

A potato pipeline – from gene discovery to commercial deployment

WP2.1 dissemination event – 21 Sept 2018



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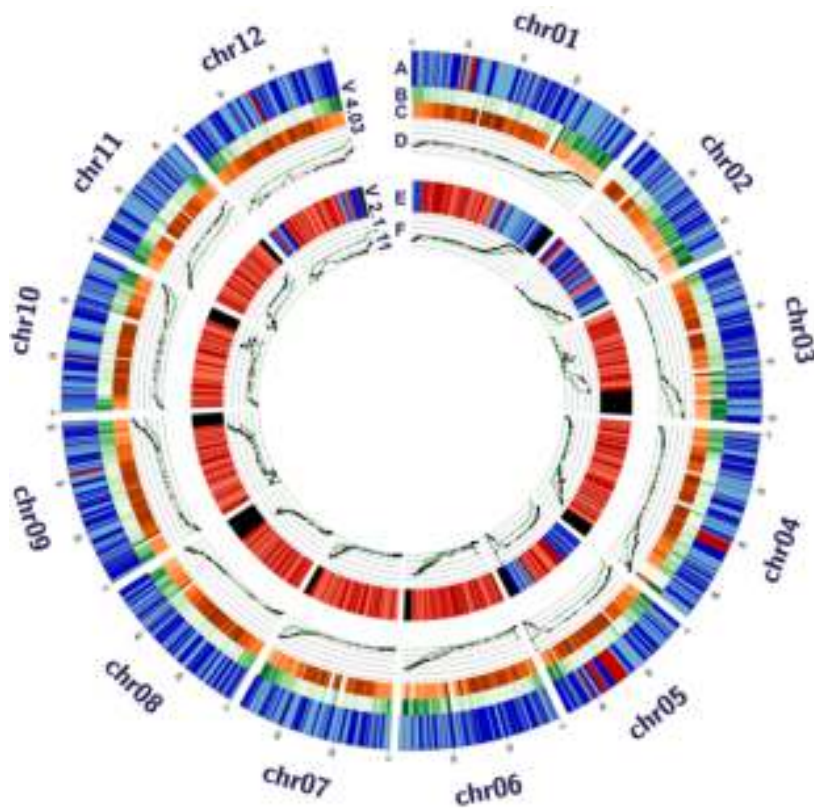
The SEFARI logo consists of the word "SEFARI" in a bold, sans-serif font, followed by a stylized sunburst or starburst icon.

Potato: an important Scottish crop



- 28,000 ha of potatoes (value £209 million) grown annually in Scotland
- Potato genome project (partly RESAS funded) has had a major impact on potato science and breeding
- Modern genetics, genomics and other approaches are underpinning the development of new potato cultivars
- JHI potato programme engaged with the potato sector in Scotland and beyond

The Potato Genome



- Partly funded by RESAS in previous 2011-2016 programme
- Underpins much of trait research in current programme
- Source of markers & gene information
- Other genomes becoming available (e.g. *S. verrucosum*, M6)

Genotyping tools



Potato work in WP2.1 is highly dependant on development of genotyping tools

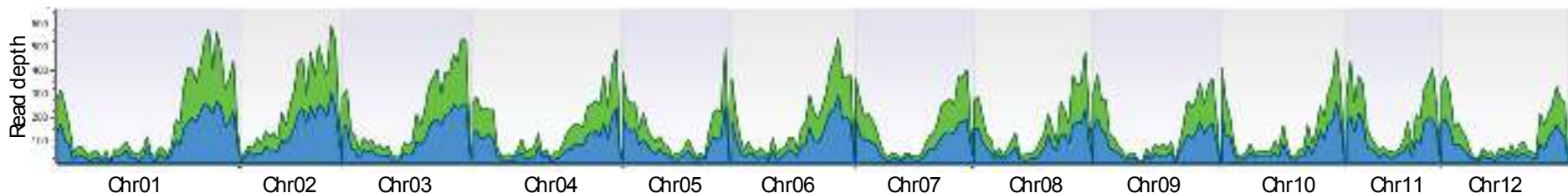
We have been involved in or led development of several initiatives in this area:

Single nucleotide polymorphism (SNP) 'arrays'

Genotyping by sequencing (GBS)

Whole-exome capture (WEC)

RenSeq (and DRenSeq)



GBS markers show genome-wide coverage in genic regions

Hutton potato germplasm



Germplasm

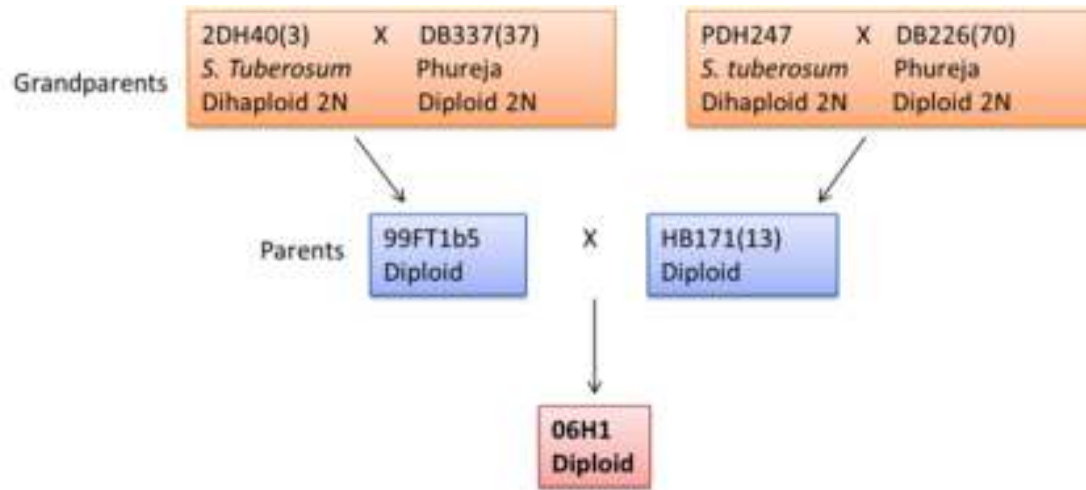
- Commonwealth Potato Collection (82 species)
- CPC 'core'
- Diploid diversity panel (Stenotomum)

Populations

- Biparental populations (e.g. 06H1, Genpop1)
- Potato Association panel (POTAPP)
- Other targeted populations (PCN, Late blight, PVY)



Diploid genetics: 06H1 population



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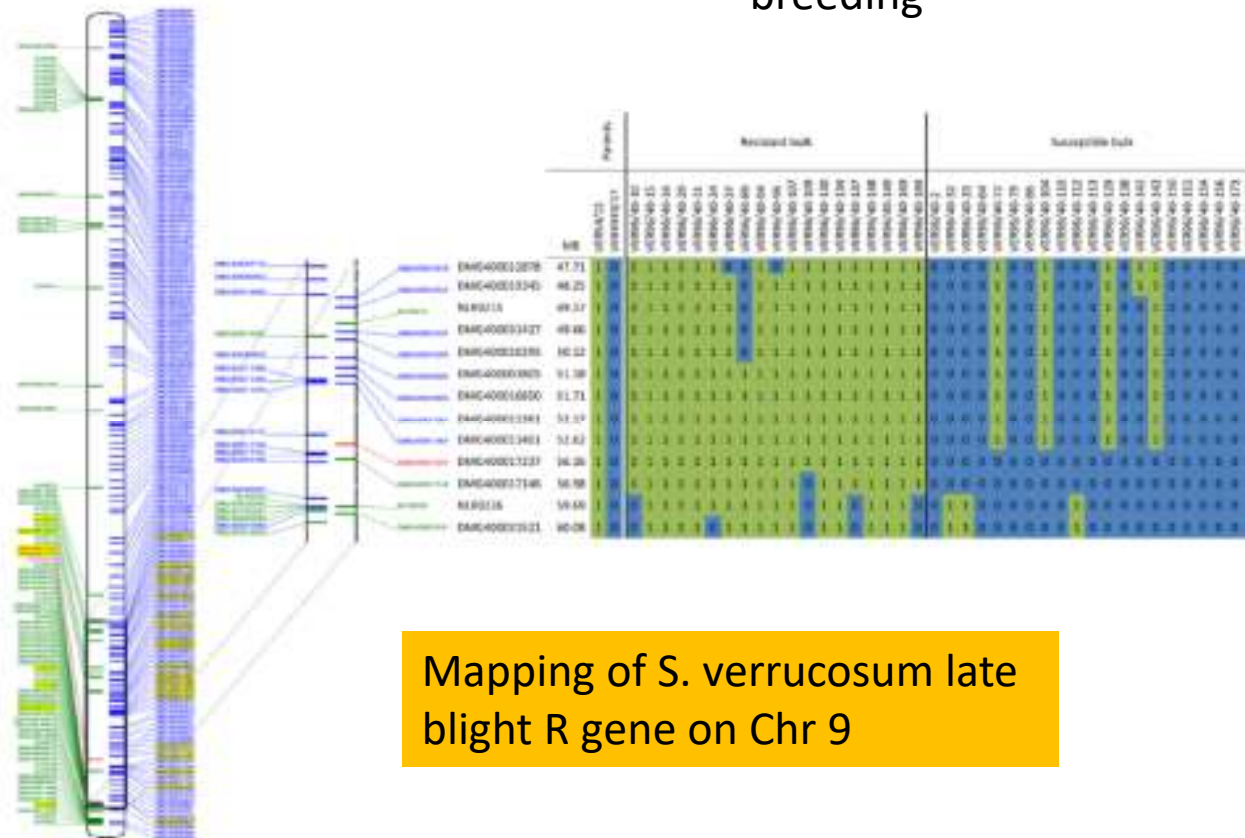
- Highly diverse ‘hybrid’ cross underpinning WP2.1
- ~350 clones genotyped with SNP markers
- ~25 traits measured in replicated field trials
- Dense genetic map & tuber shape analysis published ([Prashar et al TAG, 2014](#))
- ~3100 mapped SNPs used for QTL mapping for traits – tuber shape, yield, dormancy, quality, IRT, late blight, PVY, tuber greening, Vit C
- Candidate genes for traits identified

RenSeq: a new method for mapping novel disease resistances in potato



RenSeq: 755+ NB-LRR genes from Potato, Tomato and Pepper
48,500 probes (120 nt) (3.8 MB)

Uses a simple ‘capture’ method to resequence all resistance genes in a DNA sample
Allows the rapid mapping of resistance genes and development of tightly linked markers for use in breeding



Mapping of *S. verrucosum* late blight R gene on Chr 9

DRenSeq: a diagnostic method to identify functional R genes in a sample



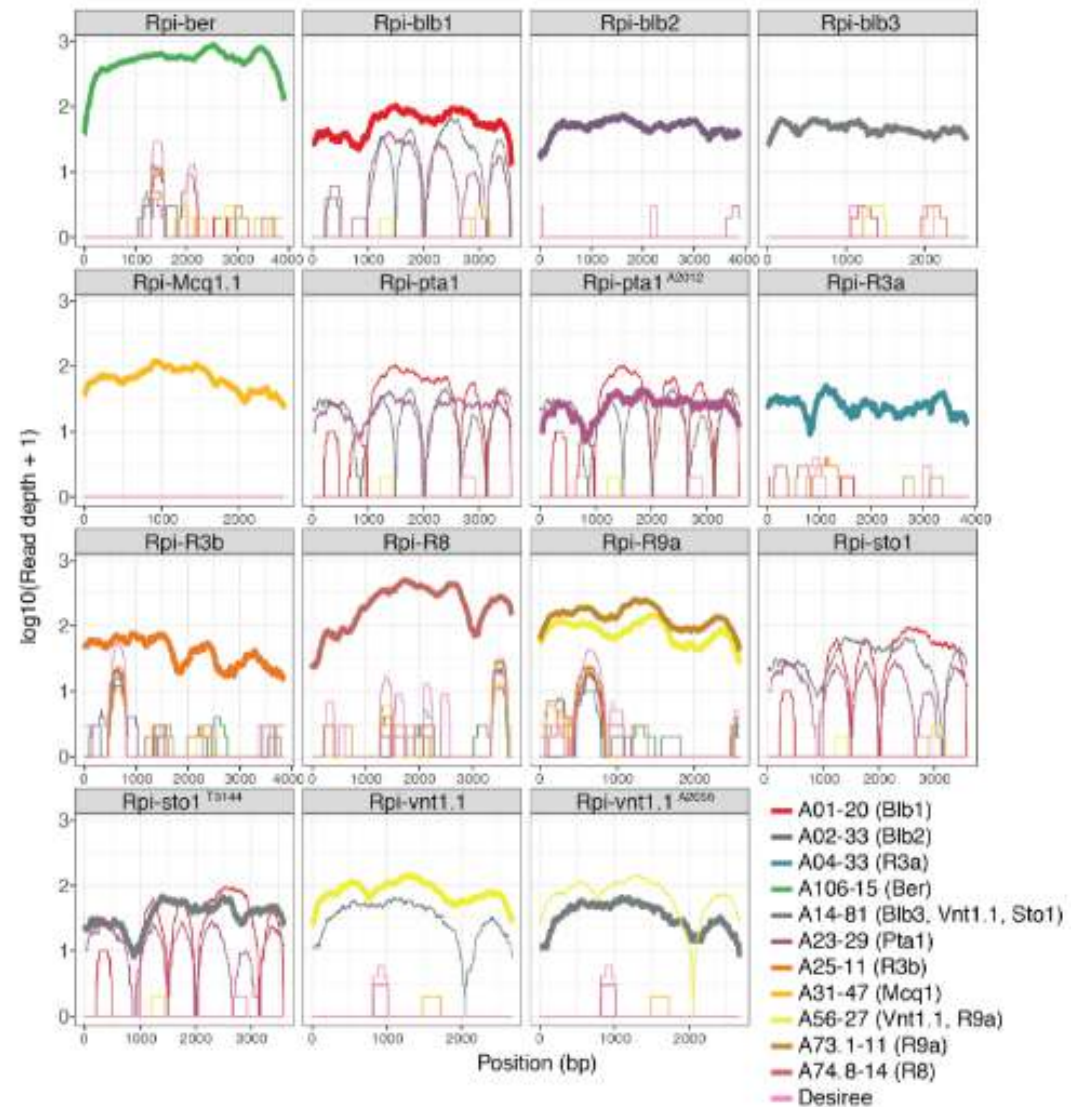
11 cloned potato R genes

Can check for 100% coverage of any one gene in a variety

Very useful diagnostic tool

High level of interest from stakeholders especially potato breeding companies.

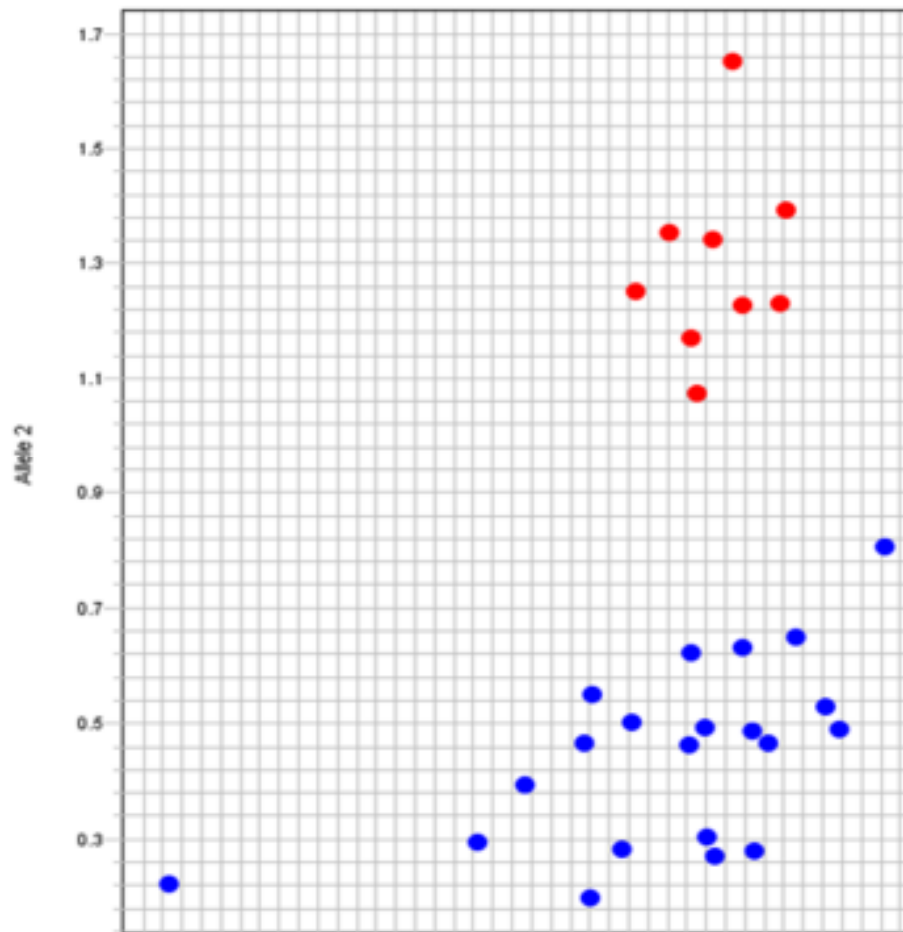
Will facilitate parental and progeny selection in potato breeding programmes



KASP marker diagnostic for presence of R8



Allelic Discrimination Plot

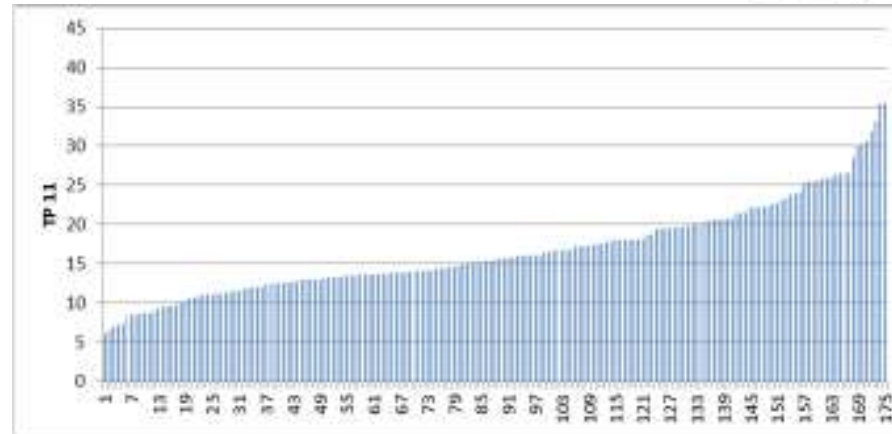


Cultivars with R8

- R8,
- Sarpo Mira
- Cammeo
- 6 R F1 clones Sarpo Mira x Maris Piper

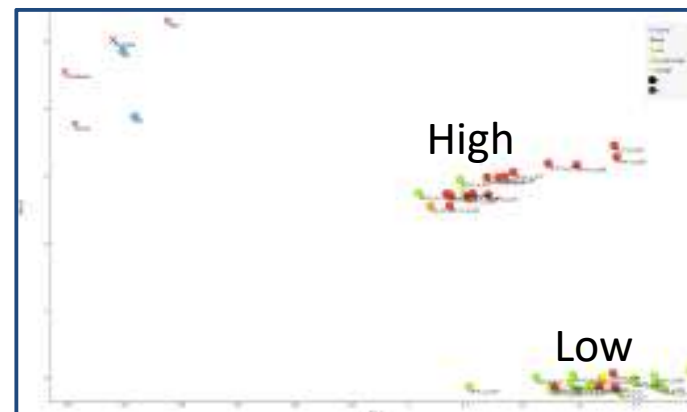
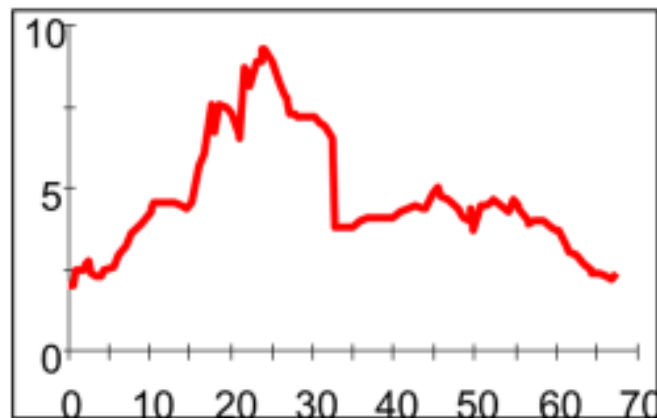
21 cultivars without functional R8

Tuber greening – a major cause of waste in the UK



Phenotyping

Variation in population



QTL on chr 9

Marker validation

Work co-funded by industrial partner

Tuber dormancy – a major storage issue



RESAS funded work led to BBSRC grant involving industry (Pepsi, Bartletts, AHDB)

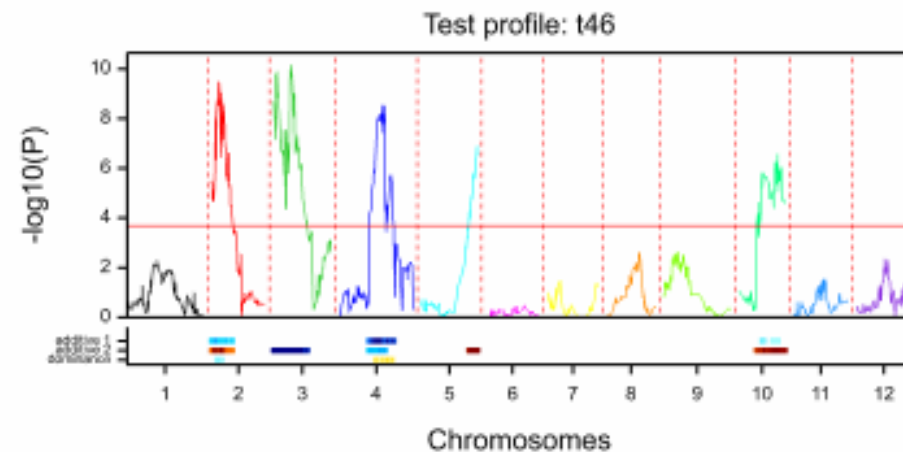
06H1 population phenotyped over two years for dormancy break and sprout growth

Data used for QTL analysis

Complex genetics of dormancy has been revealed

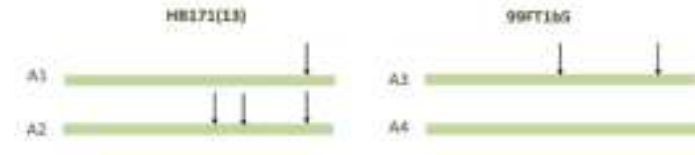
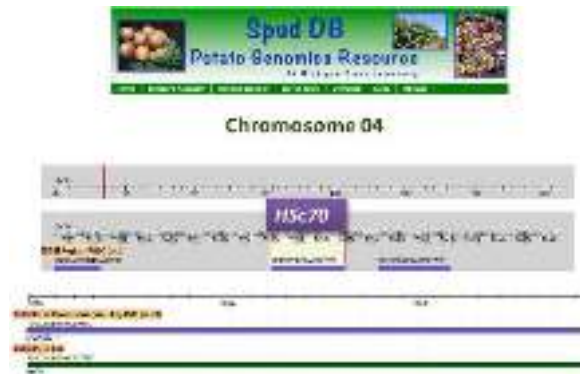
Gene on chromosome 3 has been shown to be involved in sprouting and tuber traits

Markers for dormancy identified



Hsc70 gene conferring heat tolerance

QTL for yield
at High
Temperatures
Chr 4



4 alleles

Trait measured	Genotypic mean for A1A3 (gr)	Genotypic mean for A2A3 (gr)	Genotypic mean for A1A4 (gr)	Genotypic mean for A2A4 (gr)
FW at 20°C	2.27±0.28 ^a	3.58±0.31 ^b	1.46±0.18 ^a	3.13±0.32 ^b
FW at 28°C	0.51±0.13 ^{ab}	1.24±0.20 ^c	0.35±0.08 ^a	0.92±0.15 ^{bc}
DW at 20°C	0.50±0.2 ^{ab}	0.76±0.18 ^b	0.31±0.22 ^a	0.85±0.18 ^b
DW at 28°C	0.11±0.06 ^{ab}	0.30±0.08 ^c	0.06±0.01 ^a	0.24±0.08 ^{bc}

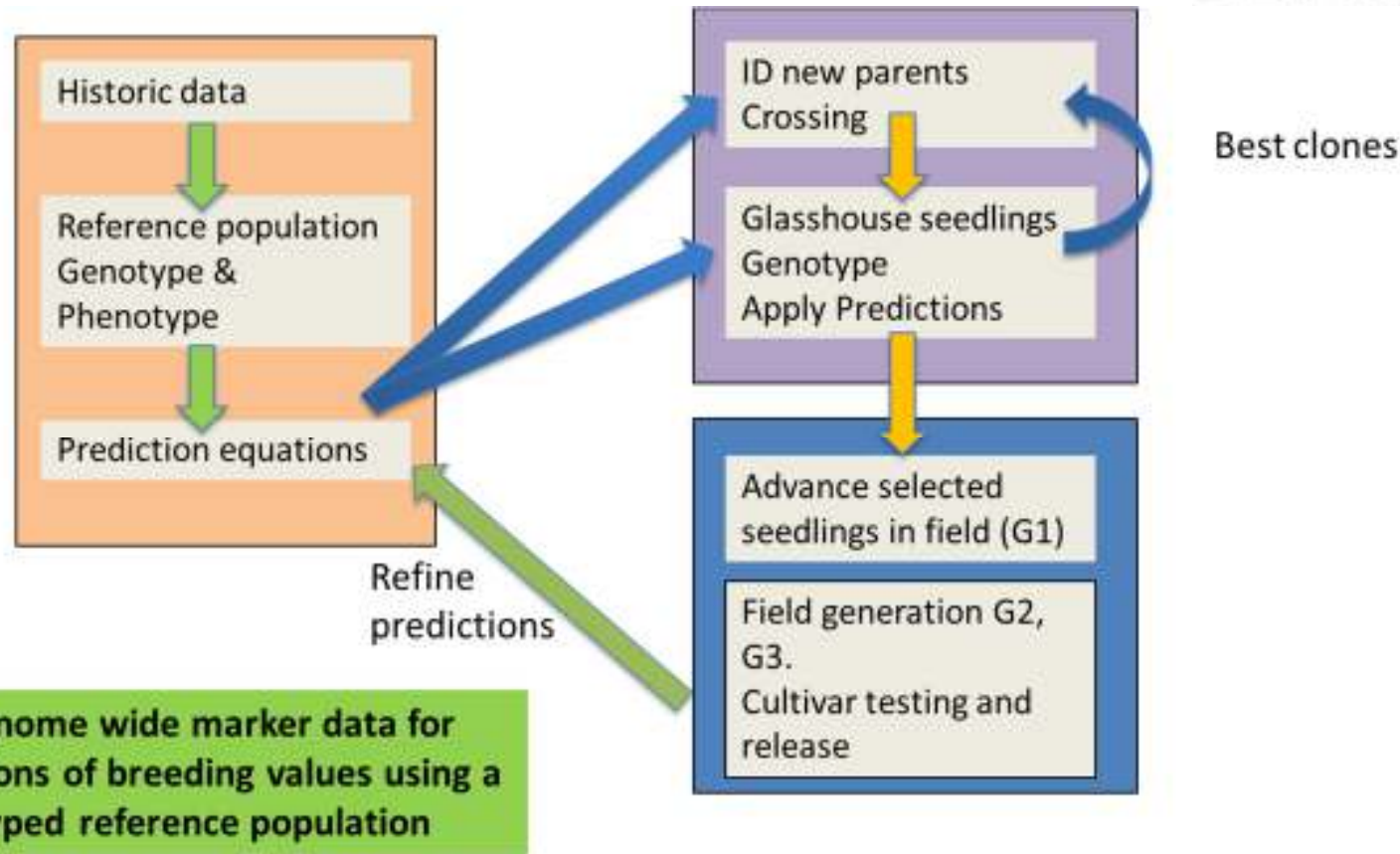
06H1 phenotyped for heat stress tolerance – gene identified on chromosome 4

One allele ‘A2’ had largest effect on tuber yield

Transgenic plants also perform better at higher temperatures

Clones from 06H1 being trialled in Africa and some industry take up (Solynta etc)

Novel breeding approaches: Genomic selection



New WP2.1 deliverable to examine the potential for using GS in UK potato breeding

Builds on work done in previous and current programme as well as industry funded work

Discussions ongoing with industrial partners regarding possible deployment of this approach

Summary



- Potato work in WP2.1 involves several disciplines – genetics, genomics, pathology, molecular physiology, bioinformatics – scientists work together as an effective team
- Frequent discussions with stakeholders ensures research is well linked in to industry needs
- Work also aiming to address challenges due to climate change as well as changing industrial priorities and novel breeding methods likely to have impact