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# The pangenome of *Aegilops tauschii* facilitates high-resolution genomics studies

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# The Open Wild Wheat Consortium

## Unlocking the Diversity of Wild Wheat

We are an international consortium of researchers with strategic interests in Triticeae breeding, genomics, genetics, pathology, and germplasm collection, preservation, and distribution.



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[www.openwildwheat.org](http://www.openwildwheat.org)

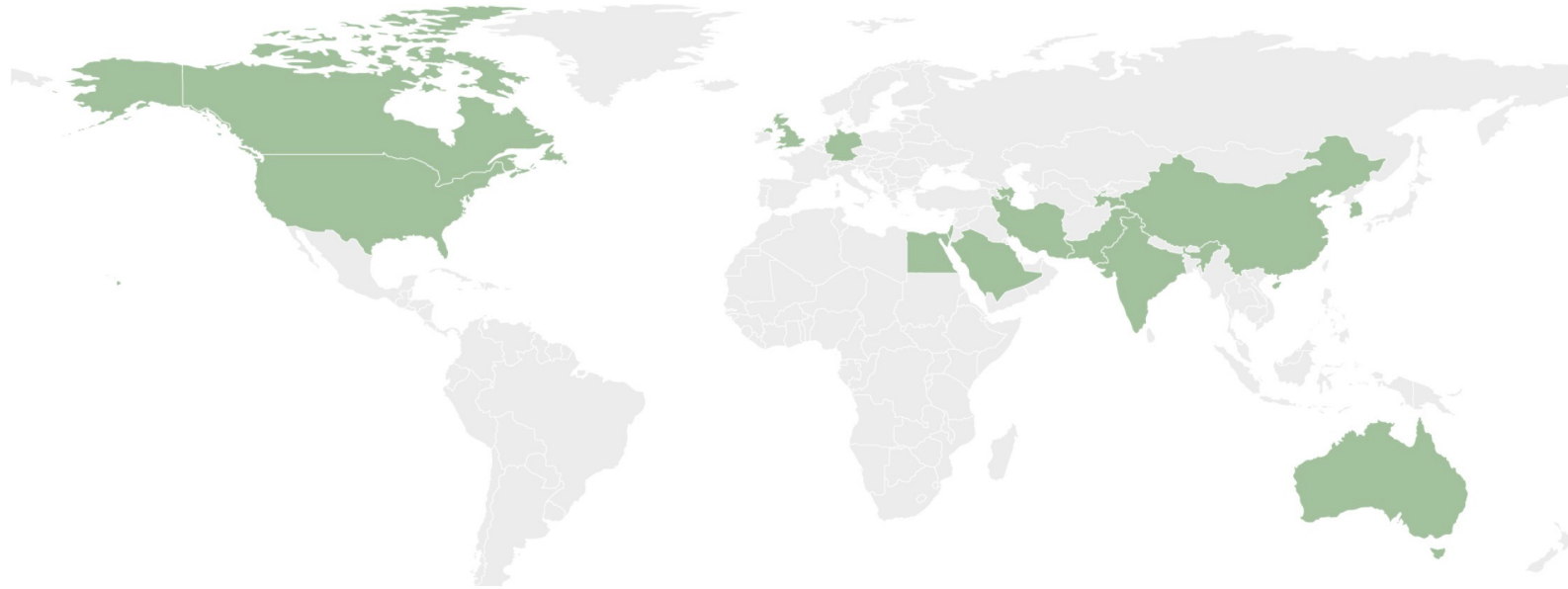


Illustration by Robyn Palessandolo

# The Open Wild Wheat Consortium

## Cross-Continental Collaboration

The Open Wild Wheat Consortium is represented by 15 countries across America, Europe, Asia, Australia, and Africa.



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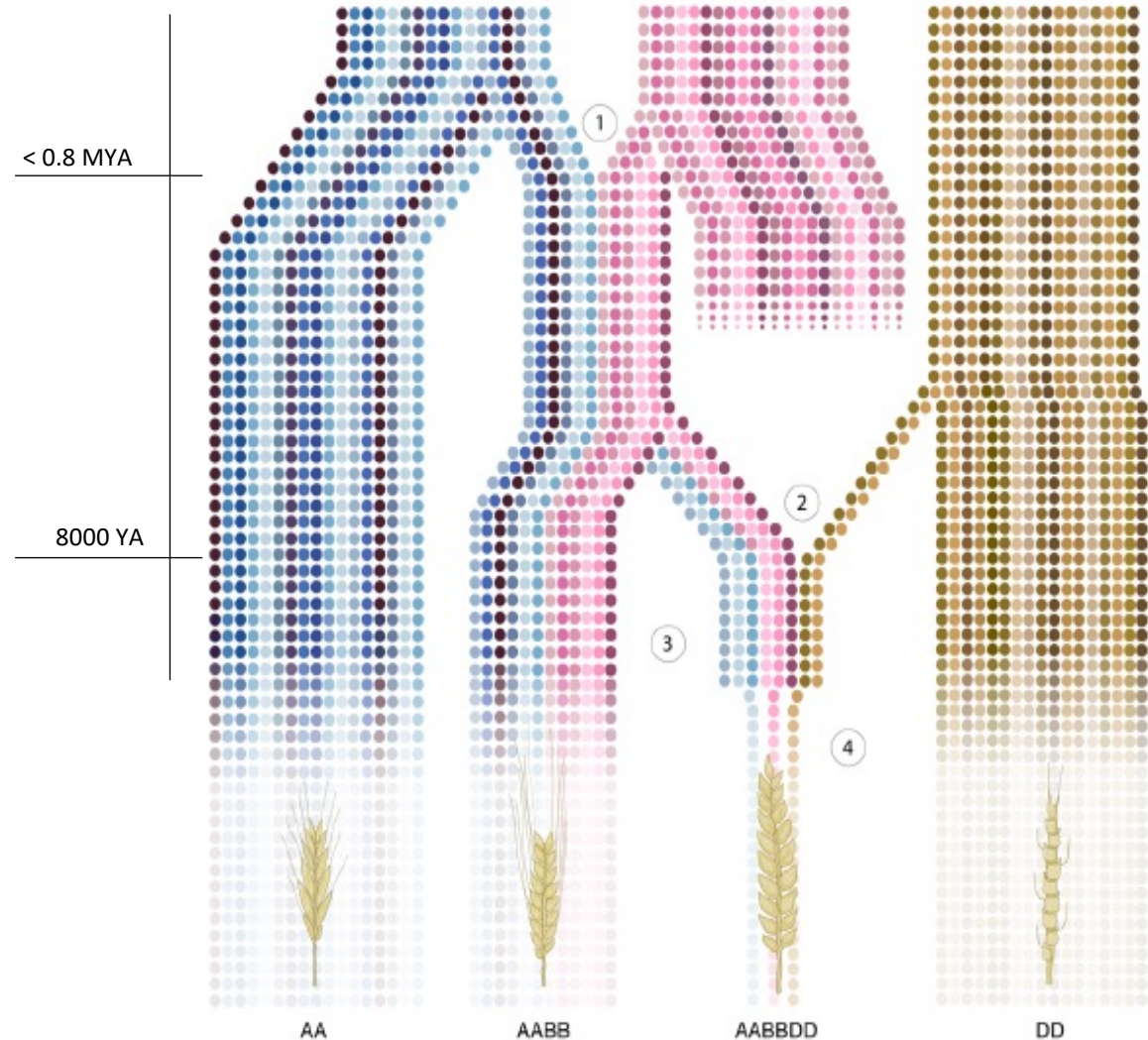
1. Agricultural Research Center, Egypt
2. Research Institute of Forests and Rangelands, Iran
3. Tel Aviv University, Israel
4. King Abdullah University of Science and Technology, Saudi Arabia
5. Quaid-i-Azam University, Pakistan
6. University of Minnesota, USA
7. Sichuan Agricultural University, Chengdu, China
8. Julius Kühn-Institut, Germany
9. National Academy of Sciences of Tajikistan, Tajikistan
10. University of British Columbia, Canada
11. University of California Davis, USA
12. Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany
13. Wheat Genetics Resource Center, Kansas State University, USA
14. National Institute of Agricultural Science, Republic of Korea
15. Institute of Crop Science, Chinese Academy of Agricultural Sciences, China
16. University of Sheffield, United Kingdom
17. Genetic Resources Institute, Ministry of Science and Education, Azerbaijan
18. John Innes Centre, United Kingdom
19. Punjab Agricultural University, India
20. University of Sydney, Australia
21. Institute of Molecular Biology and Biotechnologies, Azerbaijan
22. Kansas State University, USA
23. USDA-Agricultural Research Service, USA
24. University of Nottingham, United Kingdom
25. University of Maryland, USA
26. South Dakota State University, USA

# *Aegilops tauschii* as a source of genetic diversity for bread wheat improvement



*Aegilops tauschii*  
Wild relative of hexaploid wheat

- D-genome donor
- Diploid
- Genome size 4.36 Gb



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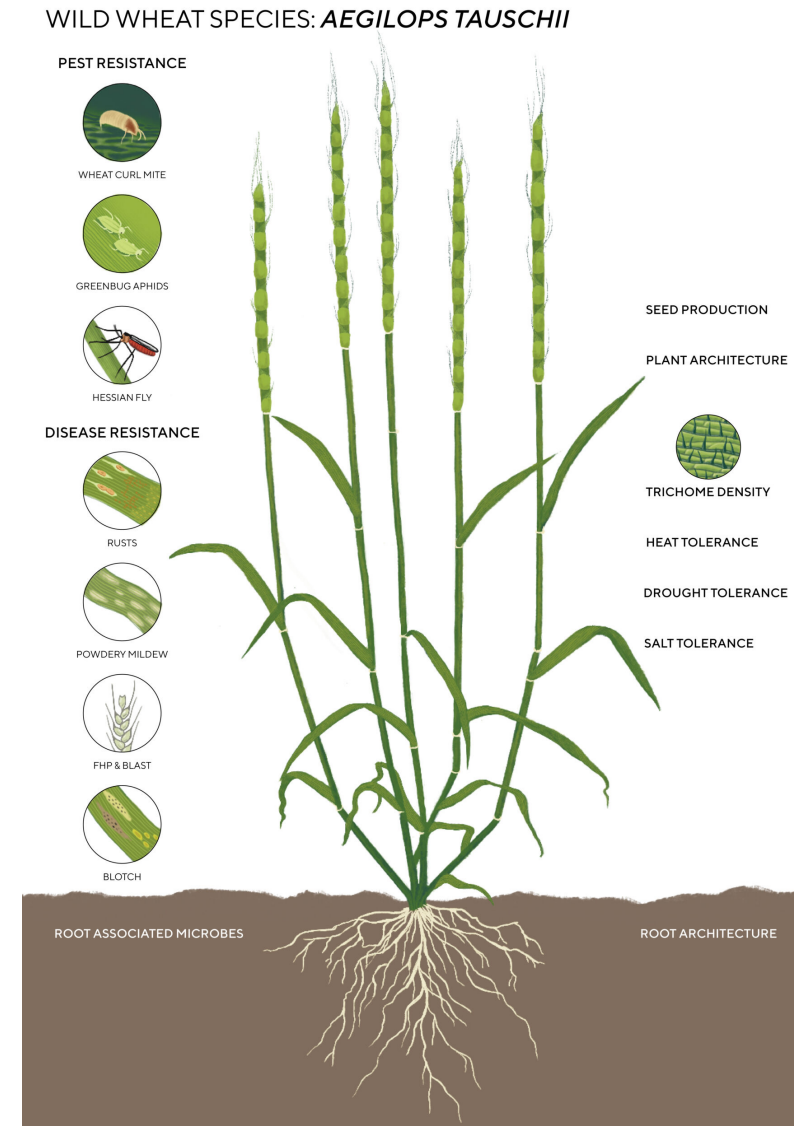


Illustration by Emma Waller. OpenWildWheat.org

# Population genomics of *Aegilops tauschii*



## OPEN WILD WHEAT

Phase I  
2017-2021

nature  
biotechnology

ARTICLES

<https://doi.org/10.1038/s41587-021-01058-4>

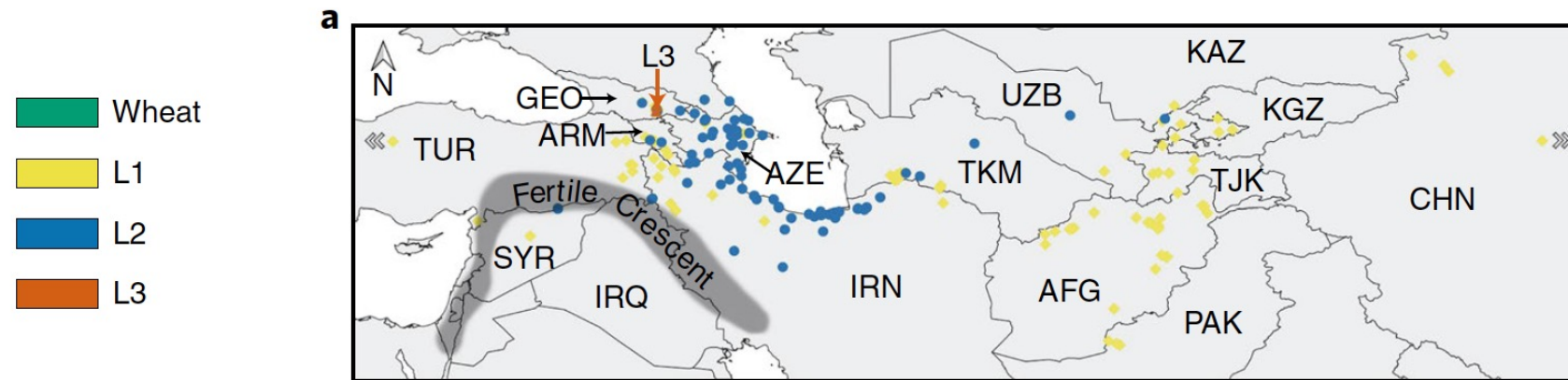


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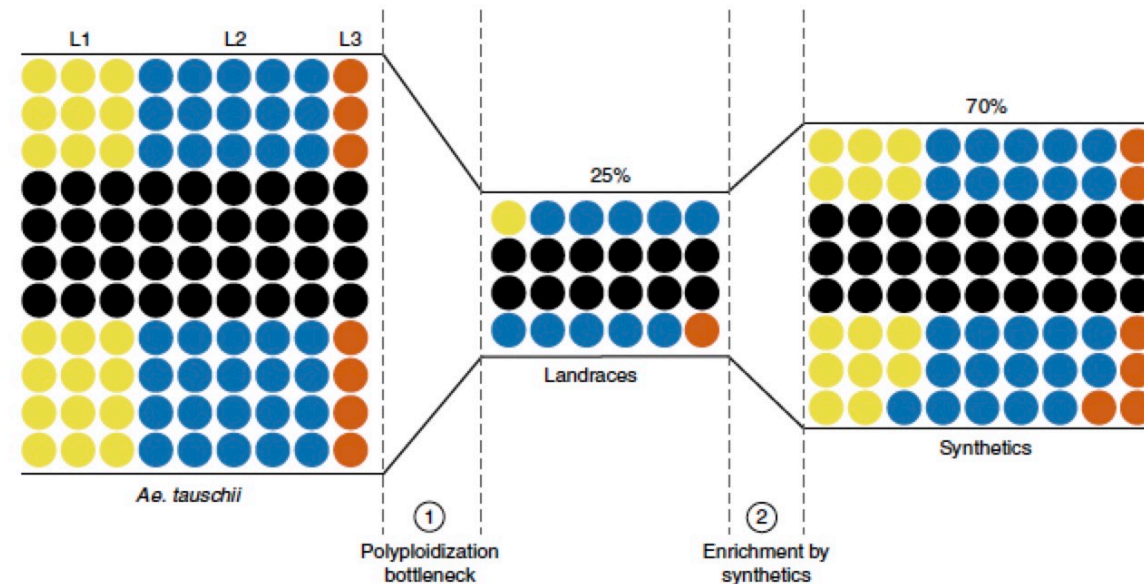
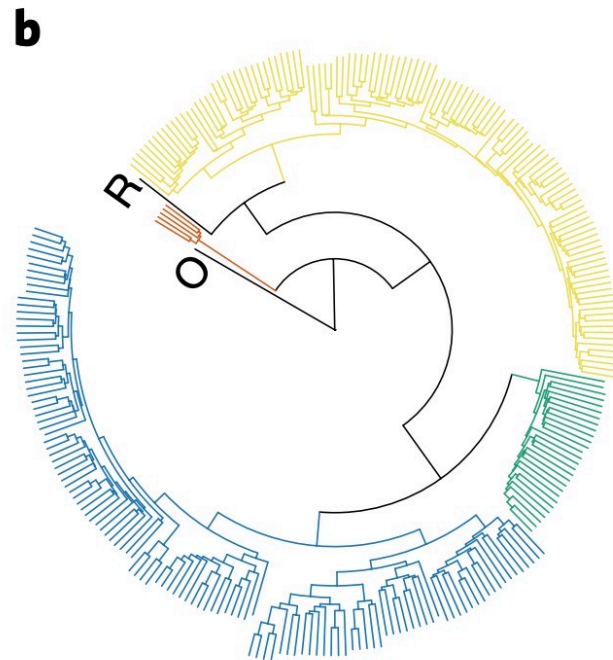
## Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement

Kumar Gaurav<sup>1,39</sup>, Sanu Arora<sup>1,39</sup>, Paula Silva<sup>2,3,39</sup>, Javier Sánchez-Martín<sup>4,39</sup>, Richard Horsnell<sup>5,39</sup>, Liangliang Gao<sup>2</sup>, Gurcharn S. Brar<sup>6,7</sup>, Victoria Widrig<sup>4</sup>, W. John Raupp<sup>2</sup>, Narinder Singh<sup>2,36</sup>, Shuangye Wu<sup>2</sup>, Sandip M. Kale<sup>8</sup>, Catherine Chinoy<sup>1</sup>, Paul Nicholson<sup>1</sup>, Jesús Quiroz-Chávez<sup>1</sup>, James Simmonds<sup>1</sup>, Sadiye Hayta<sup>1</sup>, Mark A. Smedley<sup>1</sup>, Wendy Harwood<sup>1</sup>, Suzannah Pearce<sup>1</sup>, David Gilbert<sup>1</sup>, Ngonidzashe Kangara<sup>1</sup>, Catherine Gardener<sup>1</sup>, Macarena Forner-Martínez<sup>1</sup>, Jiaqian Liu<sup>1,9</sup>, Guotai Yu<sup>1,37</sup>, Scott A. Boden<sup>1,10</sup>, Attilio Pascucci<sup>1,11</sup>, Sreya Ghosh<sup>1</sup>, Amber N. Hafeez<sup>1</sup>, Tom O'Hara<sup>1</sup>, Joshua Waites<sup>1</sup>, Jitender Cheema<sup>1</sup>, Burkhard Steuernagel<sup>1</sup>, Mehran Patpour<sup>12</sup>, Annemarie Fejer Justesen<sup>12</sup>, Shuyu Liu<sup>13</sup>, Jackie C. Rudd<sup>13</sup>, Raz Avni<sup>14</sup>, Amir Sharon<sup>14</sup>, Barbara Steiner<sup>15</sup>, Rizky Psthika Kirana<sup>15,16</sup>, Hermann Buerstmayr<sup>15</sup>, Ali A. Mehrabi<sup>17</sup>, Firuza Y. Nasyrova<sup>18</sup>, Noam Chayut<sup>19</sup>, Oadi Matny<sup>20</sup>, Brian J. Steffenson<sup>20</sup>, Nitika Sandhu<sup>21</sup>, Parveen Chhuneja<sup>21</sup>, Evans Lagudah<sup>22</sup>, Ahmed F. Elkot<sup>23</sup>, Simon Tyrrell<sup>24</sup>, Xingdong Bian<sup>24</sup>, Robert P. Davey<sup>24</sup>, Martin Simonsen<sup>25</sup>, Leif Schauser<sup>25</sup>, Vijay K. Tiwari<sup>26</sup>, H. Randy Kutcher<sup>6</sup>, Pierre Hucl<sup>6</sup>, Aili Li<sup>27</sup>, Deng-Cai Liu<sup>28</sup>, Long Mao<sup>27</sup>, Steven Xu<sup>29</sup>, Gina Brown-Guedira<sup>30</sup>, Justin Faris<sup>29</sup>, Jan Dvorak<sup>31</sup>, Ming-Cheng Luo<sup>31</sup>, Ksenia Krasileva<sup>32</sup>, Thomas Lux<sup>33</sup>, Susanne Artmeier<sup>33</sup>, Klaus F. X. Mayer<sup>33,34</sup>, Cristobal Uauy<sup>1</sup>, Martin Mascher<sup>8,35</sup>, Alison R. Bentley<sup>5,38</sup>, Beat Keller<sup>4</sup>, Jesse Poland<sup>2,37</sup> and Brande B. H. Wulff<sup>1,37</sup>

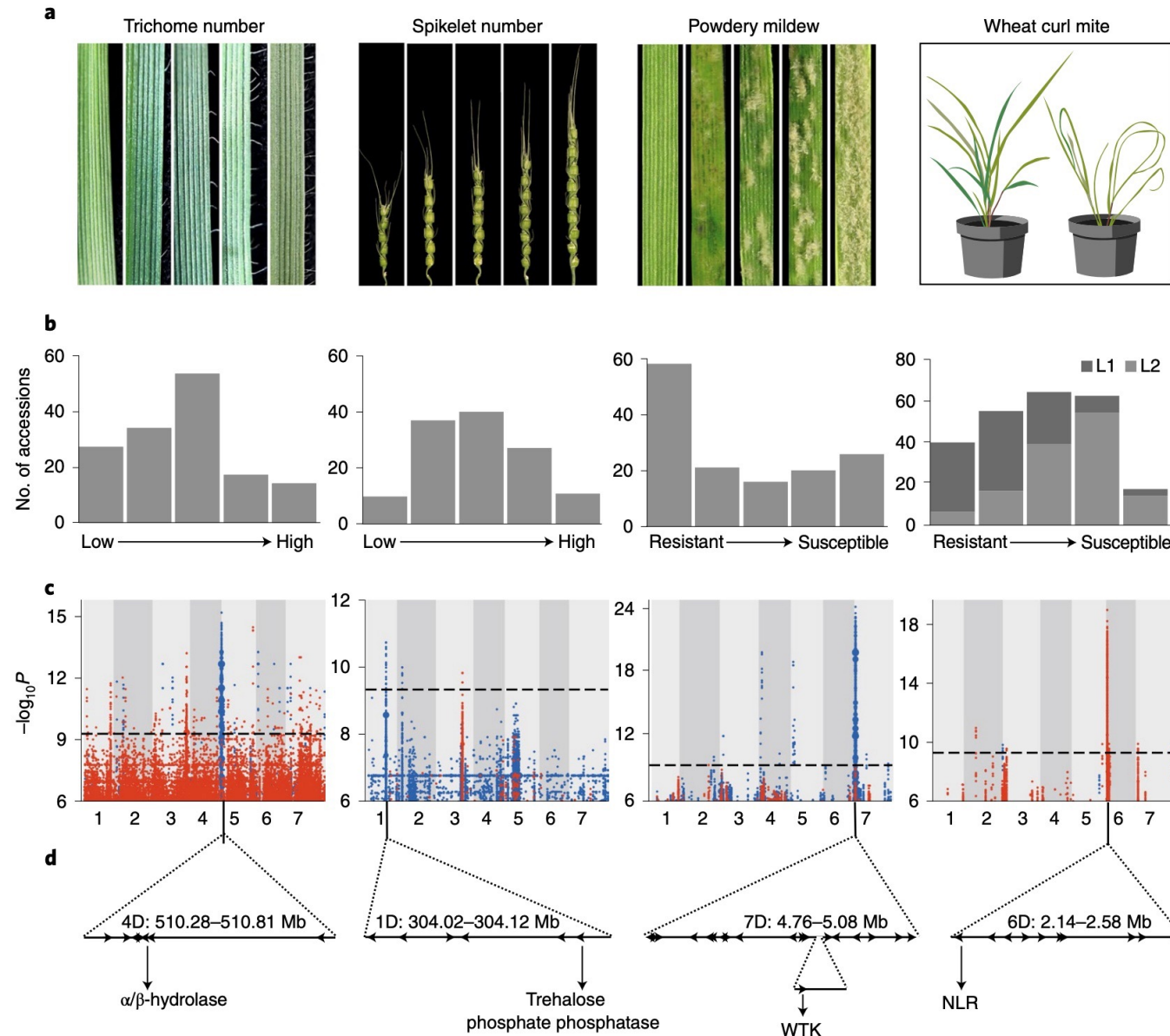
# Population genomics of *Aegilops tauschii*



Sequence-configured diversity panel of 242 non-redundant *Ae. tauschii* accessions



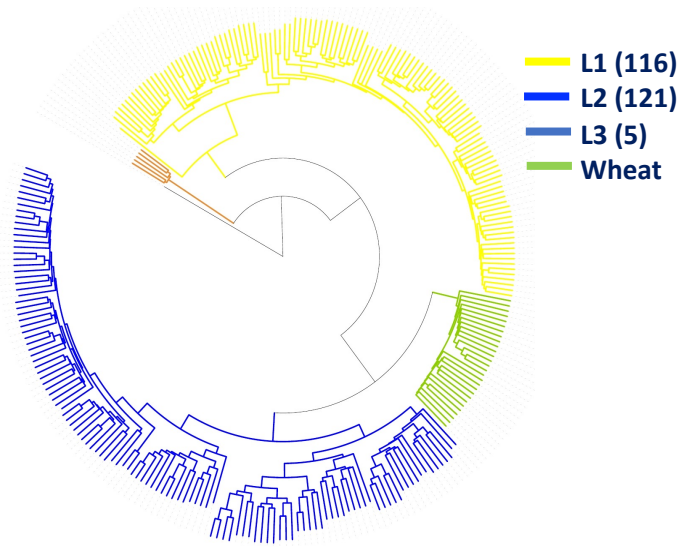
# Dissecting traits of interest using the resequenced and phenotyped panel



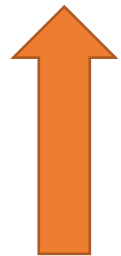


# Resource limitations of Open Wild Wheat Phase I

## Detecting rare alleles

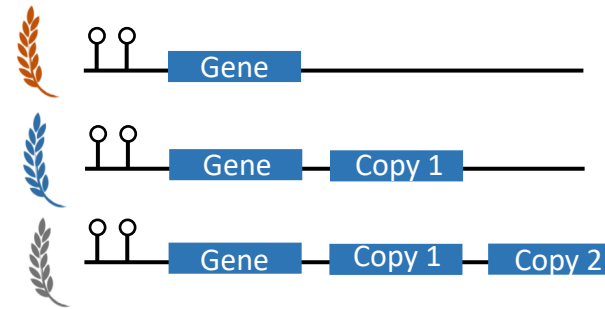


Adapted from Gaurav et al., 2021

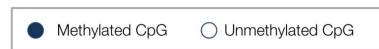
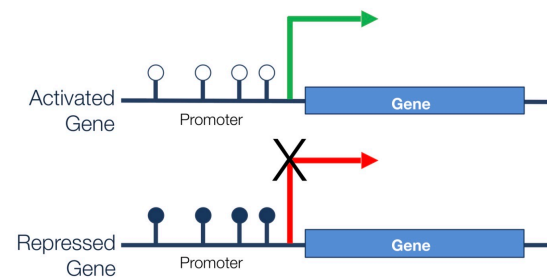


✓ Increase diversity panel size

## Detecting cryptic gene variation



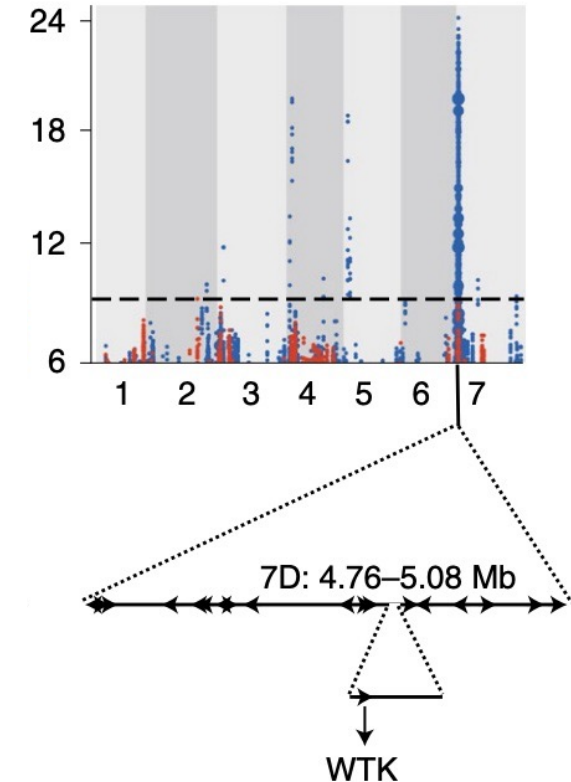
### Copy Number Variants



### DNA methylation variants

✓ Associative transcriptomics

## High-quality genome assemblies



Gaurav et al. Nature Biotechnology. 2021

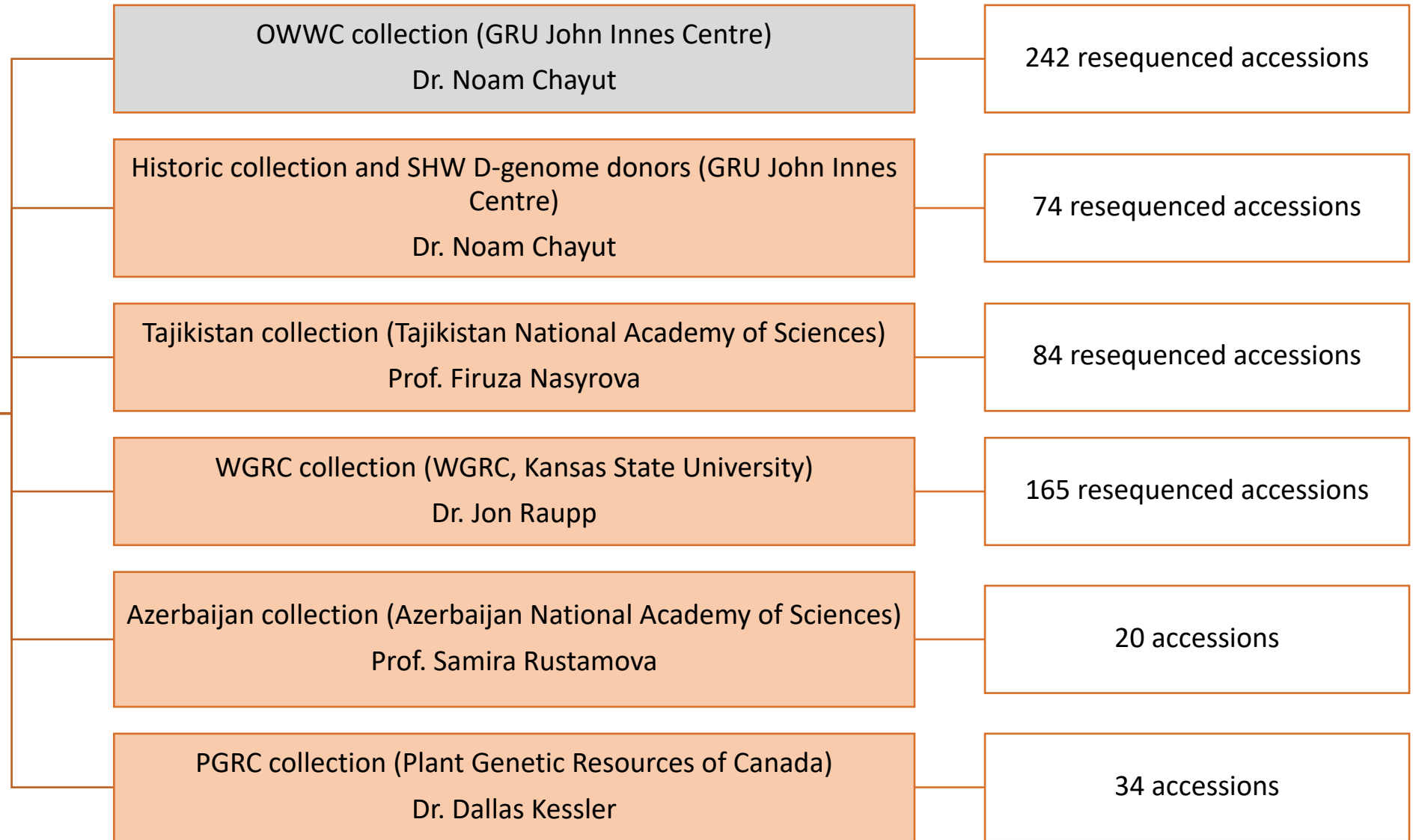
✓ Generate the pangenome

# Expanded *Aegilops tauschii* diversity panel – Open Wild Wheat Phase II



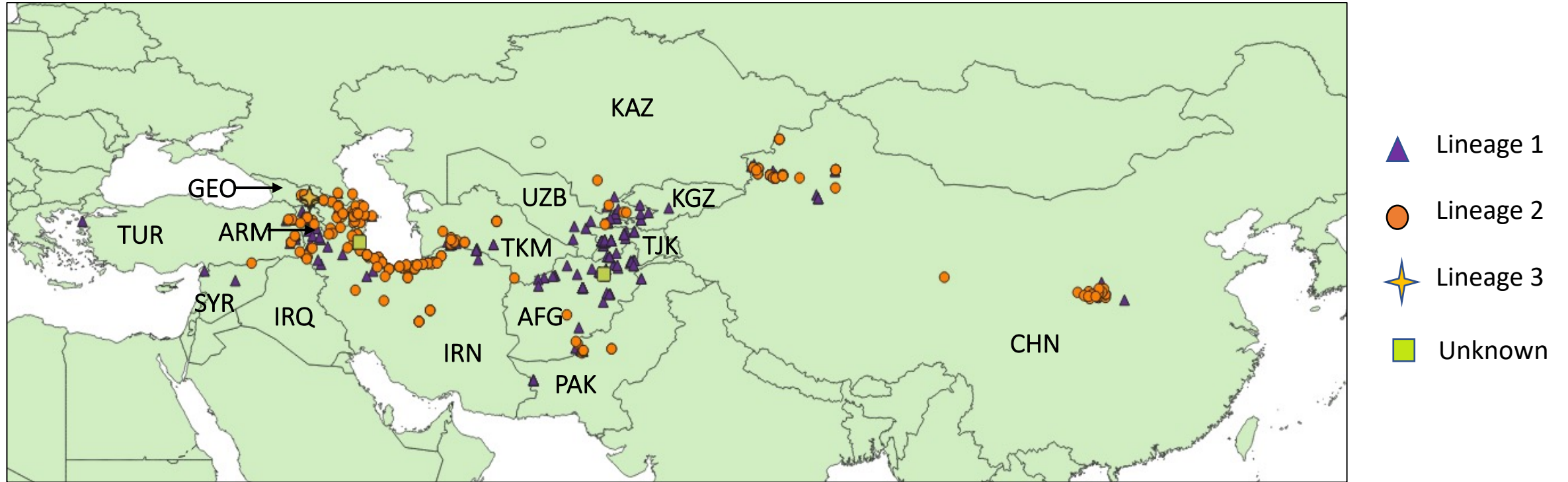
*Ae. tauschii*  
panel

652 accessions



Future additions: Pakistan collection (Quaid-i-Azam University) Prof. Awais Rasheed 33 accessions  
Iranian collection (Ilam University) Prof. Ali Mehrabi >50 accessions

# Expanded *Aegilops tauschii* diversity panel – Open Wild Wheat Phase II



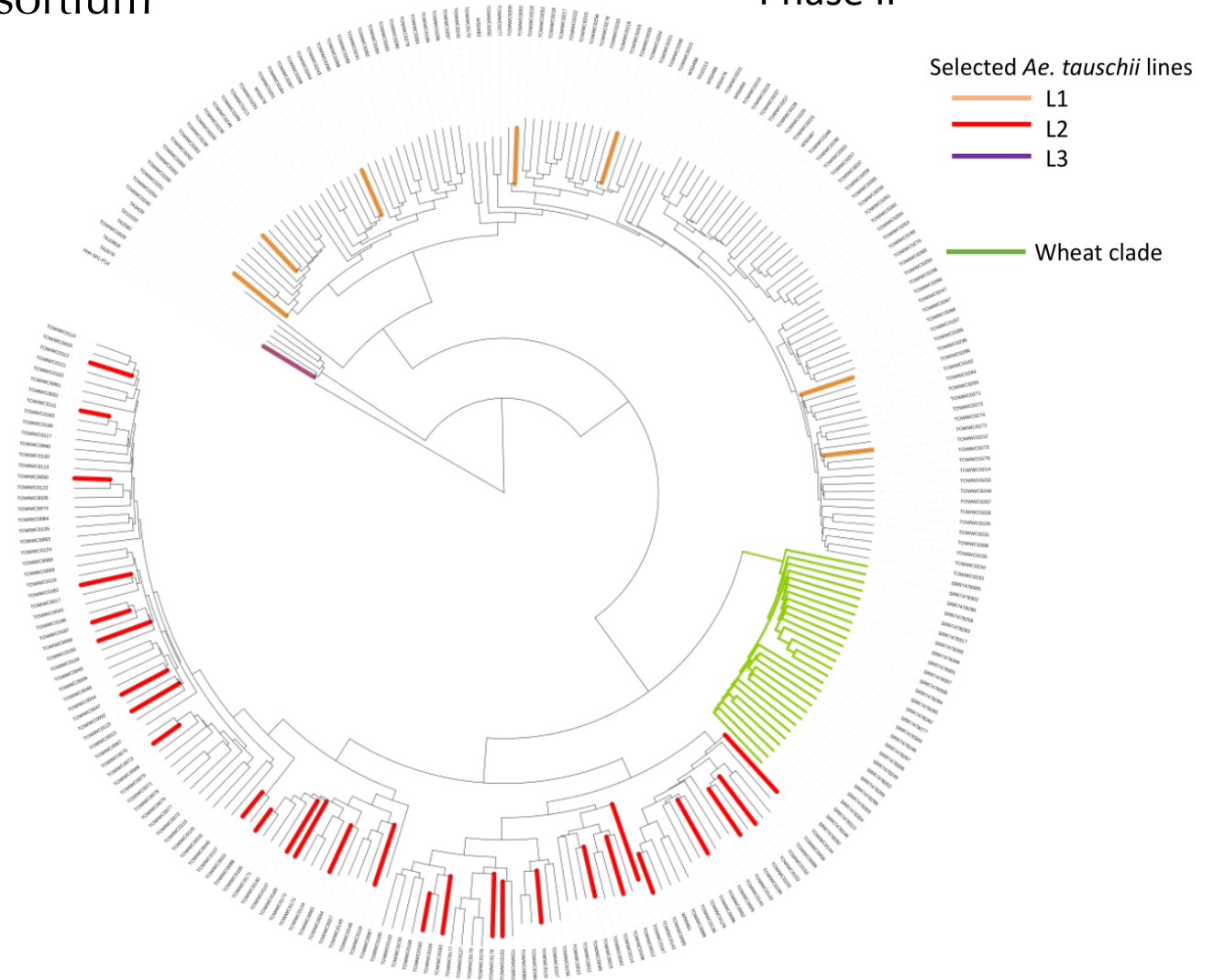
# The pangenome of *Aegilops tauschii*



43 accessions of strategic interest to the consortium

Phase II

Strategic traits of interest
Disease and pest resistance
Starch
Yield
Salinity tolerance
D-genome donors of SHW
Heat tolerance
Nitrogen use efficiency
Tiller number
Iron content
Agromorphological traits



# Sequencing and assembling the *Aegilops tauschii* pangenome

## **Lineage-level HiC-scaffolded high-coverage assemblies**

- ✓ Accessions: TOWWC0052 (L1), TA1675 (L2), TA2576 (L3)
- ✓ PacBIO CCS (HiFi) 67-97X coverage + illumina HiC 300 M reads
- ✓ HiFi + HiC phased assemblies
- ✓ HiC scaffolding to the chromosome-scale

## **Pseudo chromosome-level assemblies**

- ✓ 43 accessions
- ✓ PacBIO CCS (HiFi) 18 – 29X coverage (Mean= 23X)
- ✓ Primary assemblies
- ✓ Scaffolded using lineage-level assemblies

# Lineage-level assemblies



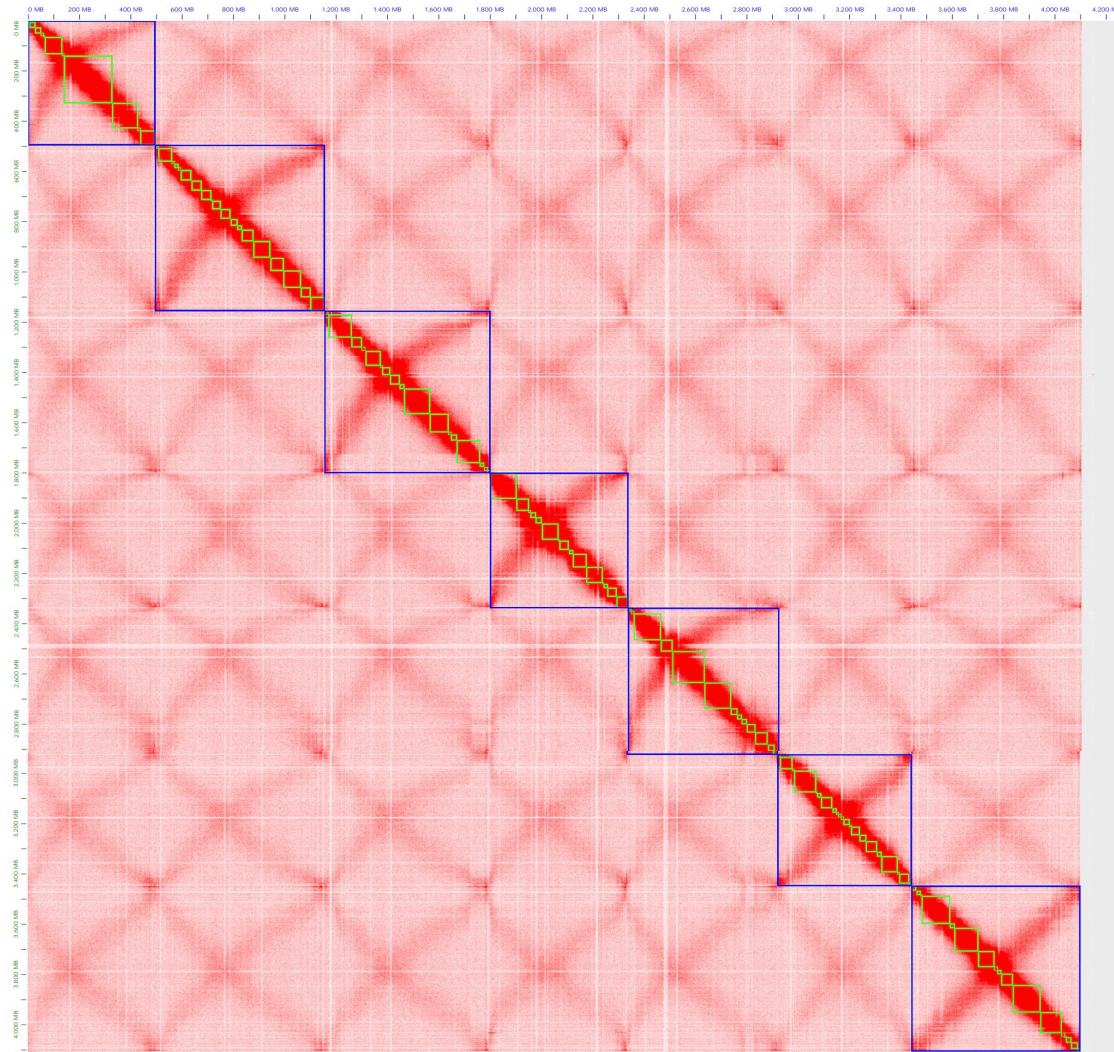
- ✓ Resource for anchoring pangenome assemblies
- ✓ High resolution for structural variant calling

Assembly ->	TOWWC0052 (L1)	TA1675 (L2)	TA2576 (L3) (reference*-scaffolded)
Superscaffolds	7	7	7
Total assembled length	4,151,983,908	4,159,914,615	4,245,074,256
Scaffolded contigs per chromosome	13-27	1-10	18-32
Unplaced assembled length	45,447,308	53,352,240	114,633,098

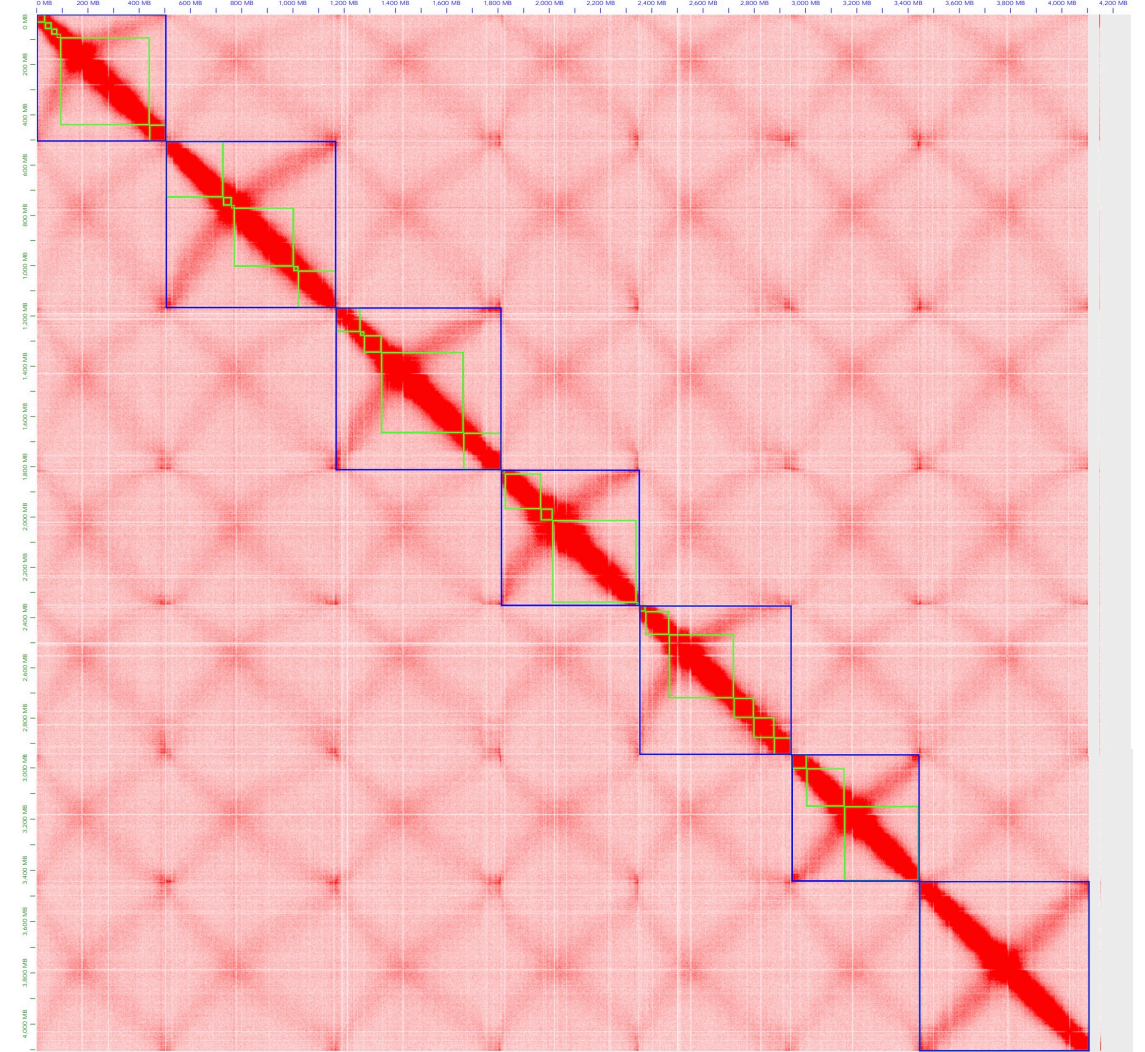
\*Reference assembly: AL8/78 v5.0 (RefSeq GCF\_002575655.2), chromosomes only

# Lineage 1 and lineage 2 HiC scaffolded assemblies

L1: TOWWC0052, 77X cov, N50= 53.38 Mb



L2: TA1675, 97X cov, N50= 221.04 Mb



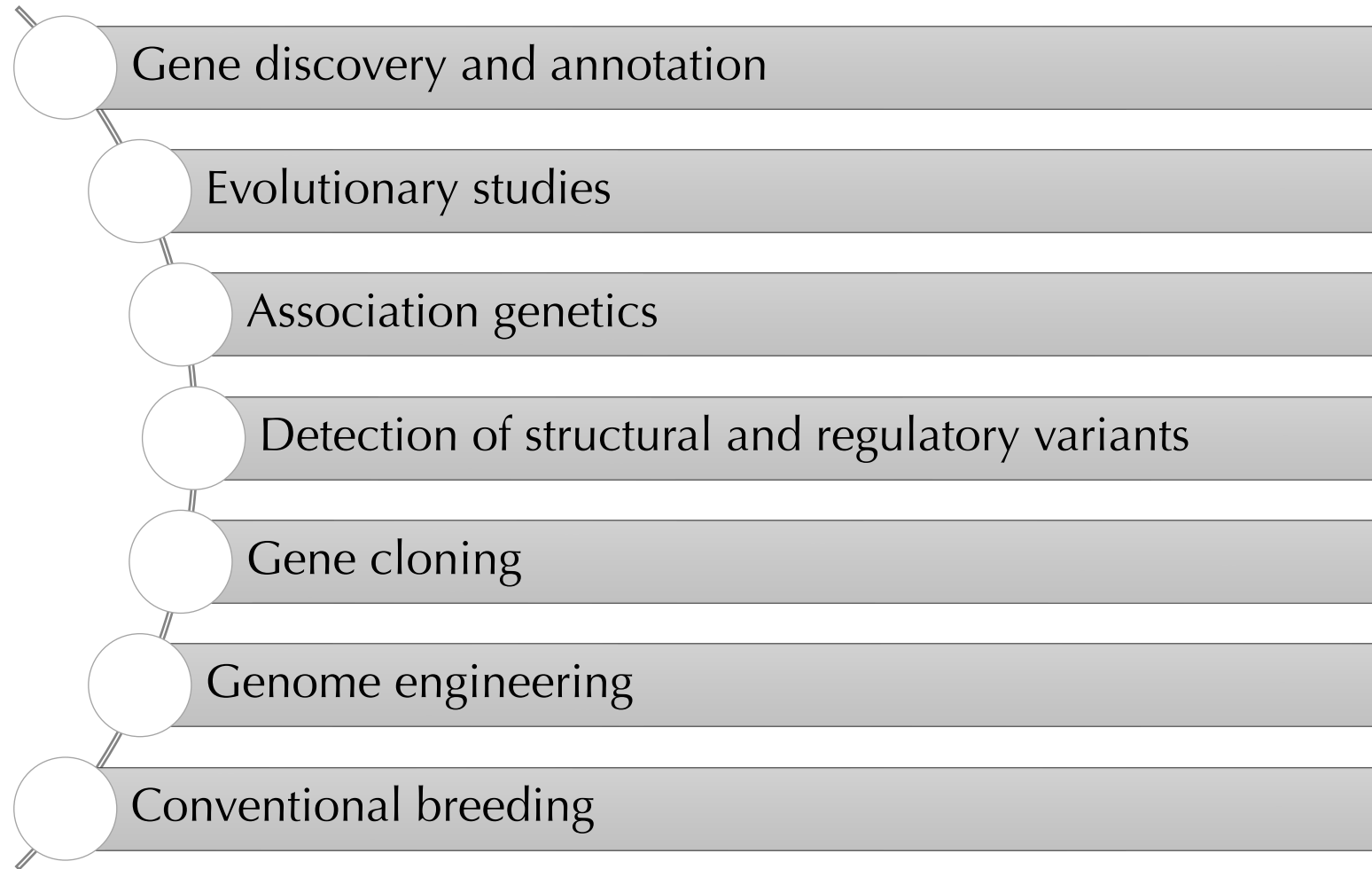
## Genome assembly summary for 43 pangenome accessions

Feature	Metric	Mean	Minimum	Maximum
Contiguity	Assembled length (Gb)	<b>4.17</b>	4.12	4.23
	Number of contigs	<b>1833</b>	1162	3687
	N50 (Mb)	<b>43.19</b>	15.01	90.33
Completeness	Complete BUSCOs (%)	<b>98.34</b>	97.95	98.64
	illumina reads <i>k</i> -mer completeness (%)	<b>98.51</b>	97.75	99.87
Correctness	Average HiFi read accuracy (%)	<b>99.86</b>	99.72	99.92
	Base-level accuracy (QV)	<b>44</b>	31	48
	Assembly unique <i>k</i> -mer count (%)	<b>0.13</b>	0.03	1.78
	Reference-based* anchoring (% of total assembled length)	<b>98.44</b>	97.28	99.23

\*Reference assembly: AL8/78 v5.0 (RefSeq GCF\_002575655.2), chromosomes only



# Applications of the *Ae. tauschii* pangenome resource



# Rapid gene cloning application

Theor Appl Genet (2013) 126:1179–1188  
DOI 10.1007/s00122-013-2045-5

ORIGINAL PAPER


## **Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from *Aegilops tauschii* to wheat**

Eric L. Olson · Matthew N. Rouse ·  
Michael O. Pumphrey · Robert L. Bowden ·  
Bikram S. Gill · Jesse A. Poland

nature  
biotechnology

ARTICLES

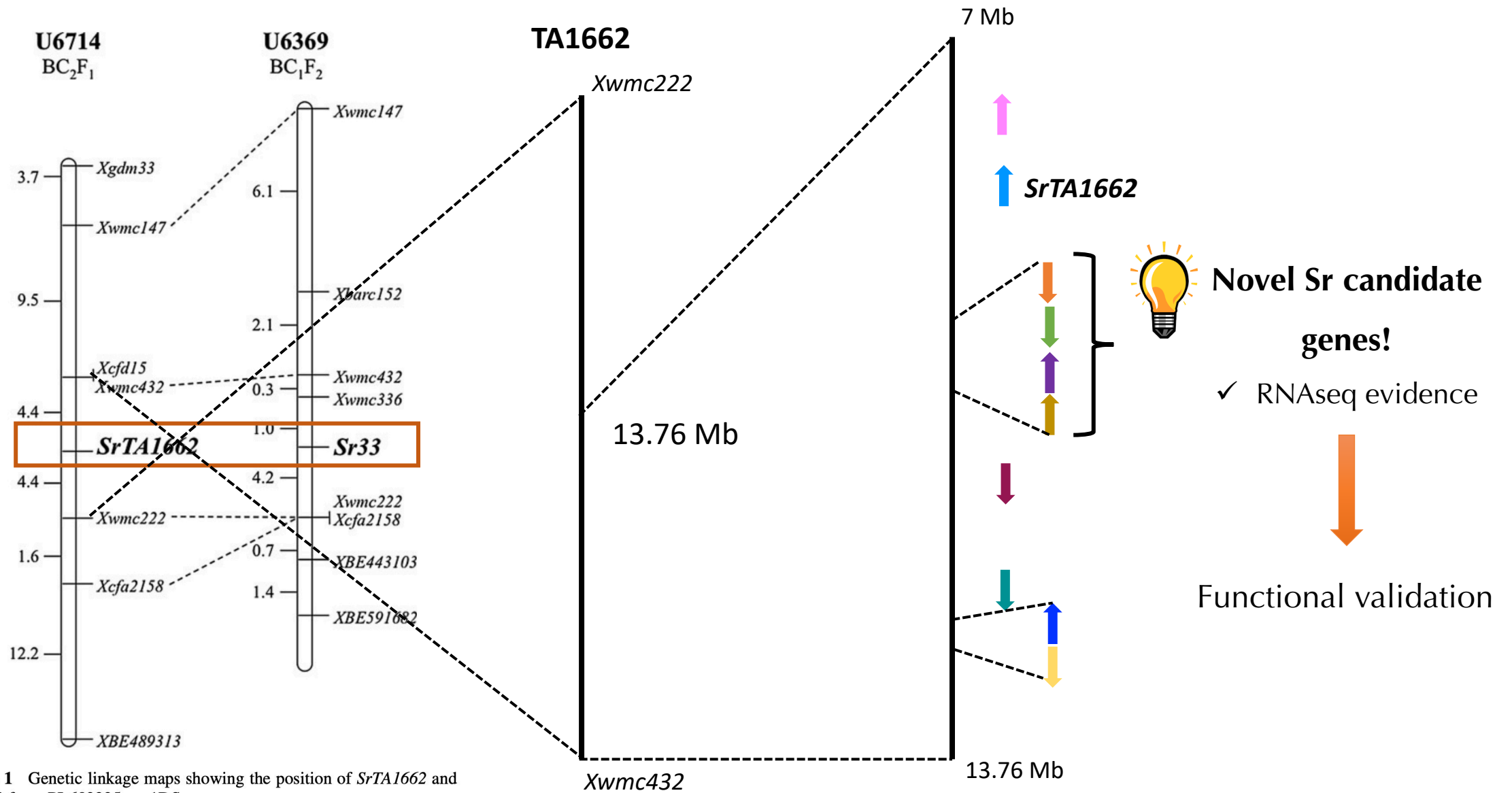
<https://doi.org/10.1038/s41587-021-01058-4>

 Check for updates

OPEN

**Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement**

# Rapid gene cloning application

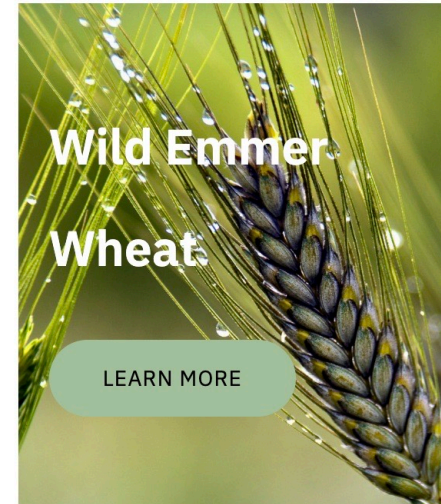


**Fig. 1** Genetic linkage maps showing the position of *SrTA1662* and *Sr33* from PI 603225 on 1DS



WILD WHEAT SPECIES

## Wild Wheat Focus Species



Brian Steffenson  
University of Minnesota

Jesse Poland  
KAUST

Wulff Lab  
KAUST



Guotai Yu  
Wulff Lab, KAUST

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- Cristobal Uauy
- Jesus Quiroz-Chavez

## The Open Wild Wheat Consortium



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