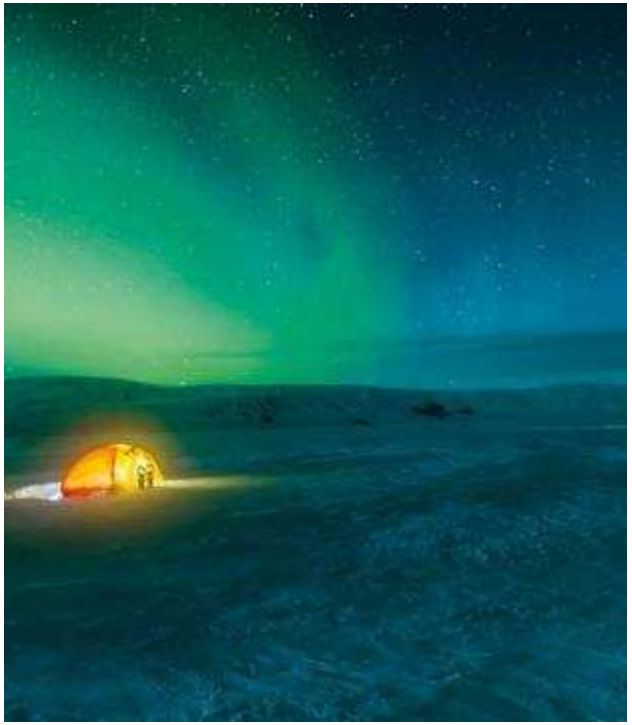
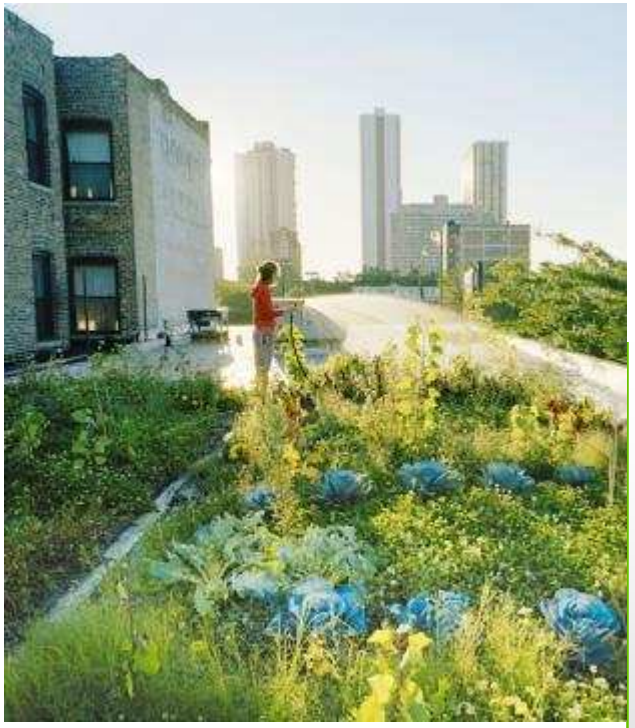




Science For A Better Life

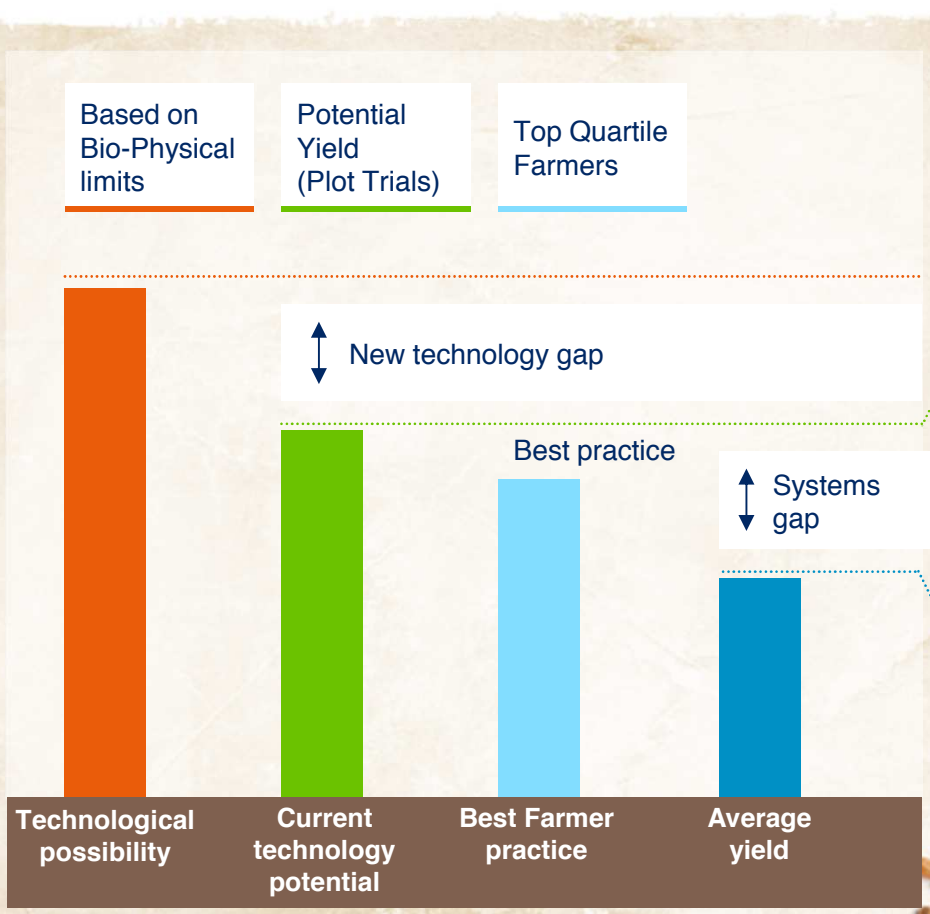
Shaping Wheat for the Future: Leveraging the Wheat genome in Crop Efficiency Research and Breeding

John Jacobs
January 12, 2016

Agenda

- Why is Bayer investing in Wheat
- Pillars of Bayer's Wheat strategy
- Examples from R&D
- Bayer and the IWGSC
- New era for the wheat genome

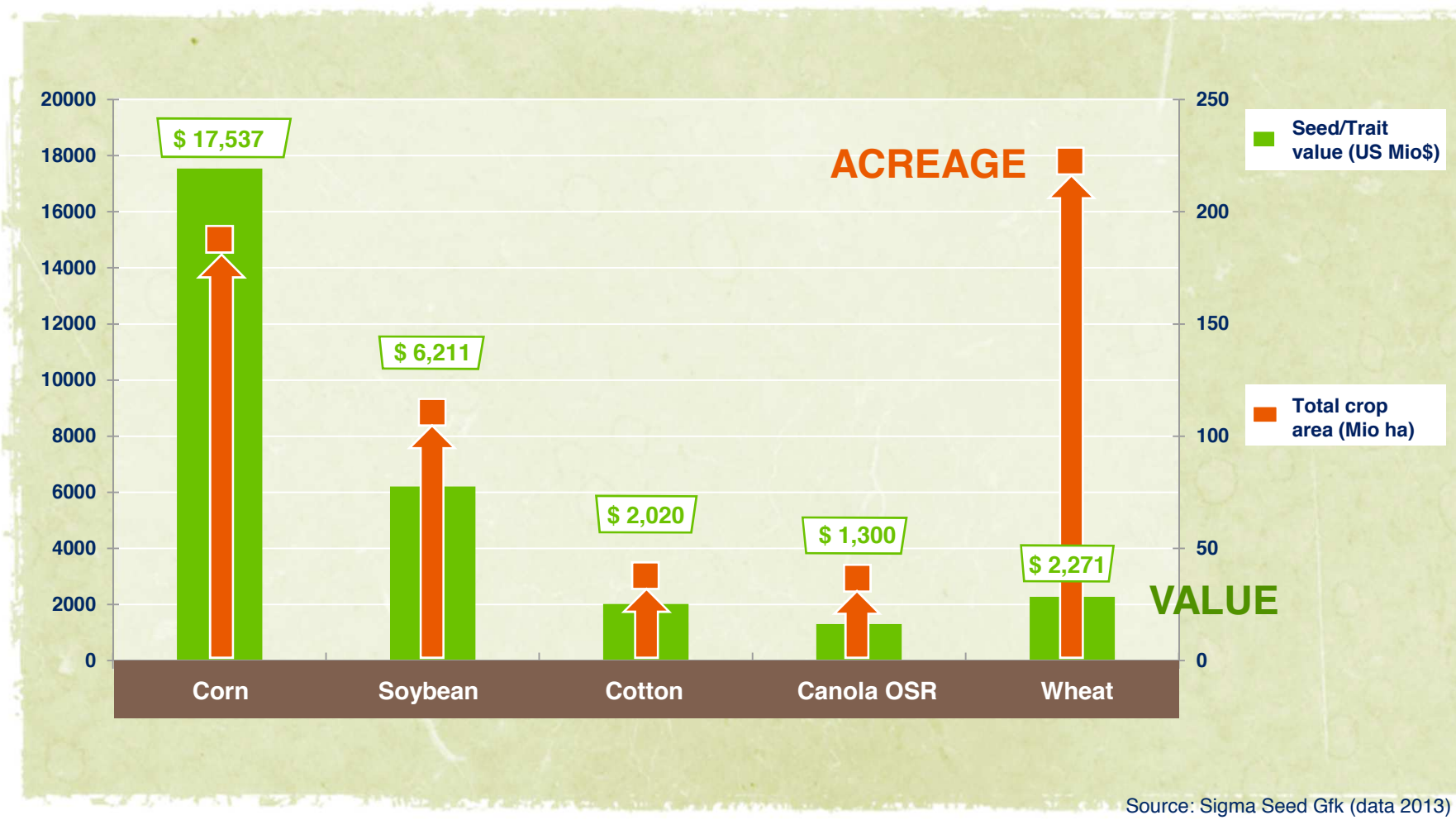
Wheat Yield Frontiers



Country	Ave. Yield t/ha	Potential Yield t/ha	% Gap
Yaqui valley, Mexico	6	9	50%
Punjab, India	4.3	6.25	45%
Haryana, India	4.2	5.75	35%
Western Australia	1.8	2.6	45%
N Dakota, USA	2.5	3.7	50%
United Kingdom	8.2	10.4	25%
Eastern China	4.7	7.0	50%
Kansas, USA	2.6	3.9	45%

Source: FAO Expert Meeting on How to Feed the World in 2050 (Rome, 24-26 June 2009)

Potential of Wheat Seed/Trait market



Source: Sigma Seed Gfk (data 2013)

Why is **Bayer** investing in the Wheat Seeds & Traits market?

No. 1

WHEAT
= key part of our business today

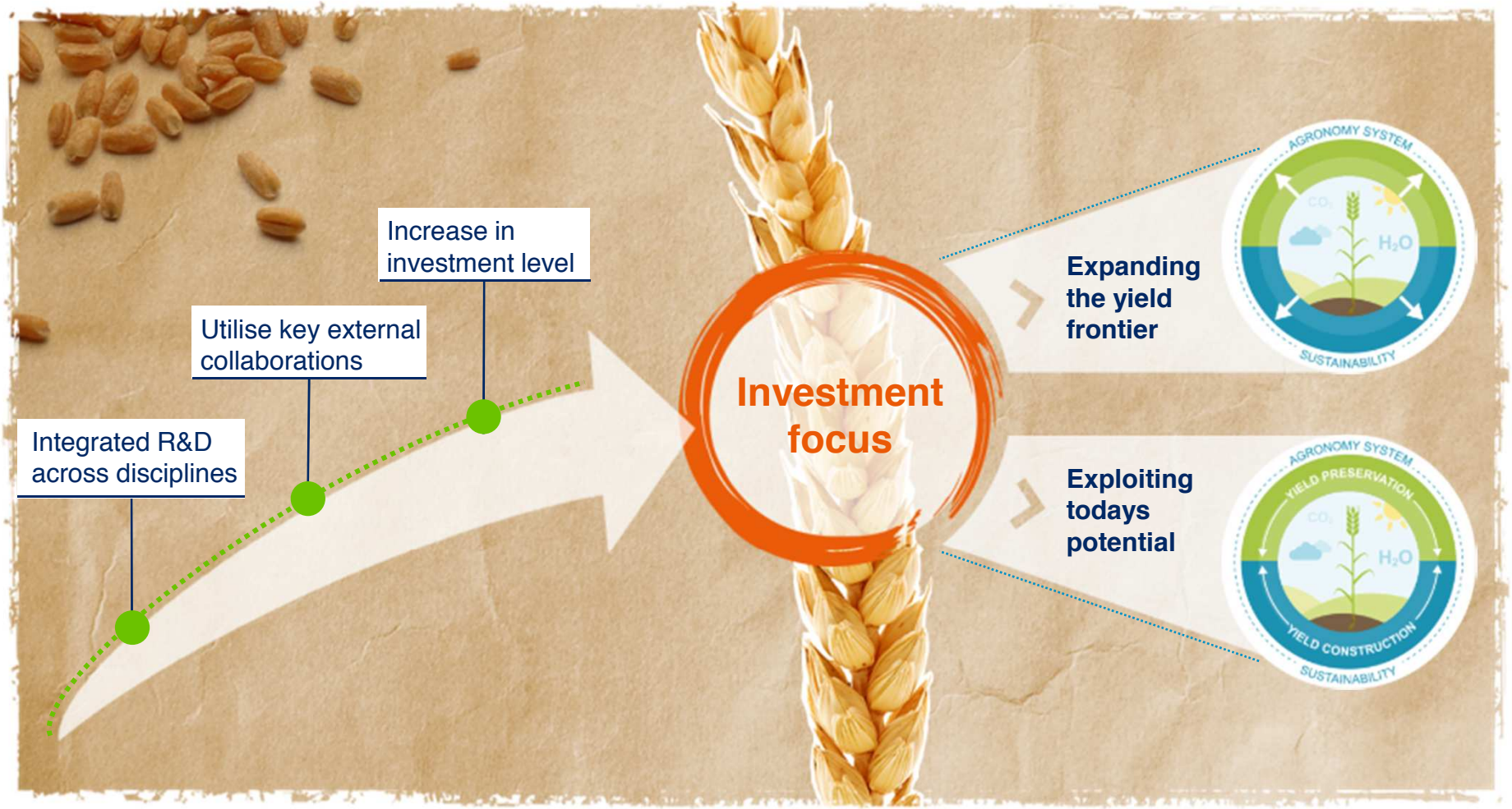
No. 2

NEW technology in breeding and traits can expand the yield frontier

No. 3

Integrating research, breeding and agronomy can deliver new solutions

Bayer CropScience investing EUR 1.5 billion in new solutions in cereals from 2010 to 2020



Bayer's Seeds and Traits strategy

Traits and technology

Build **competitive GM and non-GM trait platform** via:

- In-house expertise
- Strategic partnerships

Germplasm and breeding

- Access **global germplasm** for synthesis into a **regional breeding efforts**
- Working to bring **enhanced yield and yield stability** through **hybrids**

Enabling Technologies

Build competitive enabling technologies to rapidly process candidate traits through pipeline

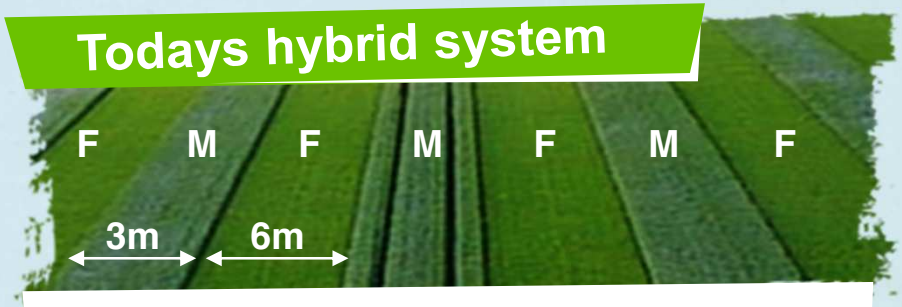
Unique technology offerings within Bayer CropScience

The hybrid wheat challenge…
How to produce economically at scale

Todays “line” varieties

Self pollinating:
- **100%** seed recovery from area

Todays hybrid system



Strip planting:
- Harvest females: **60%–70%** seed recovery
- Chemical gametocide timing critical

We test hybrid crosses

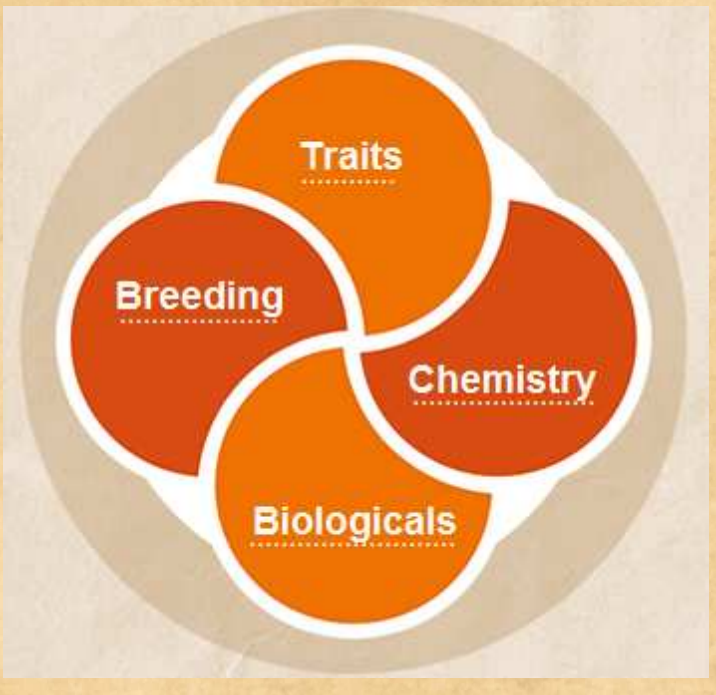
Plan to address the challenges of earlier hybrid wheat production approaches by deploying new technology

Crop Efficiency Research

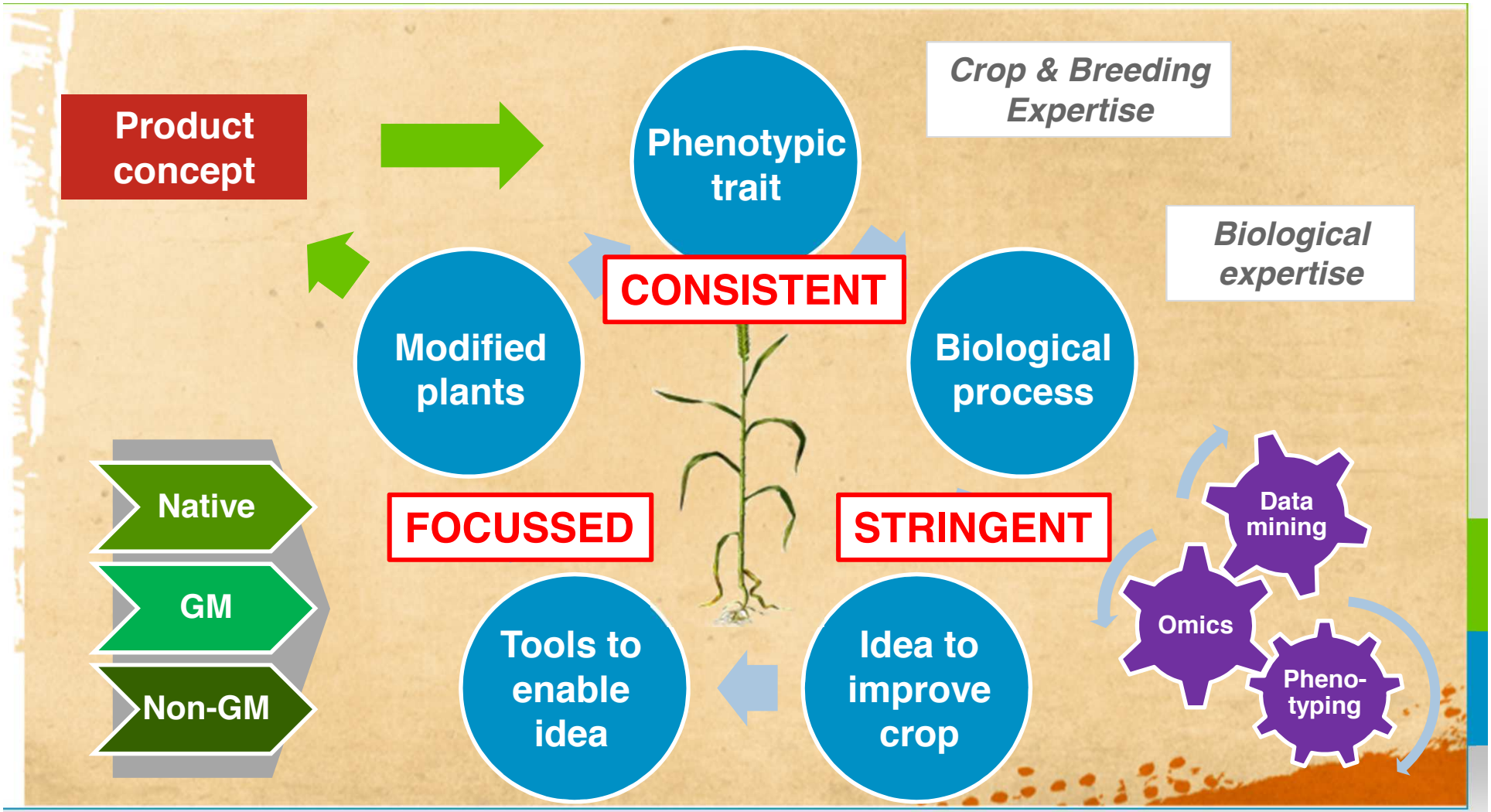
Crop Efficiency: The use of a broad range of technologies to improve plant characteristics with the primary intention of increasing yield

Expanding the yield frontier

Exploiting todays potential



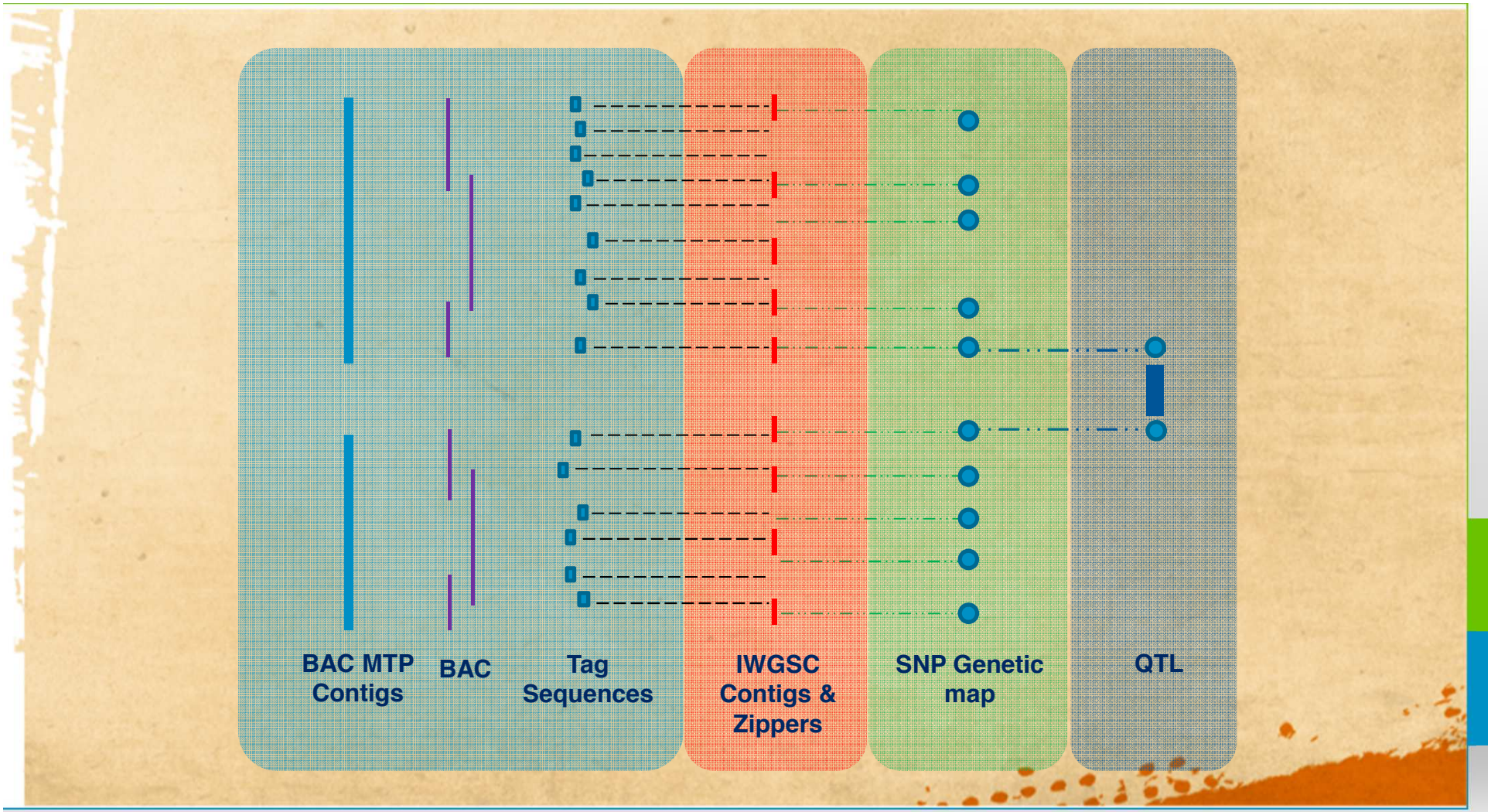
Crop Efficiency Research Strategy: focus on yield components



So where does the wheat genome fit in???

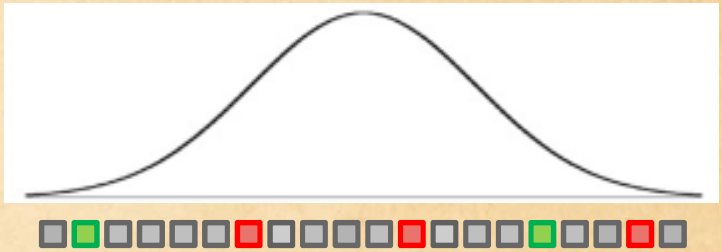
Everywhere!!!

SNP mining and QTL anchorage on sequence scaffolds

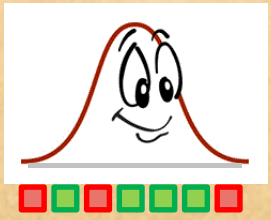


From map-based cloning to QTL Causal Gene mining

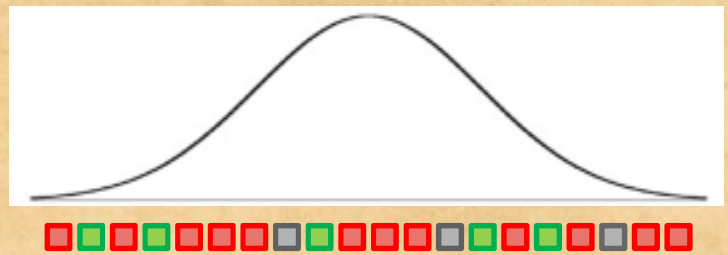
Original QTL region, few and highly fragmented sequence anchor points



Long and tedious process of map-based cloning for each locis of interest to arrive at small set of likely candidates



Original QTL region, immediate understanding of full gene content in reference line



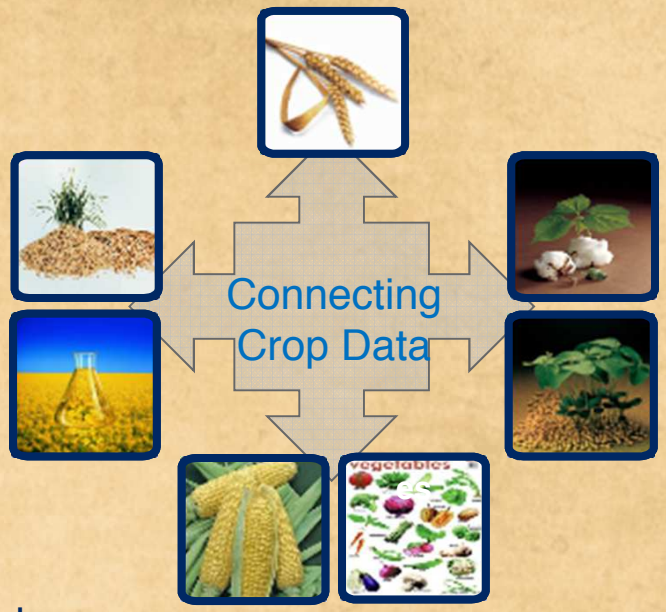
Computational overlay with other omics data allows extraction of candidate gene list for evaluation and for experimental validation

Map-based cloning process becomes cheaper and faster

Requires complete and well-annotated (reference) genome

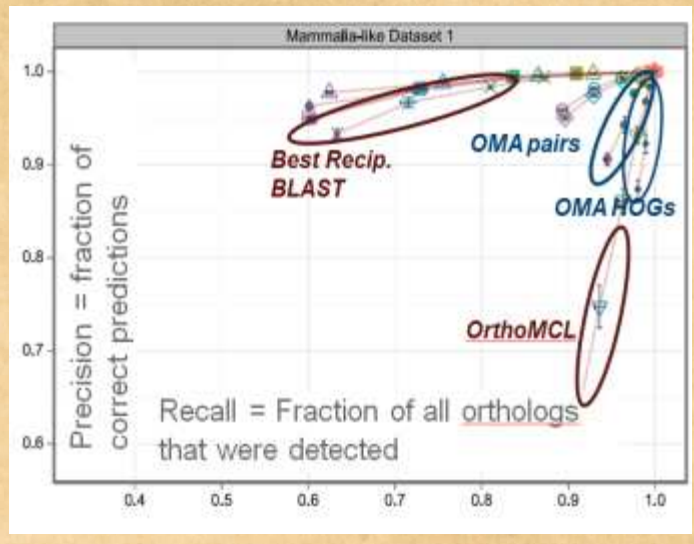
Translational biology

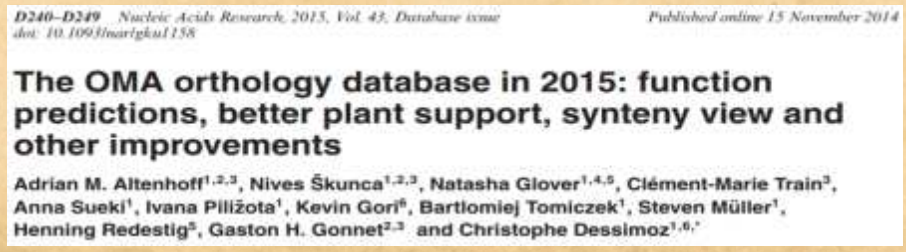
- **Translational biology**
  - Is that gene available in my crop?
  - Does it have the same expression pattern?
  - Which is the functional/structural ortholog?
  - Has it been selected for in domestication or breeding?
- **Annotation**
  - What is the function of my “new” wheat gene?
- **Sequence assembly**
  - How should I assemble these contigs? Are they part of the same gene or paralogous?



Orthology inference

- Best-Recip. BLAST/OrthoMCL perform poorly when high redundancy
- Orthologous Matrix is a better alternative
- Collaboration to develop OMA for Bayer crops
  - **Christophe Dessimoz** project lead
  - **Henning Redestig** Bayer lead
  - **Natasha Glover** Post-doc
  - **Ivana Pilizota, Alex Warwick-Vesztrocy** PhD




D240–D249 Nucleic Acids Research, 2015, Vol. 43, Database issue Published online 15 November 2014
doi: 10.1093/nar/gku1158

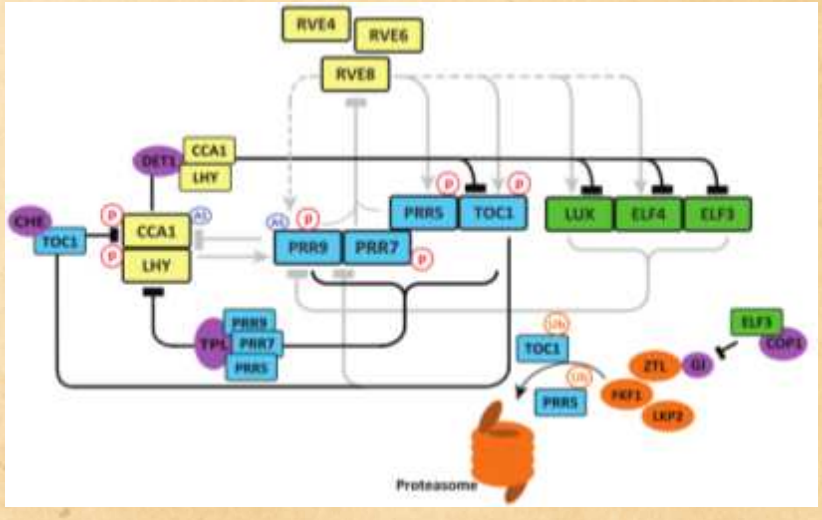
The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements

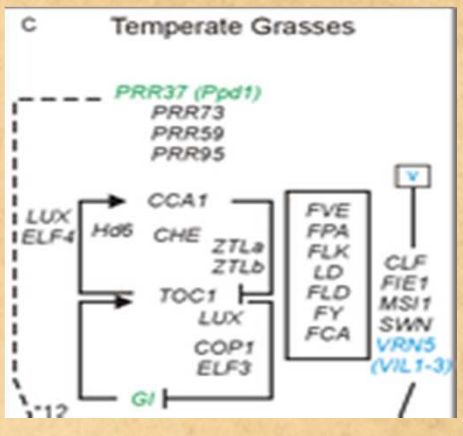
Adrian M. Altenhoff[1,2,3], Nives Škunca[1,2,3], Natasha Glover[1,4,5], Clément-Marie Train[3], Anna Sueki[1], Ivana Piližota[1], Kevin Gori[6], Bartlomiej Tomiczek[1], Steven Müller[1], Henning Redestig[5], Gaston H. Gonnet[2,3] and Christophe Dessimoz[1,6,*]

Requires complete and well-annotated (reference) genome

Translational genetics: circadian clock and wheat yield

Hypothesis: The circadian clock co-determines yield and yield associated traits in wheat





- PhD Student: Lukas Wittern
- Supervisors: Alex Webb (Cambridge), Andy Greenland (NIAB) & Matthew Hannah (Bayer)

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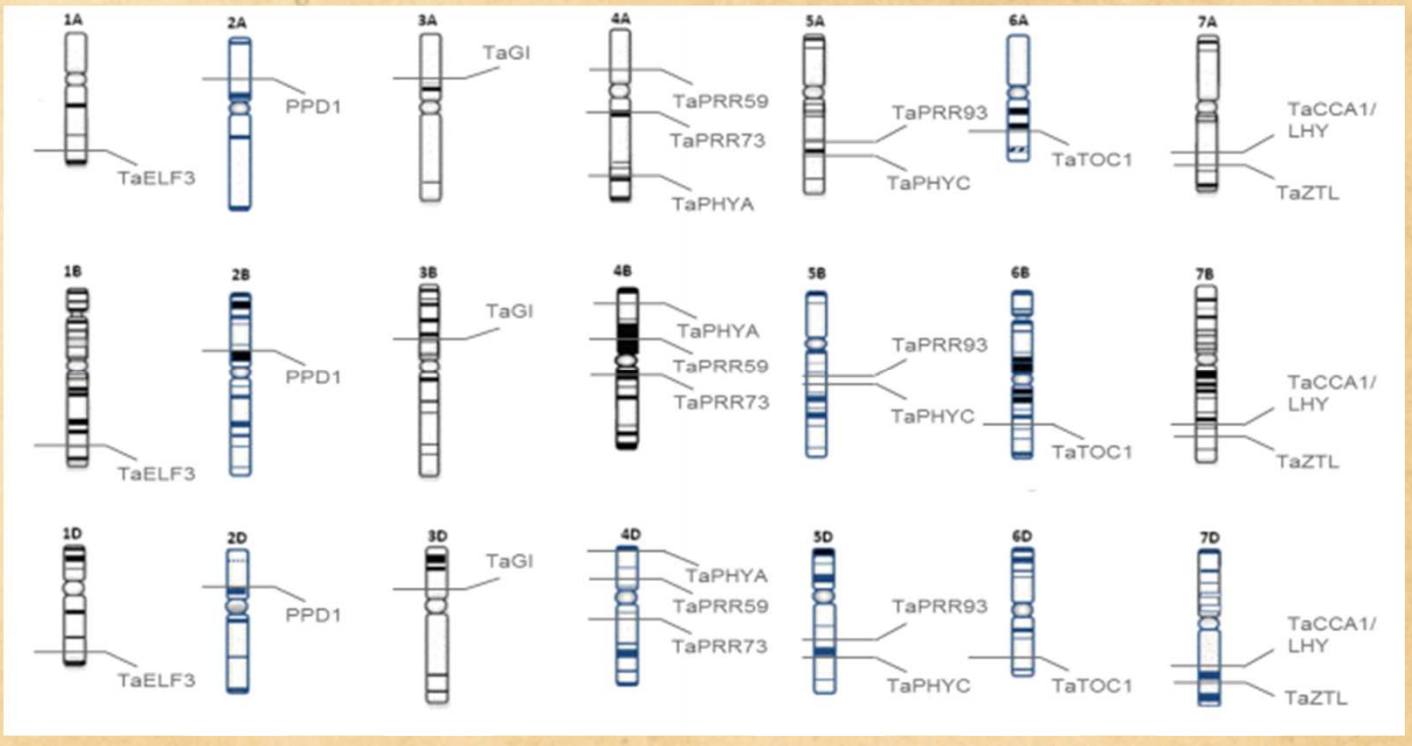
Positioning clock gene orthologs on the draft wheat genome



- 2015: Arabidopsis gene -> wheat ortholog -> CSS contig -> SNP -> genetic map
- 2016: Arabidopsis gene -> wheat ortholog -> Draft genome assembly

Requires complete and well-annotated (reference) genome

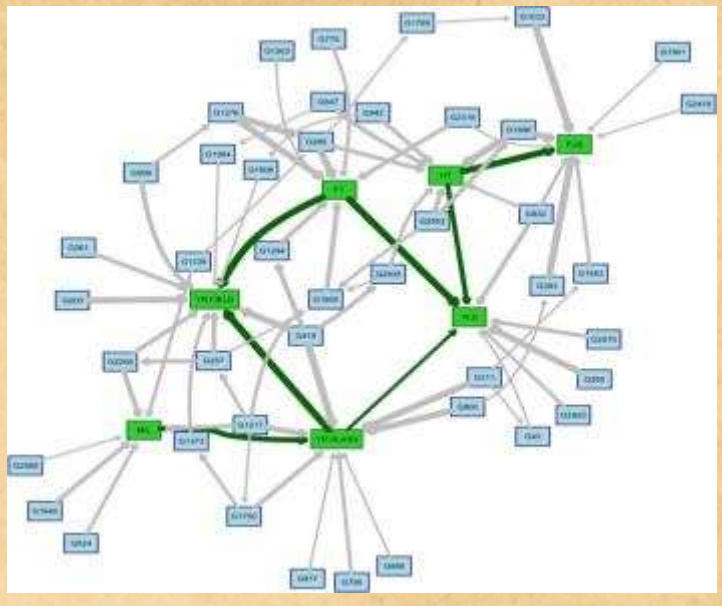
Linking clock gene orthologs to phenotypic traits…

An Eight-Parent Multiparent Advanced Generation Inter-Cross Population for Winter-Sown Wheat: Creation, Properties, and Validation

Ian J. Mackay,*,[4] Pauline Bansept-Basler,*,[1] Toby Barber,* Alison R. Bentley,* James Cockram,* Nick Gosman,*,[2] Andy J. Greenland,* Richard Horsnell,* Rhian Howells,* Donal M. O'Sullivan,*,[3] Gemma A. Rose,* and Phil J. Howell*
*The John Bingham Laboratory, National Institute of Agricultural Botany (NIAB), Cambridge, CB3 0LE, United Kingdom
ORCID ID: 0000-0002-2605-2314 (I.J.M.)

Multiple Quantitative Trait Analysis Using Bayesian Networks

Marco Scutari,*,[1] Phil Howell,† David J. Balding,* and Ian Mackay†
*Genetics Institute, University College London (UCL), London WC1E 6BT, United Kingdom, and †National Institute of Agricultural Botany (NIAB), Cambridge CB3 0LE, United Kingdom



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Bayer and IWGSC

November 2011

- Bayer joined IWGSC

December 2013

- Bayer-sponsored project (€1 mio) “Whole Genome Profiling BAC libraries and physical map construction 8 chromosome arms

November 2015

- Bayer-sponsored project (€420K) “Whole Genome Profiling of BAC minimal tiling paths for 14 chromosomes

Jointly with: CNRGV, INRA, KeyGene and Abraham Korel

	A	B	D
1S	WGP1	WGP1	WGP3
1L	WGP1	WGP1	
2S	PhysMap	PhysMap	PhysMap
2L	PhysMap	PhysMap	PhysMap
3S	WGP2		
3L	WGP2		
4S	WGP2	PhysMap	WGP3
4L	WGP2	PhysMap	
5S	WGP1	WGP2	WGP2
5L	WGP1	PhysMap	PhysMap
6S			WGP3
6L			
7S	WGP1	WGP2	WGP2
7L	WGP1	WGP2	WGP2

A new era for the wheat genome!

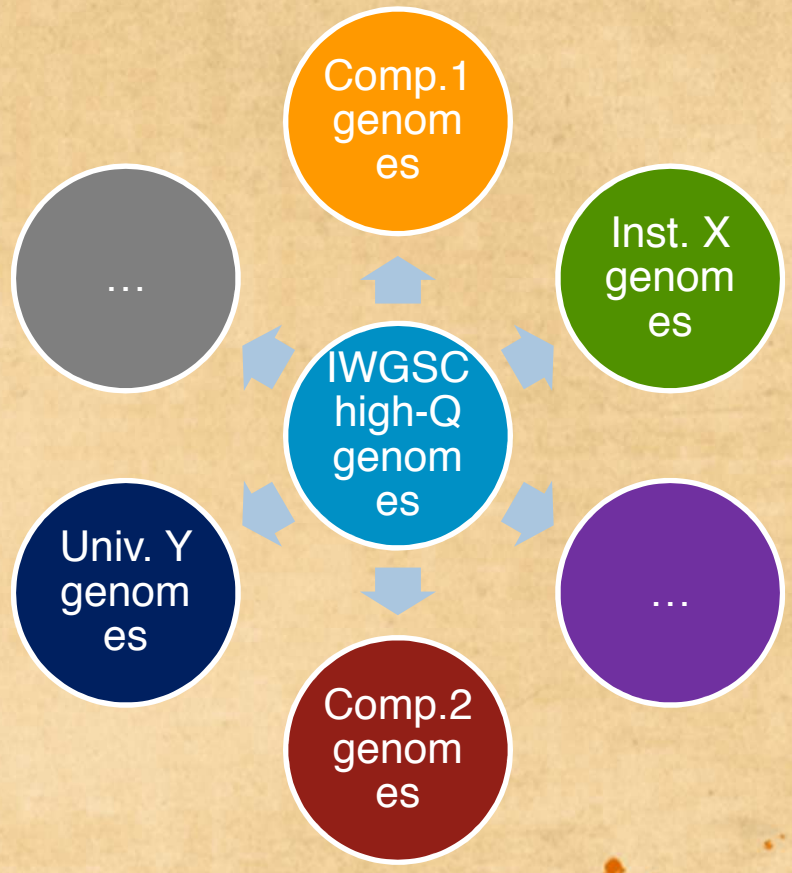
- Whole wheat genomes can be delivered in large scaffolds within a few months at a fraction of the cost
- One reference genome is not enough to capture all larger-scale variation (SV, introgressions, …)
- There will be multiple wheat genomes before the end of this year!
- Consistency and high-quality must be assured

Proposed future role of IWGSC in partnering with Industry & Academia

IWGSC can continue to serve the wheat community

- Provide core set high resolution, high-quality reference genomes
- Coordinate annotation and additional data layers on core reference genomes
- Nurture community, ensure quality and standards

Wheat community and Industry can leverage the information of public reference genomes in “private” and collaborative wheat genome projects



Wouldn't it be great if the largest crop genome had the best platform!?


Thank you

Bayer's focus on Integrated Solutions

	Chemicals	Biologicals	Traits	Seeds	Target focus
1. **Weed Management Systems** for grass & broad-leaved weeds	✓		✓		EXPLOIT
2. **Disease management** which meets regulatory demands, provides excellent disease control, & yield benefits beyond disease control	✓	✓			EXPLOIT
3. Deliver **Yield** gains	✓		✓	✓	EXPAND

Wheat Seed Investments since 2010