Unlocking the polyploid potential of wheat through genomics

Cristobal Uauy (cristobal.uauy@jic.ac.uk)
In the past 36 months...

IWGSC et al. 2018

*Earlham (varieties)*

Clavijo et al. 2017

HapMap: Jordan et al. 2015 *Genome Biology*

Gardiner et al. 2015 *Genome Biology*

Gardiner et al. 2018 *Genome Research*

in *silico* TILLING:

Krasileva et al. 2017 *PNAS*

**knetminer**

Hassani-Pak 2017

Ramirez-Gonzalez et al. 2018 *Science*


*BMC Bioinformatics*

**CerealsDB**

*Tool for the analysis of the wheat genome*

**polymarker**

Ramirez-Gonzalez et al. 2015 *Bioinformatics*

Bevan and Uauy 2013 *Genome Biology*
Wheat genome

IWGSC et al 2018 Science
Wheat genome

IWGSC et al 2018 Science
### Beyond Chinese Spring

<table>
<thead>
<tr>
<th>Variety</th>
<th>Habit</th>
<th>Origin</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Hexaploid bread wheat</em></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CDC Landmark</td>
<td>spring</td>
<td>Canada</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>ArinaLrFor</td>
<td>winter</td>
<td>Switzerland</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>Julius</td>
<td>winter</td>
<td>Germany</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>Jagger</td>
<td>winter</td>
<td>US</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>Paragon</td>
<td>spring</td>
<td>UK</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td><strong>Cadenza</strong></td>
<td>spring</td>
<td>UK</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>Synthetic W7984</td>
<td>spring</td>
<td>Mexico</td>
<td>(Chapman et al., 2015)</td>
</tr>
<tr>
<td>Robigus</td>
<td>winter</td>
<td>UK</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td>Claire</td>
<td>winter</td>
<td>UK</td>
<td>10+ Genome Project</td>
</tr>
<tr>
<td><em>Tetraploid pasta wheat</em></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Zavitan†</td>
<td>-</td>
<td>Israel</td>
<td>(Avni et al., 2017)</td>
</tr>
<tr>
<td>Svevo</td>
<td>spring</td>
<td>Italy</td>
<td>Interomics</td>
</tr>
<tr>
<td><strong>Kronos</strong></td>
<td>spring</td>
<td>US</td>
<td>10+ Genome Project</td>
</tr>
</tbody>
</table>

† Zavitan is a tetraploid wild emmer (*T. dicocoides*) accession.

* Varieties included within the 10+ Genome Project can be accessed through the Earlham Grassroot Genomics portal ([https://wheatis.tgac.ac.uk/grassroots-portal/blast](https://wheatis.tgac.ac.uk/grassroots-portal/blast)) and the 10+ Genome project portal ([http://webblast.ipk-gatersleben.de/wheat_ten_genomes](http://webblast.ipk-gatersleben.de/wheat_ten_genomes)) (subset of varieties in each). The Svevo genome can be accessed through [https://www.interomics.eu/durum-wheat-genome](https://www.interomics.eu/durum-wheat-genome) subject to Toronto agreement. Synthetic W7984 and Zavitan can be accessed through the Grassroot and 10+ Genome portal, respectively.

Adamski et al 2018 PeerJ Preprint
in silico TILLING

EMS

M₂ population

SeedStar

Genomic DNA

Exome capture

Mutation identification

Krasileva et al 2017 PNAS
Uauy et al 2009 BMC Plant Biology
Over 850 samples; developmental time course, etc

Ramirez-Gonzalez et al 2018 Science
Wheat eFP (70 tissue*development stage)

http://bar.utoronto.ca/~asher/efp_wheat/cgi-bin/efpWeb.cgi

Ramirez-Gonzalez et al 2018 Science
Visual interface (>1,000 samples)  www.wheat-expression.com

Borrill et al 2016 *Plant Physiology*
Ramirez-Gonzalez et al 2018 *Science*
Home page

This website provides background information and practical resources to help both budding wheat scientists as well as researchers looking to expand their work into wheat.

As we move into the future there is a great need to improve crops to feed the world’s growing population and to cope with climate change. One potential route to deal with this challenge is to translate fundamental plant biology research (e.g. from Arabidopsis thaliana) into crops such as wheat. However learning even simple tasks such as growing and crossing wheat plants requires time and effort, while material and methods sections in published articles are often short and cannot substitute teaching aids. This is even more true for more complex topics such as the genomics aspect of wheat.

Here we provide information and training about:

Growing wheat  Wheat genomic resources  TILLING mutant resources  Useful wheat links
Yield and quality components

- Number of spikes
- Number of spikelets
- Number of grains

Grain weight (TGW)

Carpel size
GW2 (6A)

Floral organ size
T. polonicum

Grain dimensions

Cell number and size

5A QTL

Grain development
Polyploidy buffers phenotypic variation

Functional Redundancy

Wild-type

Full mutant effect

Dosage

Additive Non-additive

50 %

Genes VRN1, PPD1, ZIP4, R-gen, AP2

QTL

Selected Variation

Hidden Variation

Borrill et al 2019 *Plant Journal*
QTL effects in wheat are subtle compared to diploid

6A QTL (Candidate gene approach)

TKW
6%

Wheat

Rice

Brinton and Uauy 2018 JIPB
Simmonds et al 2016 TAG
Wang et al 2018 TAG
**Single GW2-A mutant does not increase yield**

<table>
<thead>
<tr>
<th>Exp.</th>
<th>Genotype</th>
<th>N</th>
<th>Yield (T/ha)</th>
<th>TGW (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>17_CF</td>
<td>gw2-A1 mutant</td>
<td>24</td>
<td>9.32 ±0.1</td>
<td>47.93 ±0.3</td>
</tr>
<tr>
<td></td>
<td>wild-type</td>
<td>24</td>
<td>9.53 ±0.1</td>
<td>43.59 ±0.3</td>
</tr>
<tr>
<td></td>
<td>Difference</td>
<td></td>
<td>-2.30%</td>
<td>10.0% ***</td>
</tr>
<tr>
<td>17_CF_S</td>
<td>gw2-A1 mutant</td>
<td>24</td>
<td>6.57 ±0.1</td>
<td>49.06 ±0.6</td>
</tr>
<tr>
<td></td>
<td>wild-type</td>
<td>24</td>
<td>6.51 ±0.1</td>
<td>44.49 ±0.5</td>
</tr>
<tr>
<td></td>
<td>Difference</td>
<td></td>
<td>1.00%</td>
<td>10.3% ***</td>
</tr>
<tr>
<td>17_M</td>
<td>gw2-A1 mutant</td>
<td>24</td>
<td>12.12 ±0.1</td>
<td>49.42 ±0.4</td>
</tr>
<tr>
<td></td>
<td>wild-type</td>
<td>24</td>
<td>12.22 ±0.1</td>
<td>44.92 ±0.4</td>
</tr>
<tr>
<td></td>
<td>Difference</td>
<td></td>
<td>-0.80%</td>
<td>10.0% ***</td>
</tr>
<tr>
<td>18_M</td>
<td>gw2-A1 mutant</td>
<td>25</td>
<td>11.83 ±0.2</td>
<td>40.4 ±0.6</td>
</tr>
<tr>
<td></td>
<td>wild-type</td>
<td>25</td>
<td>11.80 ±0.2</td>
<td>37.4 ±0.6</td>
</tr>
<tr>
<td></td>
<td>Difference</td>
<td></td>
<td>0.40%</td>
<td>8.1 % ***</td>
</tr>
<tr>
<td></td>
<td>Mean Increase</td>
<td></td>
<td>-0.43%</td>
<td>9.6 % ***</td>
</tr>
</tbody>
</table>

**Quality:** Similar or higher protein concentration across trials (consistent with Zhang et al 2018).

**Currently in field first yield trials with BC₂ triple mutants.**

unpublished
Consistent effect of 5A QTL on grain length

Grain length (mm)

Grain width (mm)

Brinton et al 2017 New Phytologist
5A QTL affects cell elongation during grain development

Brinton et al 2017 New Phytologist
Evaluating interactions in the field!

Cell expansion

Grain length (5A QTL)
Brinton et al *New Phytologist* 2017

Cell division

Grain width (6A QTL)
Simmonds et al *BMC Plant Biol* 2014
Evaluating interactions in the field!

- Genetic background (Spark and Paragon)
- Environment (Morley and Church Farm)
- H₂O status
- N₂ fertilization
## Genetic Background (5A*6A in Spark and Paragon)

### Spark

<table>
<thead>
<tr>
<th></th>
<th>5A</th>
<th>6A</th>
<th>5A+6A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>-1.1%</td>
<td>6.5%</td>
<td>6.1%</td>
</tr>
<tr>
<td>TGW</td>
<td>2.0%</td>
<td>9.2%</td>
<td>16.3%</td>
</tr>
<tr>
<td>Length</td>
<td>4.0%</td>
<td>1.1%</td>
<td>6.5%</td>
</tr>
<tr>
<td>Width</td>
<td>0.2%</td>
<td>3.7%</td>
<td>5.4%</td>
</tr>
</tbody>
</table>

### Paragon

<table>
<thead>
<tr>
<th></th>
<th>5A</th>
<th>6A</th>
<th>5A+6A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>3.0%</td>
<td>1.5%</td>
<td>4.4%</td>
</tr>
<tr>
<td>TGW</td>
<td>-0.5%</td>
<td>4.6%</td>
<td>9.9%</td>
</tr>
<tr>
<td>Length</td>
<td>2.4%</td>
<td>1.4%</td>
<td>4.2%</td>
</tr>
<tr>
<td>Width</td>
<td>-1.2%</td>
<td>2.2%</td>
<td>3.1%</td>
</tr>
</tbody>
</table>
Irrigated

Non-irrigated

Normal $N_2$

High $N_2$

28 June 2018
High N$_2$

Normal N$_2$

Irrigated

Non-irrigated

6 July 2018
Spark (previous Morley)

<table>
<thead>
<tr>
<th></th>
<th>5A</th>
<th>6A</th>
<th>5A+6A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>0.0%</td>
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<td>TGW</td>
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<tr>
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<td>1.1%</td>
<td>6.5%</td>
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<tr>
<td>Width</td>
<td>0.2%</td>
<td>3.7%</td>
<td>5.4%</td>
</tr>
</tbody>
</table>

All combined (Church Farm)

<table>
<thead>
<tr>
<th></th>
<th>5A</th>
<th>6A</th>
<th>5A+6A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>2.4%</td>
<td>3.5%</td>
<td>7.5%</td>
</tr>
<tr>
<td>TGW</td>
<td>8.1%</td>
<td>4.2%</td>
<td>11.5%</td>
</tr>
<tr>
<td>Length</td>
<td>5.7%</td>
<td>0.9%</td>
<td>5.2%</td>
</tr>
<tr>
<td>Width</td>
<td>1.6%</td>
<td>1.6%</td>
<td>3.3%</td>
</tr>
</tbody>
</table>

Spark: 5A * H₂O interactions

<table>
<thead>
<tr>
<th>5A effect</th>
<th>Irrigation</th>
<th>No Irrigation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>3.0%</td>
<td>1.7%</td>
</tr>
<tr>
<td>TGW</td>
<td>9.9%</td>
<td>7.2%</td>
</tr>
<tr>
<td>Length</td>
<td>5.8%</td>
<td>5.7%</td>
</tr>
<tr>
<td>Width</td>
<td>2.4%</td>
<td>1.1%</td>
</tr>
</tbody>
</table>

Paragon: 5A * H₂O interactions

<table>
<thead>
<tr>
<th>5A effect</th>
<th>Irrigation</th>
<th>No Irrigation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>7.7%</td>
<td>1.1%</td>
</tr>
<tr>
<td>TGW</td>
<td>6.7%</td>
<td>4.3%</td>
</tr>
<tr>
<td>Length</td>
<td>7.0%</td>
<td>6.9%</td>
</tr>
<tr>
<td>Width</td>
<td>1.1%</td>
<td>-0.1%</td>
</tr>
</tbody>
</table>

- No N₂ interaction significant
- No interaction of 6A QTL with water
- 5A interactions with water
Working hypothesis on 5A QTL

- Early 5A effect on cell expansion leads to consistently longer grains.
- Longer grains have the potential to fill more towards end of grain filling.
- This depends on growing conditions.
- If longer grains fill more, then increase in TGW and yield is higher.
Fine mapping of the 5A QTL for grain length

NIL introgression

QTL interval
365 Mbp

Fine mapped interval
75 Mbp; 461 genes
Haplotype-based analysis of QTL interval


Rapid identification and validation of candidate genes

- eFP browser
- Model species orthologs
- RNA-Seq timecourse

Double mutant, speed breeding, and phenotyping

```
   aaBB
   F1  oo
   AAbb
```

Speed Breeding

10 months

F2 seed

Brinton et al 2018 BMC Plant Biology
Watson et al 2018 Nature Plants
Validation of 5A QTL based on double mutants (Kronos)

Field 2018

5A QTL candidate gene

Wildtype

Double (null)
Final thoughts

Genomic tools for biology

Polyploidy hides useful phenotypic variation

Combining complementary modes of action

Cloning yield component QTL is possible