



Mining the Watkins Collection for Improved Architecture Alleles in Wheat.

**Plant and Animal Genome Conference XXIX
IWGSC Workshop**

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**ROTHAMSTED
RESEARCH**



Rothamsted Research



Rothamsted Research, Harpenden, England

- A charity founded in 1843.
- Studying crops, livestock and soil.
- Broadbalk Experiment started in 1843.

Plant Sciences department:

- **Wheat** and oilseed crops are the major crops studied:
 - **Omega-3 rich *Camelina sativa*.**
 - **Low acrylamide wheat** - the first genome edited wheat field trial in Europe.
 - **High fibre wheat** for healthier white bread.

Wheat Architecture and Hormonal Signalling Group:

- Studying predominantly **gibberellin (GA) signalling**.
- Novel ***Rht* dwarfing alleles** developed.

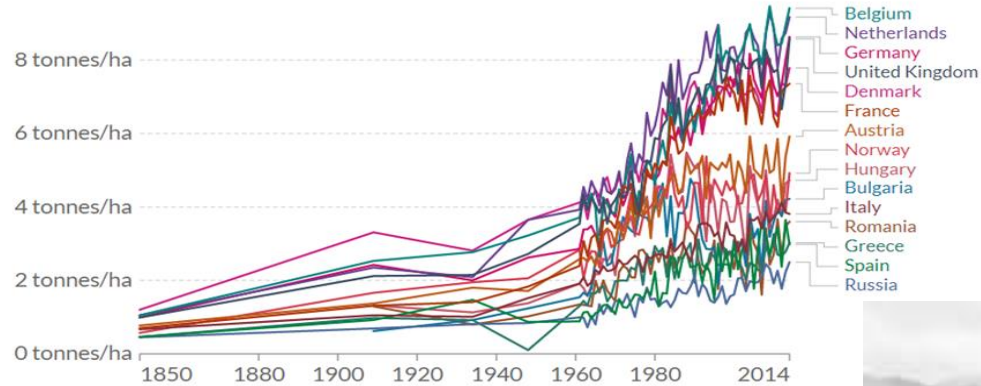


The Green Revolution

Long-term wheat yields in Europe

Wheat yields across selected countries in Europe, measured in tonnes per hectare.

Our World in Data



Source: Bayliss-Smith (1984) and Food and Agriculture Organization of the United Nations
OurWorldInData.org/crop-yields • CC BY

The great increases in cereal yields during the **Green Revolution** were achieved partly by the introduction of **dwarfing alleles** through the work of **Norman Borlaug**.



Rothamsted Archives

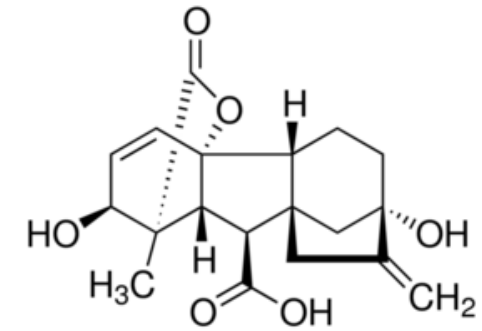


ROTHAMSTED RESEARCH

The Gibberellin (GA) and Plant Architecture



Tanimoto, E. (2012)



Gibberellin



Stem and leaf
elongation



The Gibberellin Signalling

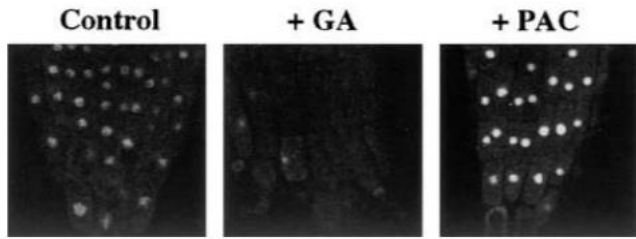
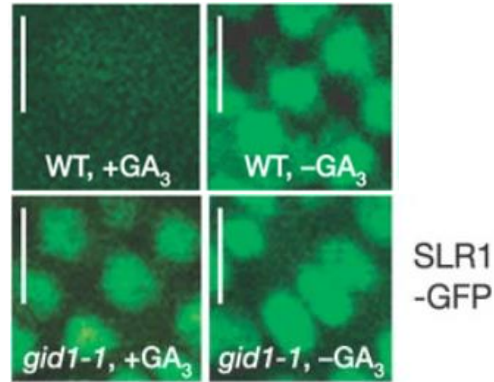
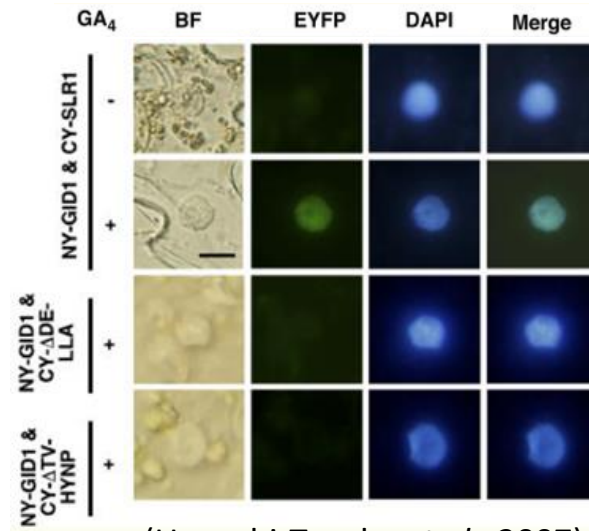


Figure 4. Effects of GA and PAC Treatment on the RGA Promoter-Expressed GFP-RGA Protein.

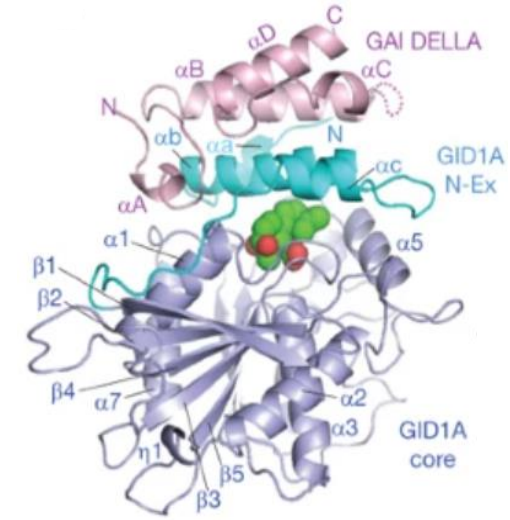
(Silverstone *et al.*, 2001)



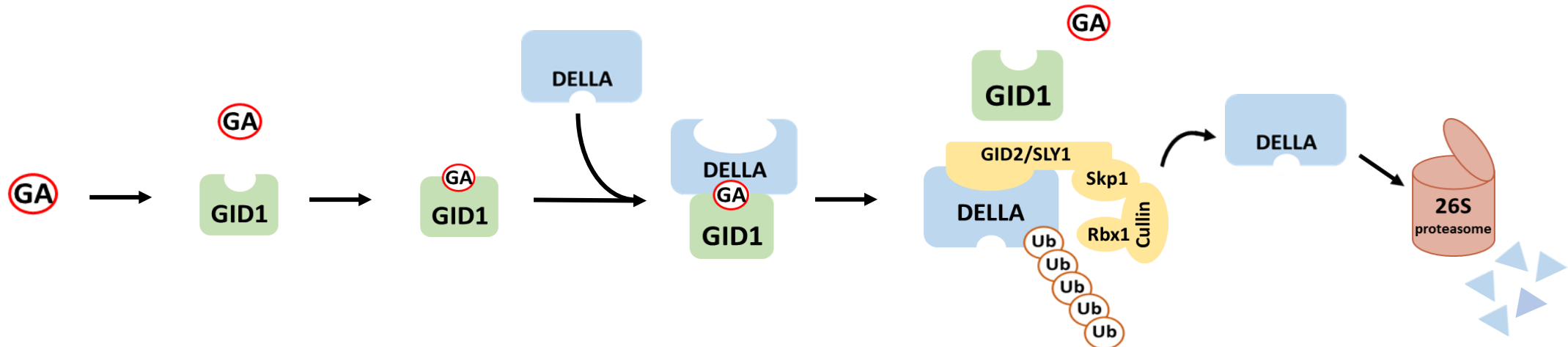
(Ueguchi-Tanaka *et al.*, 2005)



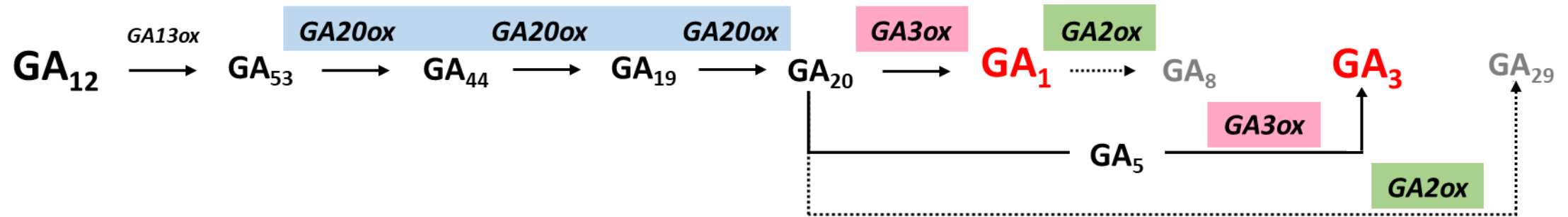
(Ueguchi-Tanaka *et al.*, 2007)



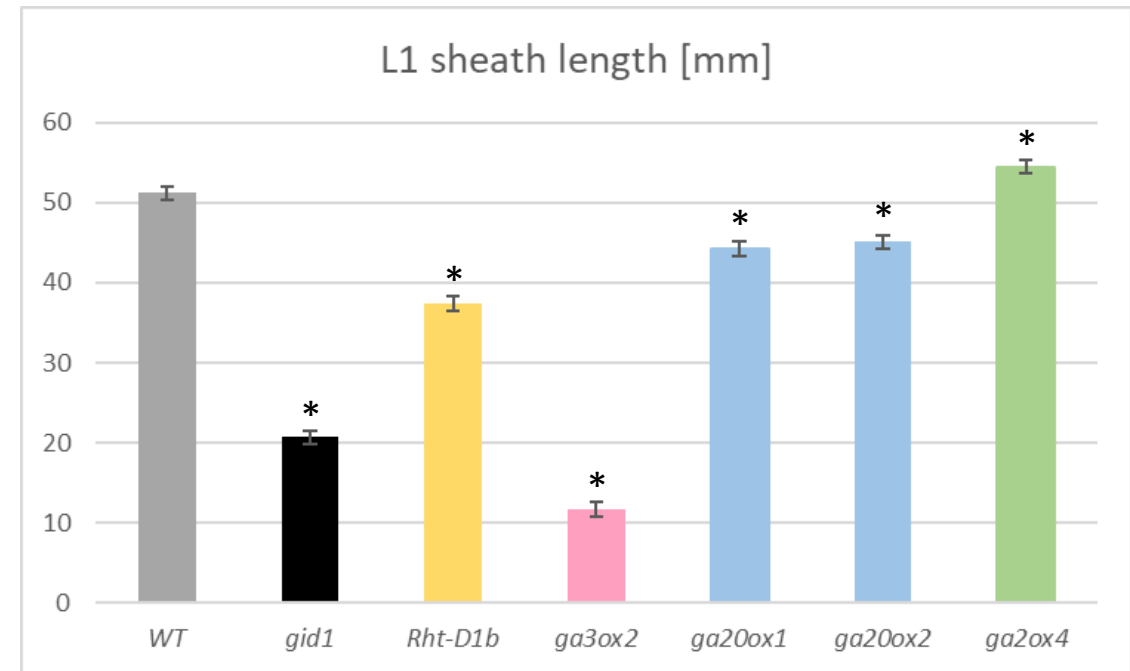
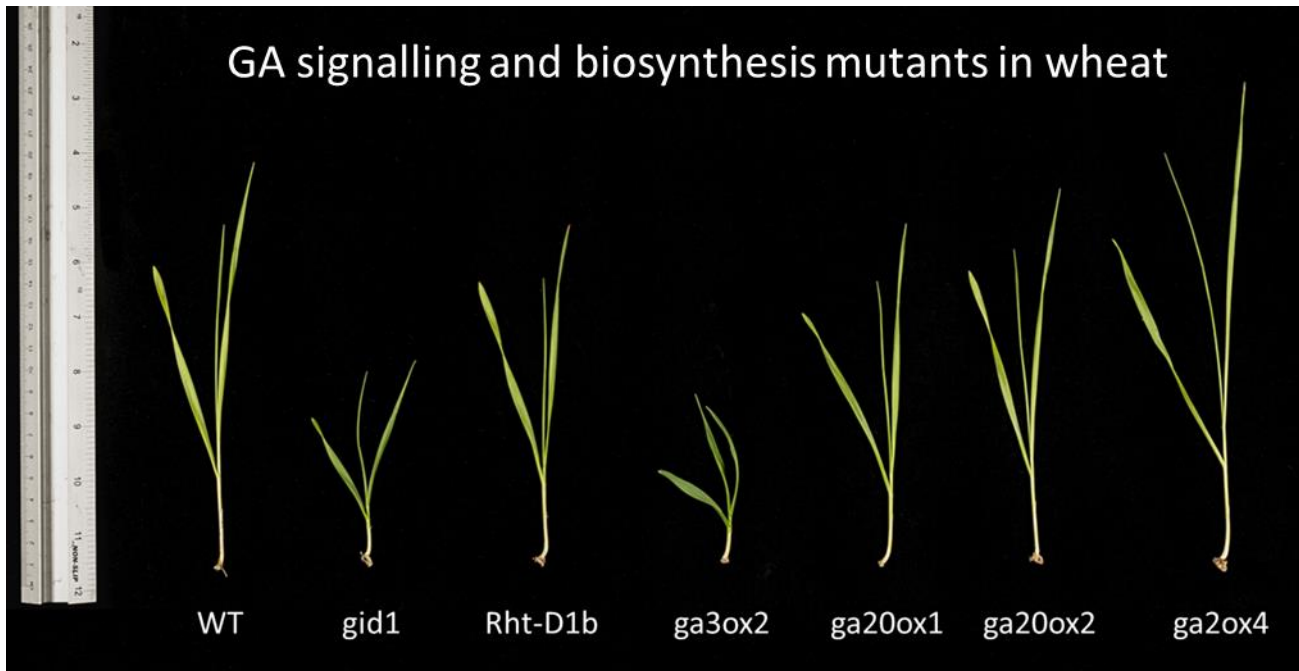
(Murase *et al.*, 2008)



The Gibberellin Biosynthesis



GA signalling and biosynthesis mutants in wheat



Dwarfing Genes of Green Revolution



Li *et al.*, (2018)

sd-1 contains a mutation in *OsGA20ox2* gene.

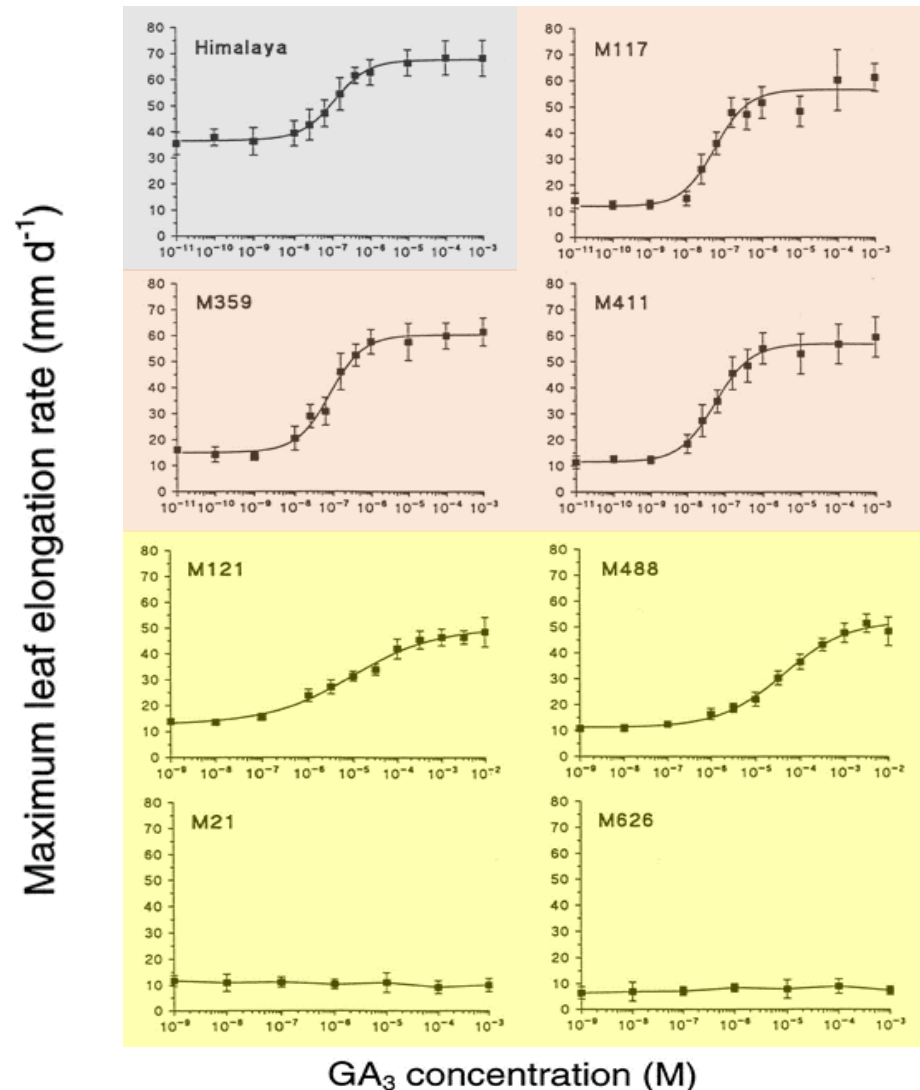


Pearce *et al.*, (2011)

Dwarfing alleles *Rht-B1b* and *Rht-D1b* contain a mutation in *Rht-1* gene that result in accumulation of RHT-1 (DELLA) protein.

GA Dose-Response Assays Identified GA Mutants in Barley

GA dose-response assays were used to identify **GA mutants** in barley.

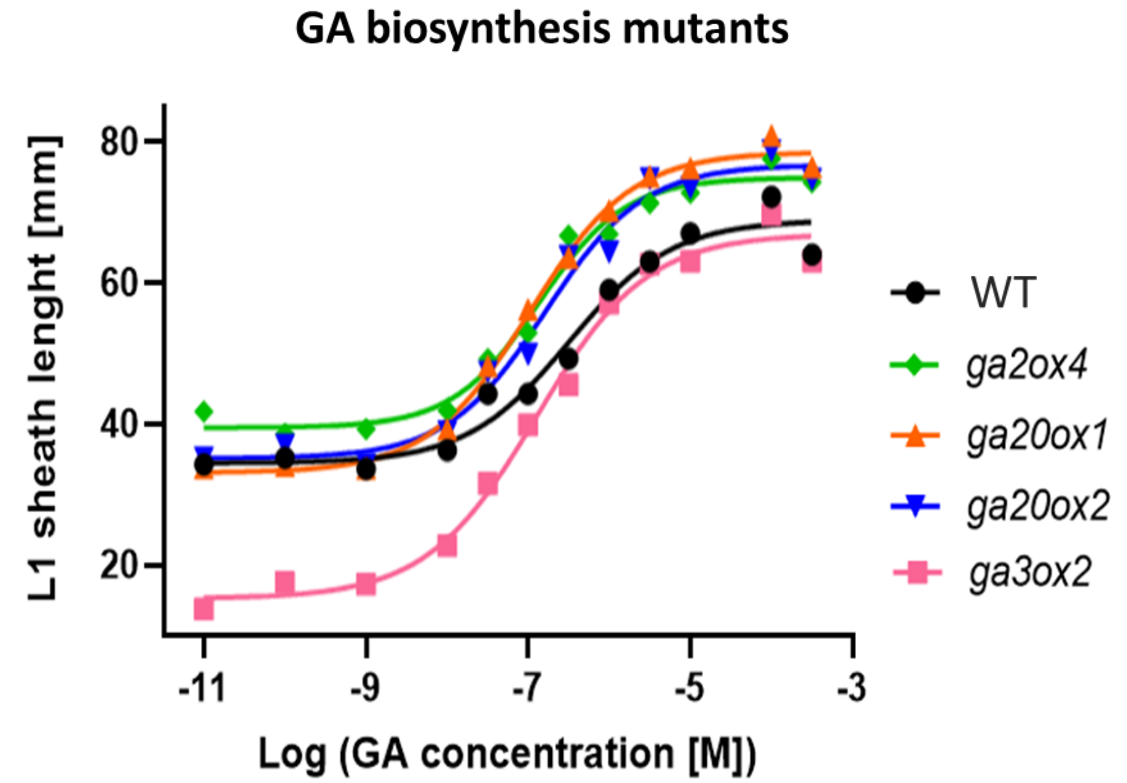
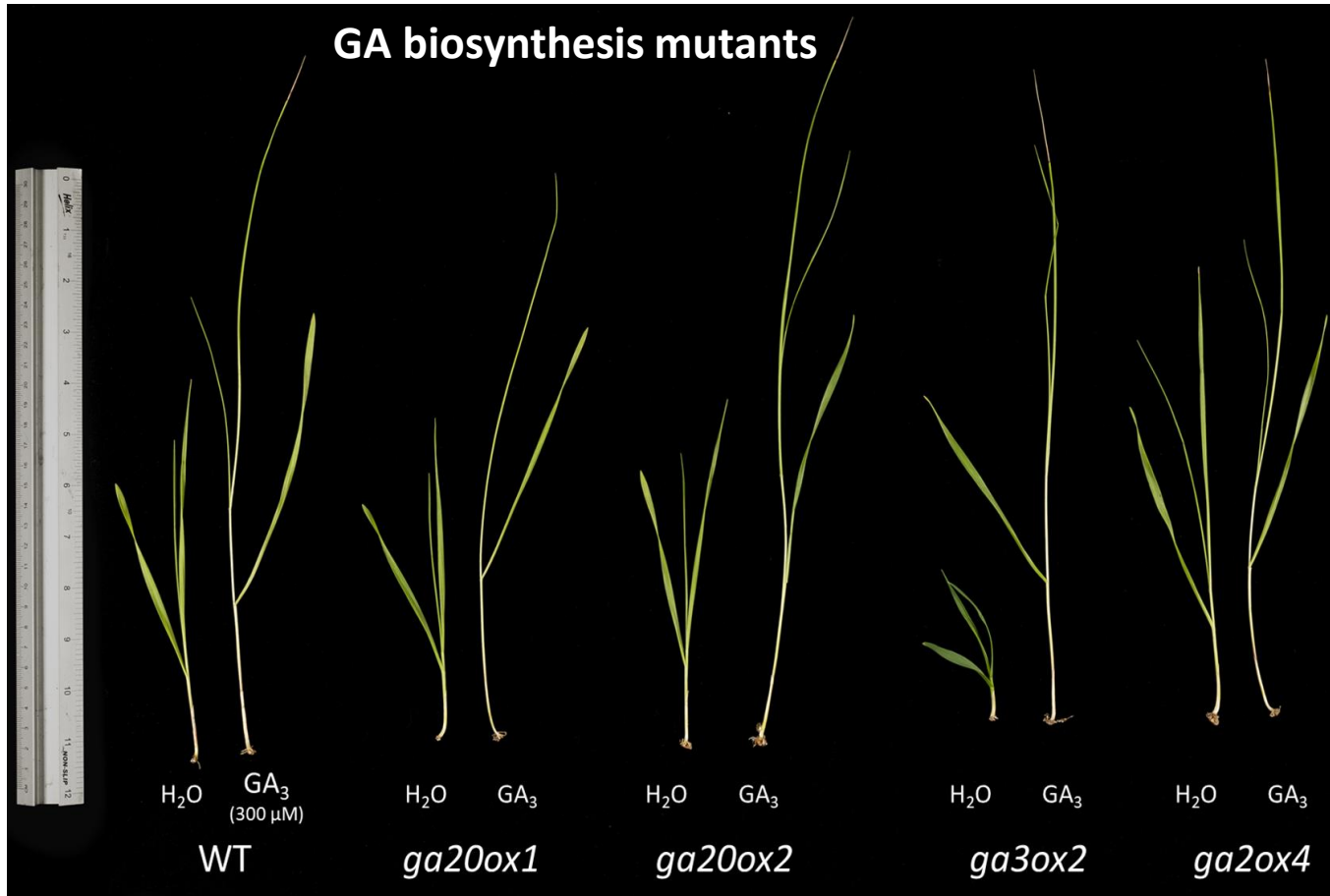


GA biosynthesis mutants respond to the same range of GA concentrations.

GA signalling mutants either require higher GA concentrations to respond, or, they are completely unresponsive to the GA treatment.

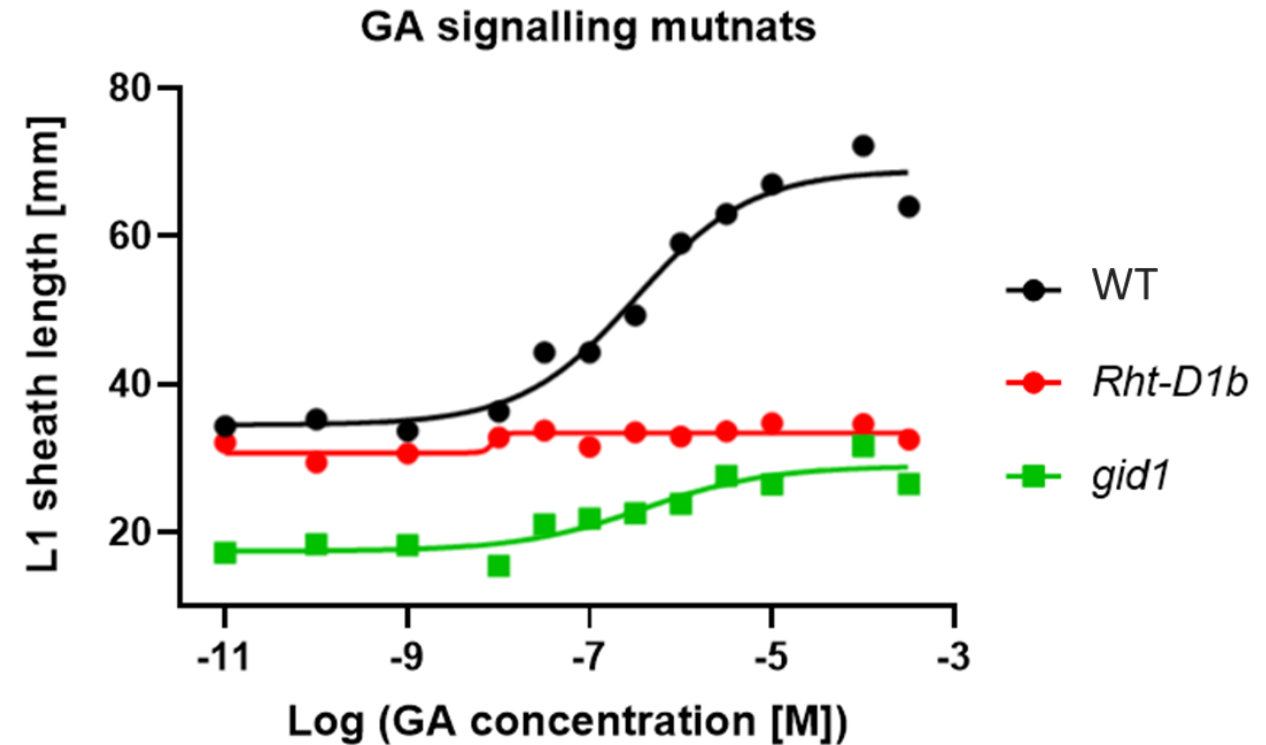
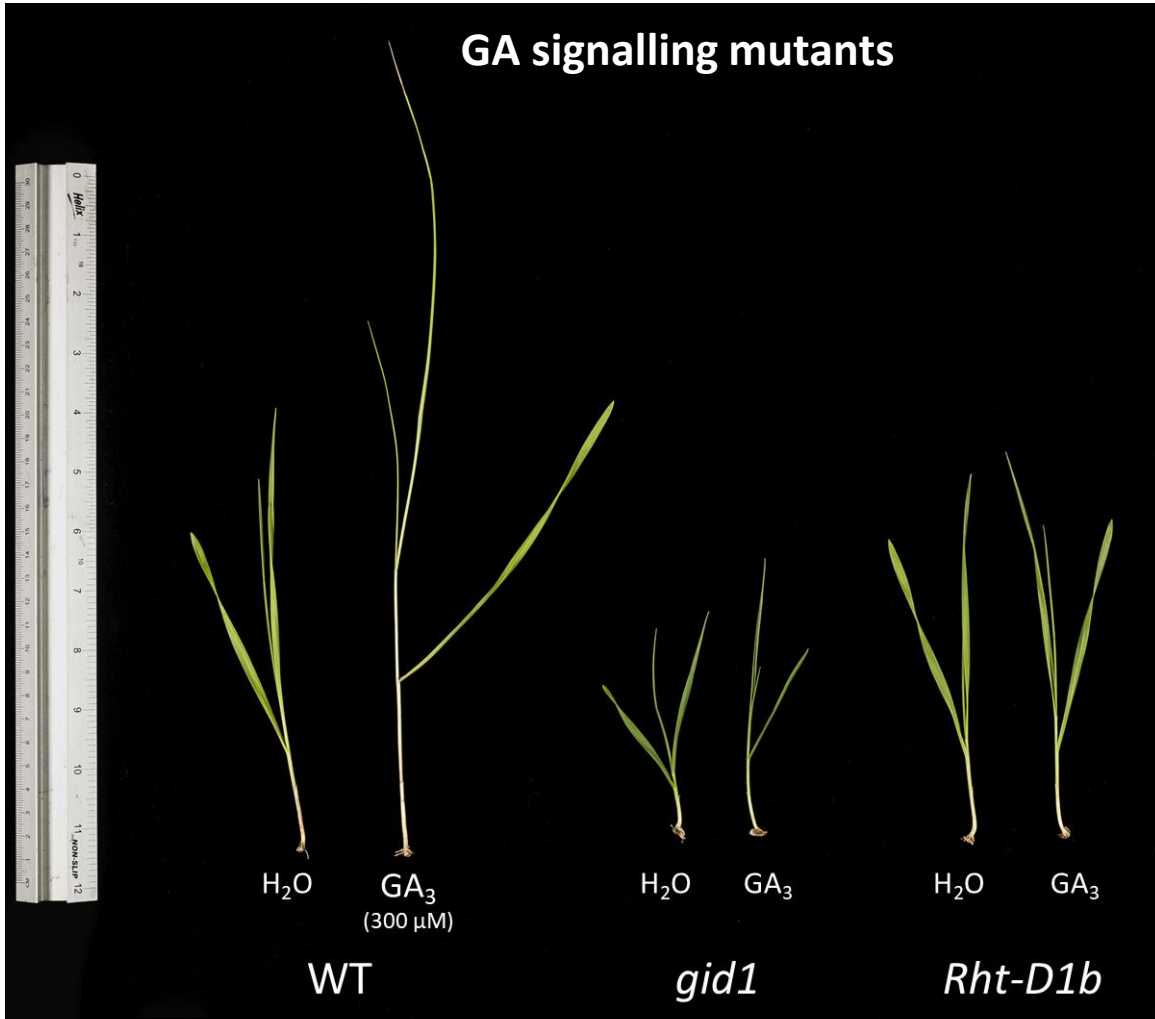
GA Dose-Response Assays of GA Biosynthesis Mutants in Wheat

GA biosynthesis mutants in wheat respond to the GA treatment like the WT plant.



GA Dose-Response Assays of GA Signalling Mutants in Wheat

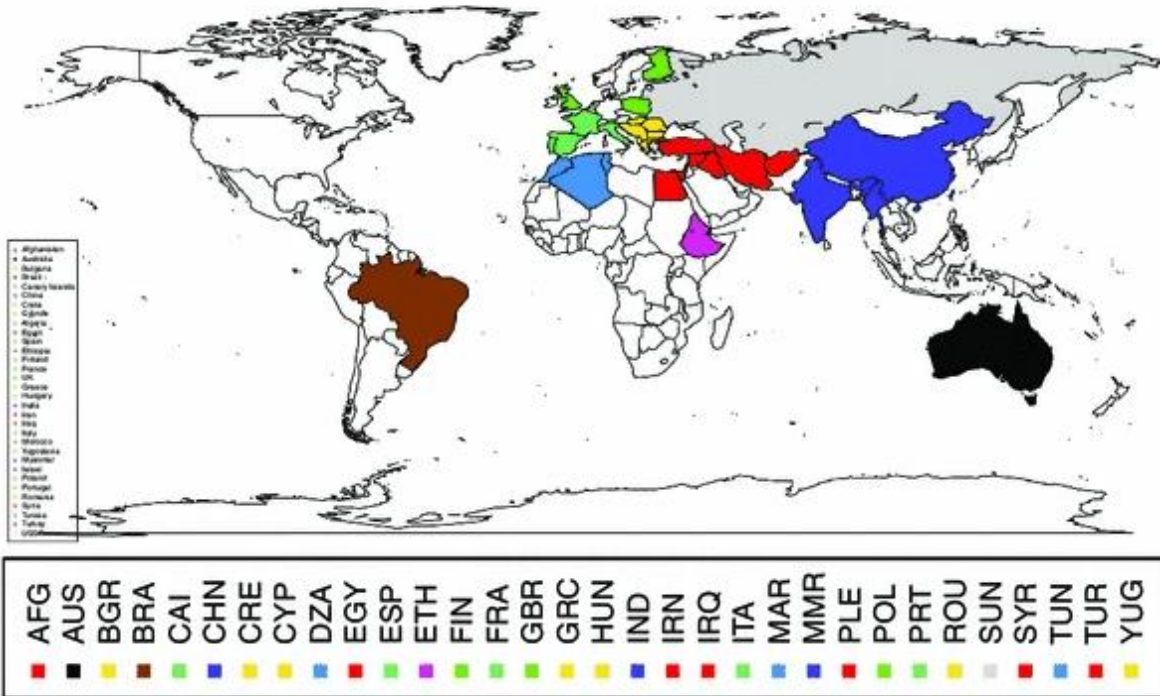
GA signalling mutants in wheat show **reduced or no response** to the GA treatment.



The Watkins Collection

Watkins Collection represents bigger genetic diversity to that of modern elite lines.

AE Watkins: Countries of Origin - Regions



Wingen *et al.*, (2014).

Collection assembled by **A. E. Watkins** from the School of Agriculture in Cambridge in the **1920s** and **1930s** from **32 countries**.

Originally contained over **7,400 landraces**; many were lost during the Second World War. The collection today consists of **826 accessions**.

Watkins Collection preserve a much **higher level of genetic diversity** than present in the modern cultivars.

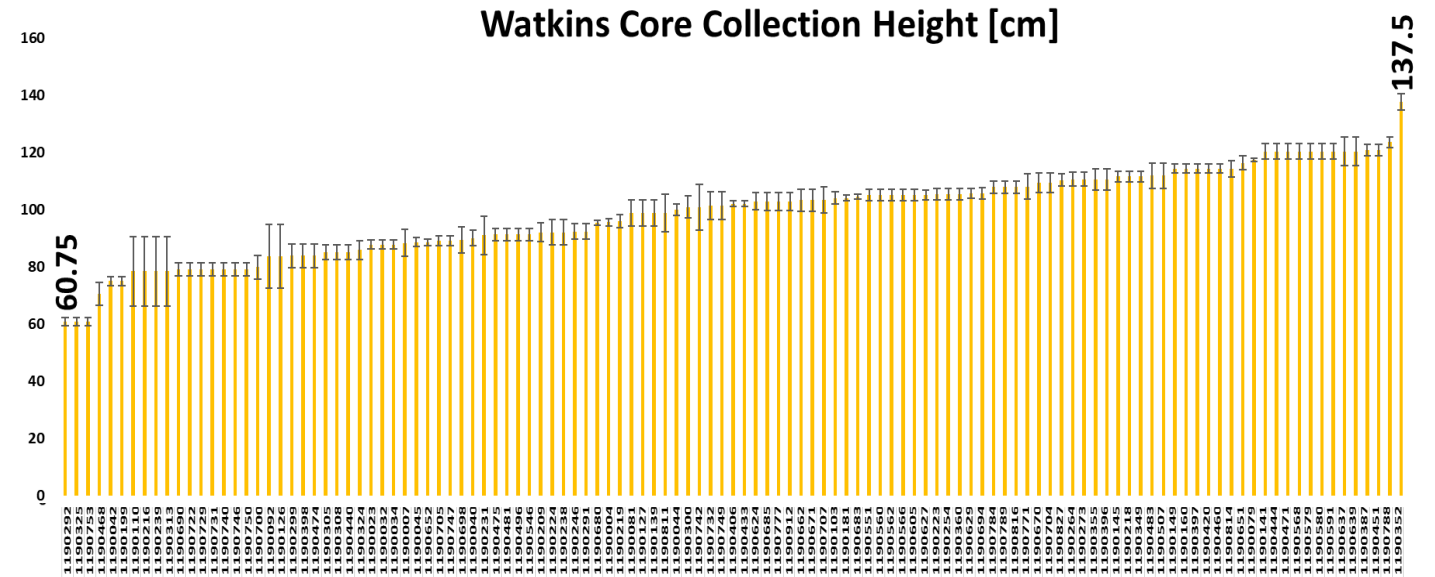
Core Collection: The core set contains **119 LCs** and preserves **98%** of the total **genetic diversity**.

The Watkins Core Collection Phenotype

Diversity of canopy architecture in Watkins accessions



Prof. K Hammond-Kosack



Data taken from: http://wisplandrangepillar.jic.ac.uk/results_resources.htm

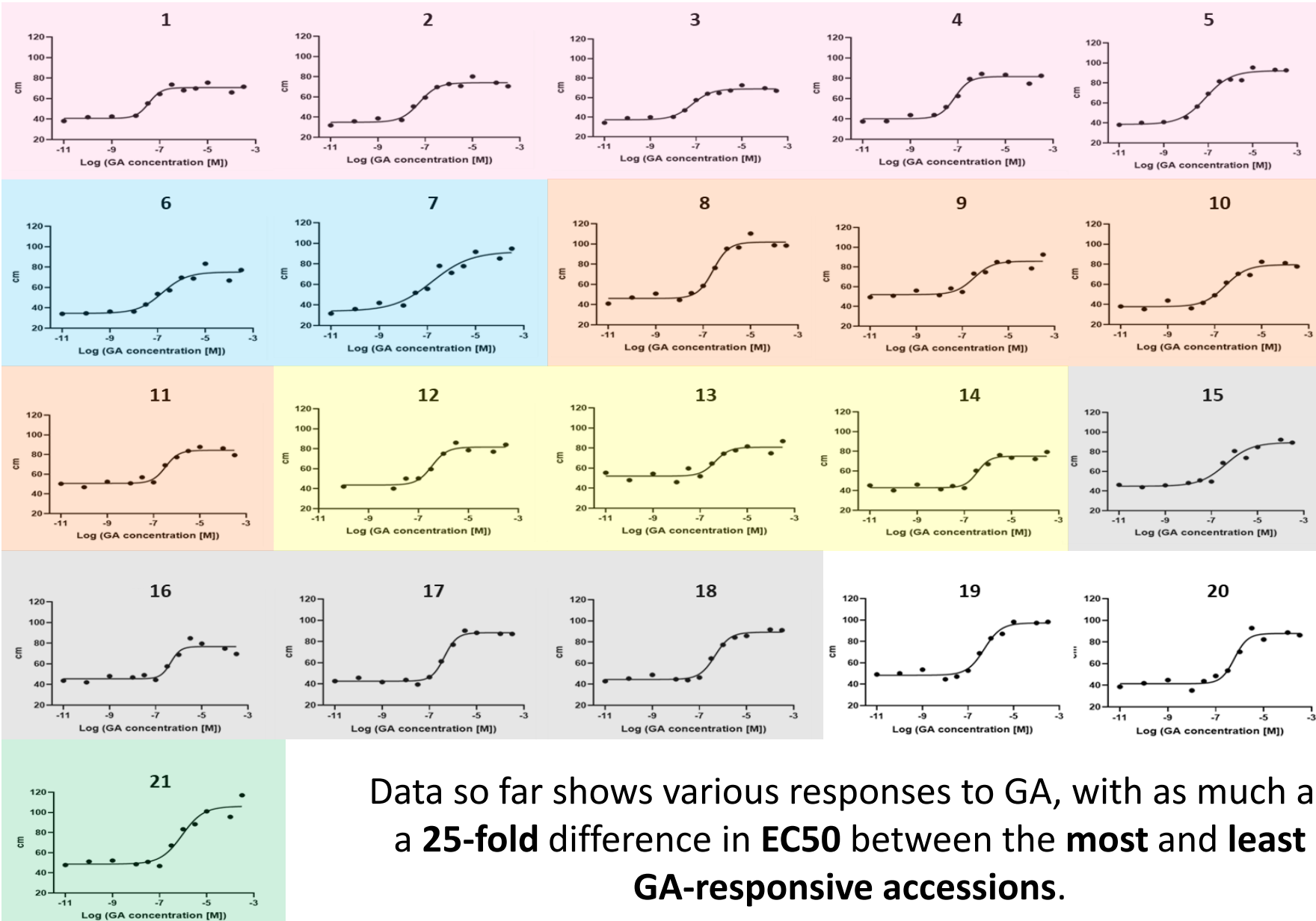
The variety of height phenotypes of the Watkins accessions may suggest **differences in GA regulation between the lines.**

GA dose-response assays will help identify lines with altered GA response.

GA hormone analysis will complement the studies to identify lines with **altered GA biosynthesis or signalling.**



GA Dose-Response Assays of Watkins Core Collection

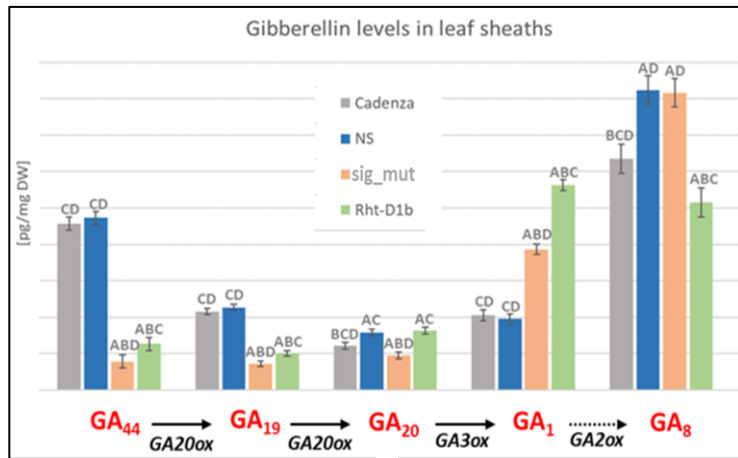


Watkins Accession	EC50 [nM]
1	34.97
2	56.18
3	66.45
4	72.55
5	76.9
6	157.3
7	160.1
8	261.9
9	281.4
10	282.7
11	283.4
12	324.3
13	338.6
14	348.7
15	400.7
16	419.5
17	425.2
18	453.3
19	505.7
20	592.5
21	893.3

Data so far shows various responses to GA, with as much as a **25-fold** difference in **EC50** between the **most** and **least** GA-responsive accessions.

Tools for Allele Discovery

Hormone Data



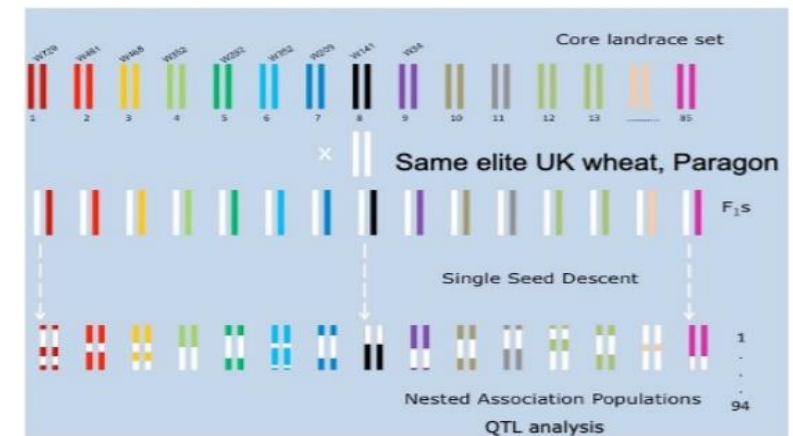
Rht-1 and other signalling mutants in wheat tend to exhibit distorted GA precursors, bioactive GA and GA catabolites levels. GAs levels will identify lines with perturbations in GA metabolism and complement the GA sensitivity data.

Wat-Seq Data

Chromosome	Position	Base	Variant	Variant_frequency	Missing_frequency	Gene_JWGS	Gene_Name (AP)	Variant type	AA_posn	AA change(s)	VEP score	
chr4A	58247793	T	G	0.5%	0.2%	TraesCS4A02G271000.1	Rht-A1	missense_variant	596	K/Q	0	deleterious
chr4A	58247929	G	C	0.1%	0.2%	TraesCS4A02G271000.1	Rht-A1	missense_variant	550	H/Q	0	deleterious
chr4A	582478149	G	T	3.5%	0.2%	TraesCS4A02G271000.1	Rht-A1	missense_variant	477	S/Y	0	deleterious
chr4A	582478337	C	A	0.1%	0.2%	TraesCS4A02G271000.1	Rht-A1	missense_variant	414	E/D	1	tolerated
chr4A	582478585	C	T	10.2%	0.0%	TraesCS4A02G271000.1	Rht-A1	missense_variant	332	G/S	0.04	deleterious
chr4B	30861393	G	T	0.3%	0.6%	TraesCS4B02G043100.1	Rht-B1	missense_variant	4	E/D	0.71	tolerated
chr4B	30861424	G	C	8.1%	1.0%	TraesCS4B02G043100.1	Rht-B1	missense_variant	15	G/R	0.43	tolerated
chr4B	30861456	G	A	8.2%	0.8%	TraesCS4B02G043100.1	Rht-B1	missense_variant	25	M/I	0.42	tolerated
chr4B	30861476	C	G	0.1%	1.4%	TraesCS4B02G043100.1	Rht-B1	missense_variant	32	A/G	0.38	tolerated
chr4B	30861571	C	T	2.4%	0.5%	TraesCS4B02G043100.1	Rht-B1	stop_gained	64	#N/A	#N/A	#N/A
chr4B	30861995	A	G	16.2%	0.2%	TraesCS4B02G043100.1	Rht-B1	missense_variant	205	E/G	0.35	tolerated
chr4B	30862010	T	G	0.1%	0.4%	TraesCS4B02G043100.1	Rht-B1	missense_variant	210	V/G	0.41	tolerated
chr4B	30862292	T	C	3.7%	0.3%	TraesCS4B02G043100.1	Rht-B1	missense_variant	304	L/P	0.05	tolerated
chr4B	30862294	C	A	3.8%	0.2%	TraesCS4B02G043100.1	Rht-B1	missense_variant	305	L/I	0	deleterious
chr4B	30862471	C	T	0.1%	0.2%	TraesCS4B02G043100.1	Rht-B1	missense_variant	364	P/S	0.03	deleterious
chr4B	30862531	C	G	0.3%	0.1%	TraesCS4B02G043100.1	Rht-B1	missense_variant	384	Q/E	0.01	deleterious
chr4B	30862771	C	T	0.1%	0.1%	TraesCS4B02G043100.1	Rht-B1	missense_variant	464	P/S	0	deleterious
chr4B	30863176	G	A	0.5%	0.2%	TraesCS4B02G043100.1	Rht-B1	missense_variant	599	G/S	0	deleterious
chr4D	18781242	G	T	7.0%	0.8%	TraesCS4D02G040400.1	Rht-D1	stop_gained	61	#N/A	#N/A	#N/A
chr4D	18781272	G	A	0.5%	0.3%	TraesCS4D02G040400.1	Rht-D1	missense_variant	71	G/S	0.73	tolerated
chr4D	18781335	C	T	0.2%	0.2%	TraesCS4D02G040400.1	Rht-D1	missense_variant	92	H/Y	0	deleterious
chr4D	18781647	G	A	0.2%	0.2%	TraesCS4D02G040400.1	Rht-D1	missense_variant	196	G/S	0.8	tolerated
chr4D	18782342	C	G	0.4%	0.3%	TraesCS4D02G040400.1	Rht-D1	missense_variant	427	D/E	0.61	tolerated
chr4D	18782577	G	A	0.5%	0.1%	TraesCS4D02G040400.1	Rht-D1	missense_variant	506	G/S	0.43	tolerated
chr4D	18782652	G	A	0.7%	0.1%	TraesCS4D02G040400.1	Rht-D1	missense_variant	531	E/K	0	deleterious
chr4D	18782770	C	T	0.1%	0.1%	TraesCS4D02G040400.1	Rht-D1	missense_variant	570	T/I	0	deleterious

Genomic data for all Watkins accessions was generated by Prof. Shifeng Cheng from Agricultural Genomics Institution at Shenzhen, China (AGIS). SNPs identified in Wat-Seq data mapped onto GA biosynthesis and signalling genes.

NAM Lines



http://www.wgin.org.uk/information/documents/Stakeholders%20Meetings/WGIN_SM_21/WGIN_SM_presentations/pdf/Designingfuturewheat-wgin2021.pdf

60 segregating biparental populations including 55 landrace accessions from the core collection that cover all of the 9 ancestral groups crossed to a modern spring elite variety Paragon. A consensus map for the NAM panel contains 2406 markers on 2498 loci (Wingen *et al.*, 2017).



Thank you

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