



植物生物信息与 功能表观组学课题组

<http://bioinfo.sibs.ac.cn/zhanglab/index.php>

张一婧

复旦大学生命科学学院

2021/09/01



研究团队

<http://bioinfo.sibs.ac.cn/zhanglab/index.php>



Welcome to join us !



“干” “湿” 结合

已毕业硕博连读同学7名

1名获上海市超级博后支持

2名获博士生国家奖学金

1名获地奥一等奖学金

2名获先正达齐尔顿奖学金

课题组的人员组成

课题组的人员构成

1 名导师全面负责每位同学的课题

2 名实验员帮助进行实验验证; 2 名负责实验探索的同学 7 名负责计算工作的同学

课题组的中坚力量

2-4 年级的同学 (硕士二年级、博士一二年级)

攻读硕博时间

5-6 年

<http://bioinfo.sibs.ac.cn/zhanglab/index.php>

毕业生去向



2013级
2018年国家奖学金

Harvard Medical School
Massachusetts General Hospital



2013级

University of Oxford

部分发表文章

1. 表观组揭示小麦多倍体优势形成机制

1. Jia J[#], Xie Y[#], Cheng J[#], Kong C[#], Wang M, Gao L, Zhao F, Guo J, Wang K, Li G, Cui D, Hu T, Zhao G*, Wang D*, Ru Z*, **Zhang Y***. (2021) Homology-mediated Inter-chromosomal Interactions in Hexaploid Wheat Lead to Specific Subgenome Territories Following Polyploidization and Introgression. *Genome Biology* 22:26
2. Wang M[#], Li Z[#], Zhang Y[#], Zhang Y[#], Xie Y, Ye L, Zhuang Y, Lin K, Zhao F, Guo J, Teng W, Zhang W, Tong Y, Xue Y*, **Zhang Y***. (2021) The epigenomic atlas delineates the specificity of subgenome-divergent development and stress responses encoded in wheat regulatory elements. *Plant Cell* koab028
3. Li Z[#], Wang M[#], Lin K[#], Xie Y[#], Guo J, Ye L, Zhuang Y, Teng W, Ran X, Tong Y, Xue Y, Zhang W* and **Zhang Y***. (2019) The bread wheat epigenomic map reveals distinct chromatin architectural and evolutionary features of functional genetic elements. *Genome Biol* 20, 139

2. 生物信息平台与方法开发

1. Qi M[#], Li Z[#], Liu C[#], Hu W, Ye L, Xie Y, Zhuang L, Zhao F, Teng W, Zheng Q, Fan Z, Xu L, Lang Z, Tong Y*, and **Zhang Y***. (2018) CGT-seq: epigenome-guided de novo assembly of the core genome for divergent populations with large genome, *Nucleic Acid Research*, gky522.
2. Ran X[#], Zhao F[#], Wang Y[#], Liu J, Zhuang Y, Ye L, Qi M, Cheng J, **Zhang Y*** (2020) Plant Regulomics: A Data-driven Interface for Retrieving Upstream Regulators from Plant Multi-omics Data, *The Plant Journal*, 101:237

3.

部分工作的中文宣传稿

[六倍体小麦为什么具有广泛的环境适应性？张一婧研究组合作解析普通小麦亚基因组非对称调控机制](http://www.cemps.cas.cn/kyjz/kyjz2019_176534/202102/t20210203_5884770.html)

http://www.cemps.cas.cn/kyjz/kyjz2019_176534/202102/t20210203_5884770.html

[六倍体小麦为何如此稳定？张一婧研究组合作揭示同源转座子维持普通小麦多倍体亚基因组高级结构稳定性](http://www.cemps.cas.cn/kyjz/kyjz2019_176534/202101/t20210111_5854802.html)

http://www.cemps.cas.cn/kyjz/kyjz2019_176534/202101/t20210111_5854802.html

[张一婧研究组合作完成普通小麦精细表观组图谱绘制及全基因组顺式作用元件鉴定](http://www.cemps.cas.cn/kyjz/kyjz2019/201908/t20190826_5370245.html)

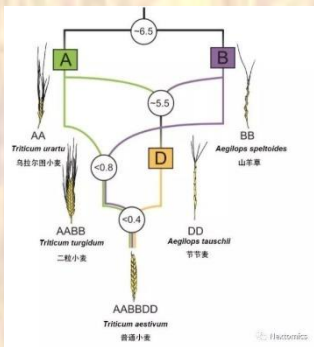
http://www.cemps.cas.cn/kyjz/kyjz2019/201908/t20190826_5370245.html

小麦的表观与转录机制其独特的研究价值

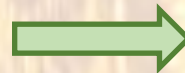
1. 基因组庞大 (16 Gb, > 人类基因组5倍, 水稻的40倍, 拟南芥的20倍)



2. 基因组复杂, 异源多倍体 (BBAADD) 3套亚基因组



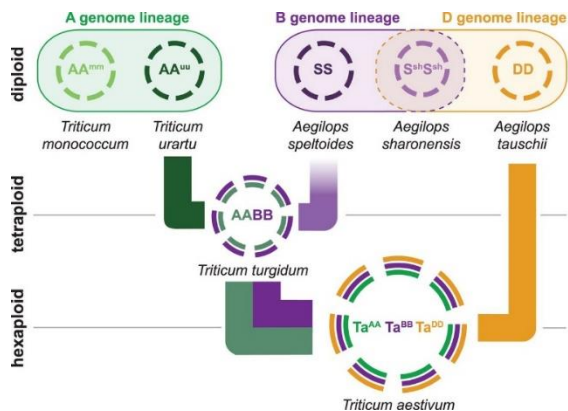
二倍体祖先



六倍体栽培种

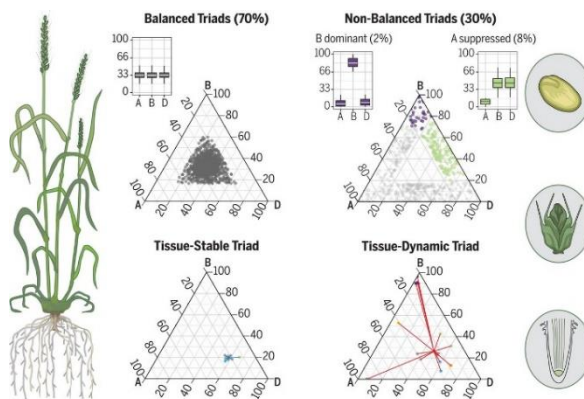
研究目标一：多倍化优势的分子机制

小麦的多倍化历程



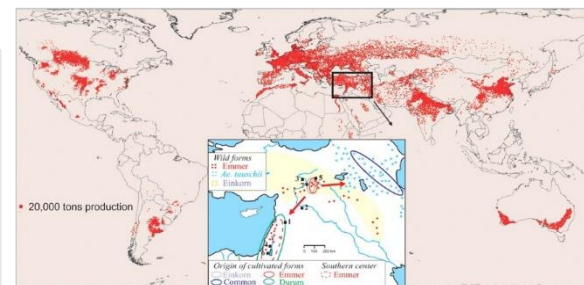
IWGSC Science 2014

亚基因组的分化



R. H. Ramírez-González et al. Science 2018

多倍体小麦具有广泛的环境适应能力

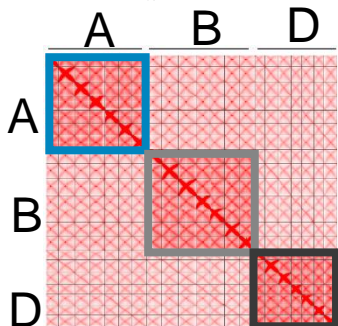


揭示小麦多倍化与驯化过程中基因调控网络演化规律与机制

研究目标一：小麦多倍体优势机制

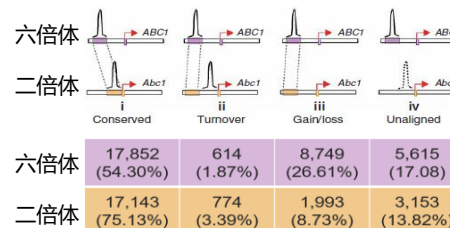
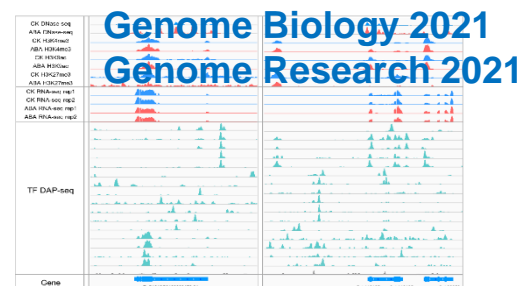
亚基因组稳定性

DNA序列 ↔ 高级结构 ↔ 多倍体稳定性



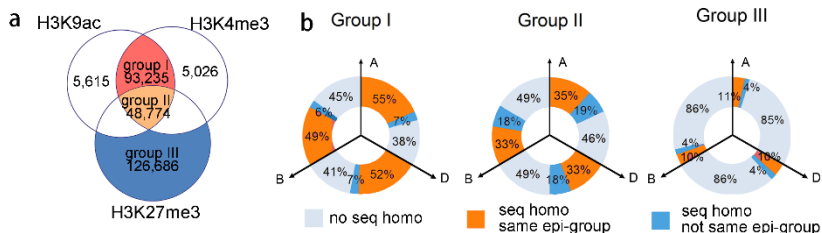
Genome Biol 2021

调控网络演化



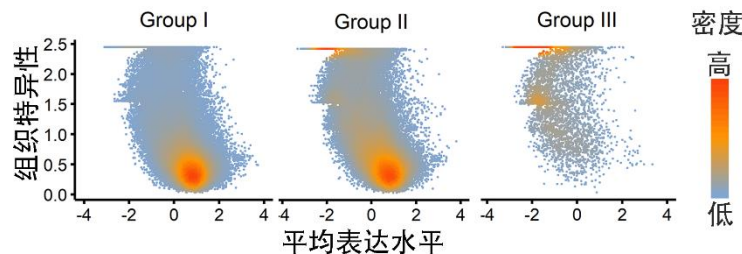
小麦多倍体优势

亚基因组功能分化



DNA调控元件的分化

Plant Cell 2021



发育特异性基因的亚基因组分化

研究目标二：测序辅助图位克隆

The Wheat Genome Reference Sequence

— HOW BREEDERS USE IT —

The availability of a reference genome for a crop helps plant breeders to speed up the development of new improved varieties

Gene discovery

CTGCA
TCTGA
CTCCT
GAGAA
GT TCA

Plant scientists use the information provided in a reference genome sequence to identify and locate genes responsible for desirable agronomic traits (such as high yield, stress tolerance and disease resistance), isolate those genes and study how they function.

Once a gene is known, this information can – for example – be utilized to tap into the natural diversity of the crop to discover new versions of the gene with more favorable features than those found in the variety used to produce the reference sequence and use those to introduce improved traits into commercial varieties.

Gene improvement

TGGCC
ATTCT
CCCAT

The information provided in a reference genome sequence can also be used to look for modified and improved versions of the genes into mutant collections and/or create modified and improved versions by genetic engineering.

Marker-assisted breeding



Molecular markers are easily identifiable fragments of DNA sequence that are located close to a specific gene. With a reference sequence in hand, breeders have an unlimited source of molecular markers close to or within the genes of interest.

They can use these markers to identify suitable parents containing the traits of interest for new crosses and track down the presence of the genes of interest in the descendants during the selection process.

New varieties breeding



Ultimately, breeders use markers and genes to speed up the development of new varieties with specific characteristics such as higher yield, tolerance to a stress (heat, water scarcity, high salt content in soil) or resistant to a specific disease (such as rust diseases and Fusarium head blight disease).

核心需求：基因挖掘与机制研究服务于基因克隆

困难：基因组庞大而复杂，至今利用图位克隆获得的小麦基因有限

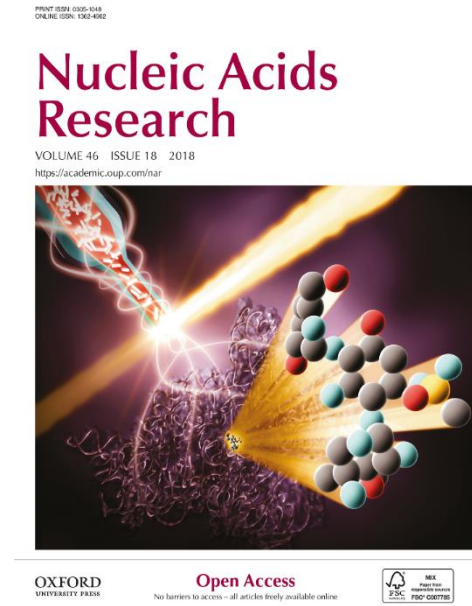
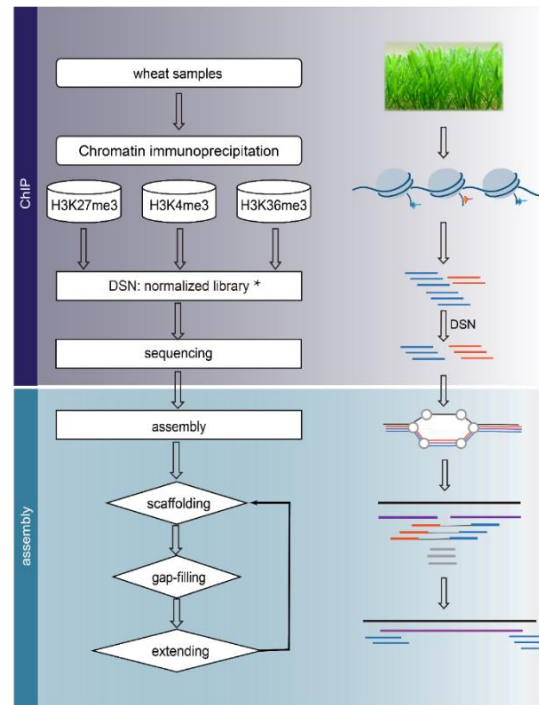
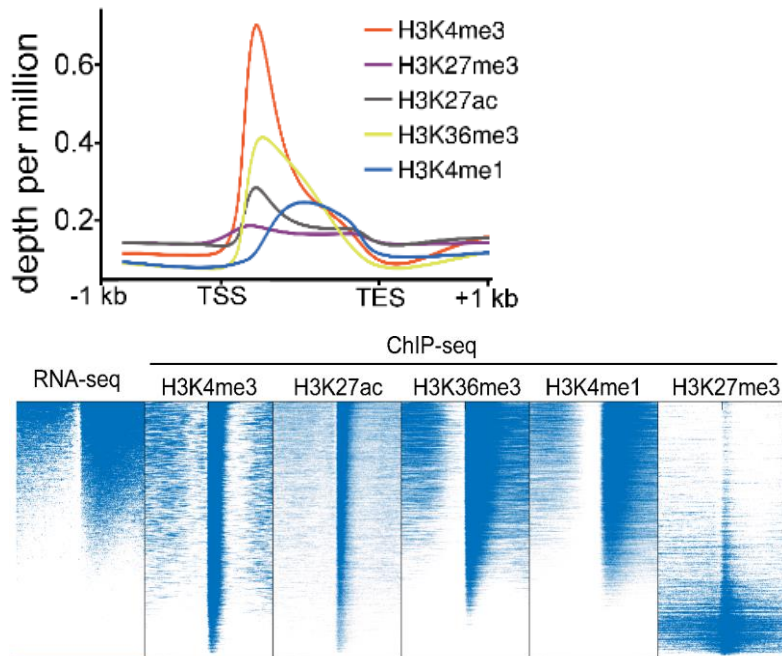
方向：开发测序辅助的图位克隆手段

步骤：

1. 低成本刻画群体多态性
2. 结合测序与遗传学实验开发图位克隆计算流程

研究目标二：测序辅助图位克隆

通过富集基因附近表观修饰位点获得核心基因组序列，包括启动子和基因区序列

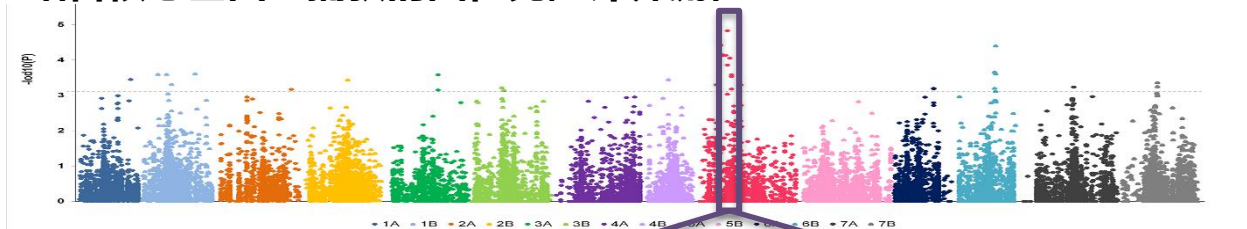


Nucleic Acid Res. (2018)

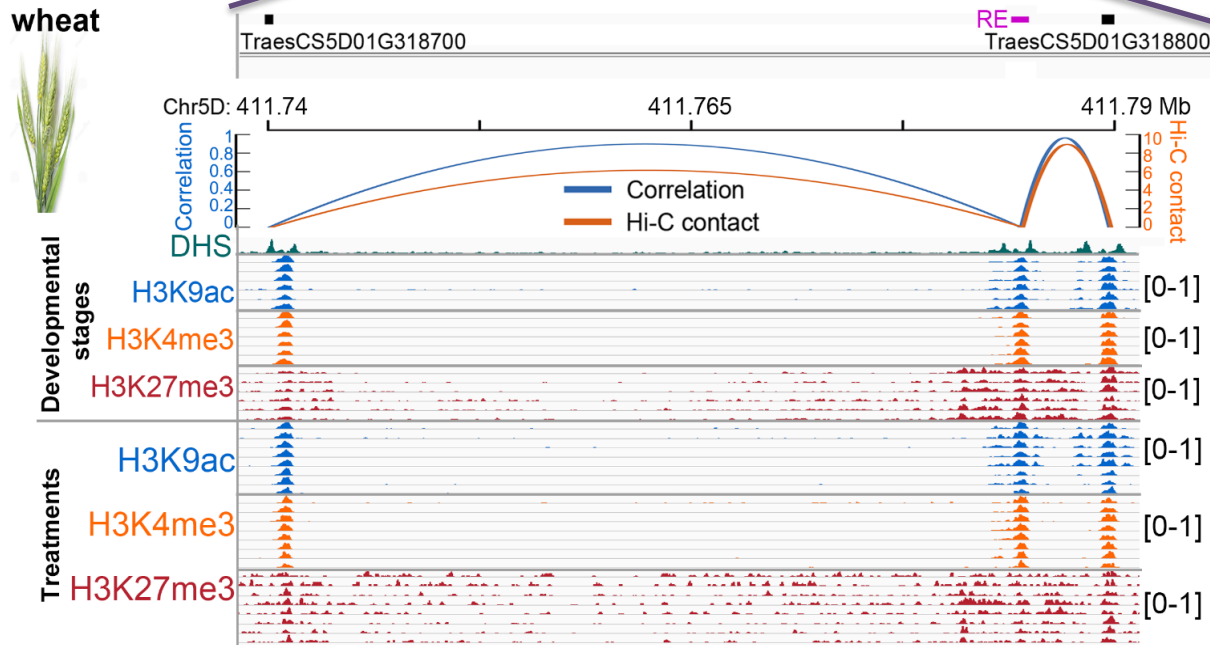
研究目标二：测序辅助图位克隆

综合多组学证据精准定位关键基因和DNA 功能元件

1. 结合核心基因组捕获的图位克隆计算流程



2. 关键位点挖掘平台



统计学帮助你寻找值得托付的课题组

一、导师

1. 学品

简化SCI index,

1) 简单的参数帮助你粗略了解

✓ 均值

✓ 中位值

✓ 极大值

2) 分布函数帮助你精细了解

✓ 正态分布

✓ 泊松分布

✓ 均匀分布

3) 随机过程帮助你动态了解

2. 人品

二、同学及科研氛围

我们欢迎怎样的成员

知之者不如好之者，好之者不如乐之者
喜欢安静深入思考问题

祝大家找到心仪的课题组

