21st Century Plant Breeding

What has the last decade seen?

- Consolidation: mergers, acquisitions, alliances.
- Centralisation of service functions.
- International expansion/aspect.
- Large companies have > access to supporting technology than smaller companies.

How will this evolve?

- Every tool in the box is needed if we are to cope with the food security "perfect storm".
- Should we expect the private sector to pay for it all from a seed royalty income of ~£35m pa?
- Can small players still succeed?
- Need to apply a new "toolkit" to support future crop productivity.

What’s in the current toolkit?

- Germplasm
- Phenotyping
- Yield, agronomics, quality
- Breeding systems
- Pedigree breeding
- Some predictive markers
- Some accelerated breeding

Led by skilful interrogation of phenotype

...and the new toolkit?

- Everything in the old toolkit PLUS
- Novel sources of variation
- Markers/trait dissection
- Population structures
- Accelerated breeding
- Hybrids
- Genomic selection
- Genetic modification
- Gene editing

Genomic Selection


Trait effects of all genes or chromosomal positions are estimated simultaneously without significance testing so there is reduced bias.

- Requires high marker density.
- Estimate a trait effect for every marker or interval.
- Statistical problem: more markers than individuals....
Genomic Prediction works half the time

Cross validation r

- NL / RL historical data 0.8
- old to new 0.2
- AxC mapping population 0.5
- low to high 0.2
- TG within countries 0.5
- between countries 0.3

In collaboration with Marco Scutari (Oxford)

Association mapping panel of 376 elite winter bread wheat varieties from northern Europe

Panel genotyped with ~3000 markers:
- 2712 genome-wide DArT markers
- SNP markers (Biogemma)
- Gene markers (Ppd, Rht, Vrn)

All methods predict on the basis of kinship to some extent

Each allele in each individual carries information about:
- QTL alleles in LD carried by the individual
- Genetic relationships with other individuals

Combining information

Differentially-penalised ridge regression (DiPR)

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Bentley et al. (2014) TAG 127: 2619-2633
Genomic selection

“Phenomic” selection

Exploiting new diversity


“Phenomic” Selection

Genomic selection

“Phenomic” selection

Exploiting new diversity

Accessing new diversity

NIAB Breeder’s toolkit
http://www.niab.com/pages/id/419/Breeders_Toolkit
**Exploiting new diversity**

Re-synthesised wheat's have basic faults and no inherent values as varieties

**BUT**

Modern wheat and synthetic wheat are crossable, allowing incorporation of novel DD diversity

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**NIAB pre-breeding team**

International genebanks

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John Hickey, Gregor Gorjanic (Roslin)

Dave Laurie, Adrian Turner, Simon Griffiths (JIC)

WISP partners

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