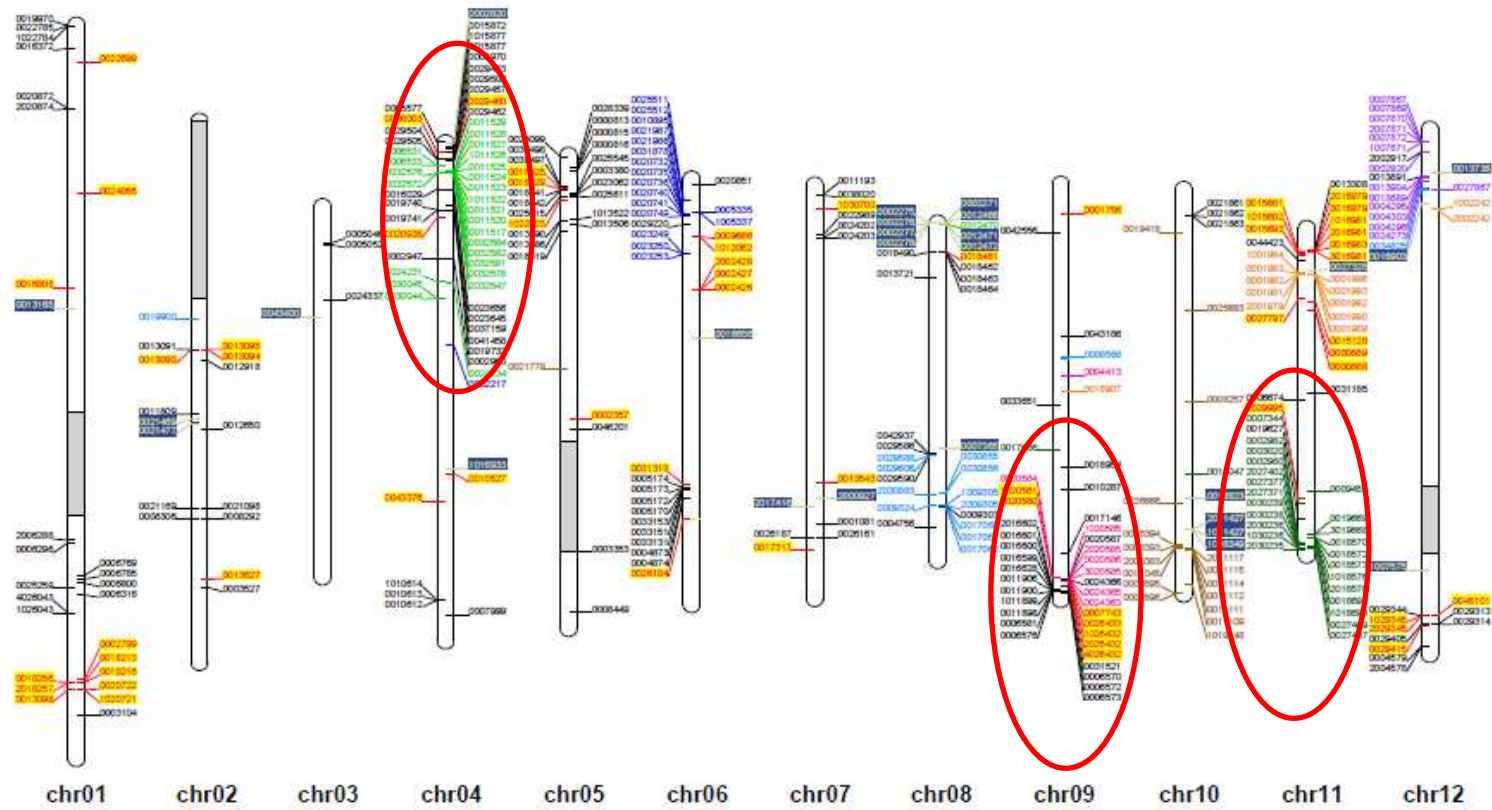
Look for candidate genes



Benefits for Potato Genetics

- Identifying the actual genes for important traits will get easier.
- Developing markers diagnostic for a trait locus is possible.
- ~430 resistance genes in genome.
- BUT better genetic & functional tools are needed.
- Need to 're-sequence' other genotypes of potato.

Potato Resistance Genes



How will genome help potato breeding?

- Identify QTLs with large effect on the traits of interest.
- Build traits of industry wide importance into all breeding material.
 - PCN & late blight resistance.
 - Sustainability traits.
- Better parental identification a priority.
- Can this be assisted by use of biotechnology?

Requirements for progress

- Industry **must** work together to agree the key targets.
- Markers for important traits can be developed – need clear deployment route (IP issues?).
- Use of GM approaches **must** be considered as a component of our strategy for crop improvement.
- GM could have benefits for ‘single gene’ traits (major resistances) and for larger effect quality characters (sugars, acrylamide etc).
- Novel breeding methods require evaluation:
 - Genomic selection.
 - Diploid hybrid breeding (www.solynta.com).