



**Susceptibility to Fusarium Head  
Blight by Wheat is Regulated by  
Silencing RNAs of Pathogen Origin**

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- Fusarium head blight (FHB, also called scab) is an industry threatening disease for cereal crops in the world
  - Severe yield loss
  - Health-threatening by mycotoxin
- The same pathogens cause *Gibberella* ear rot in maize

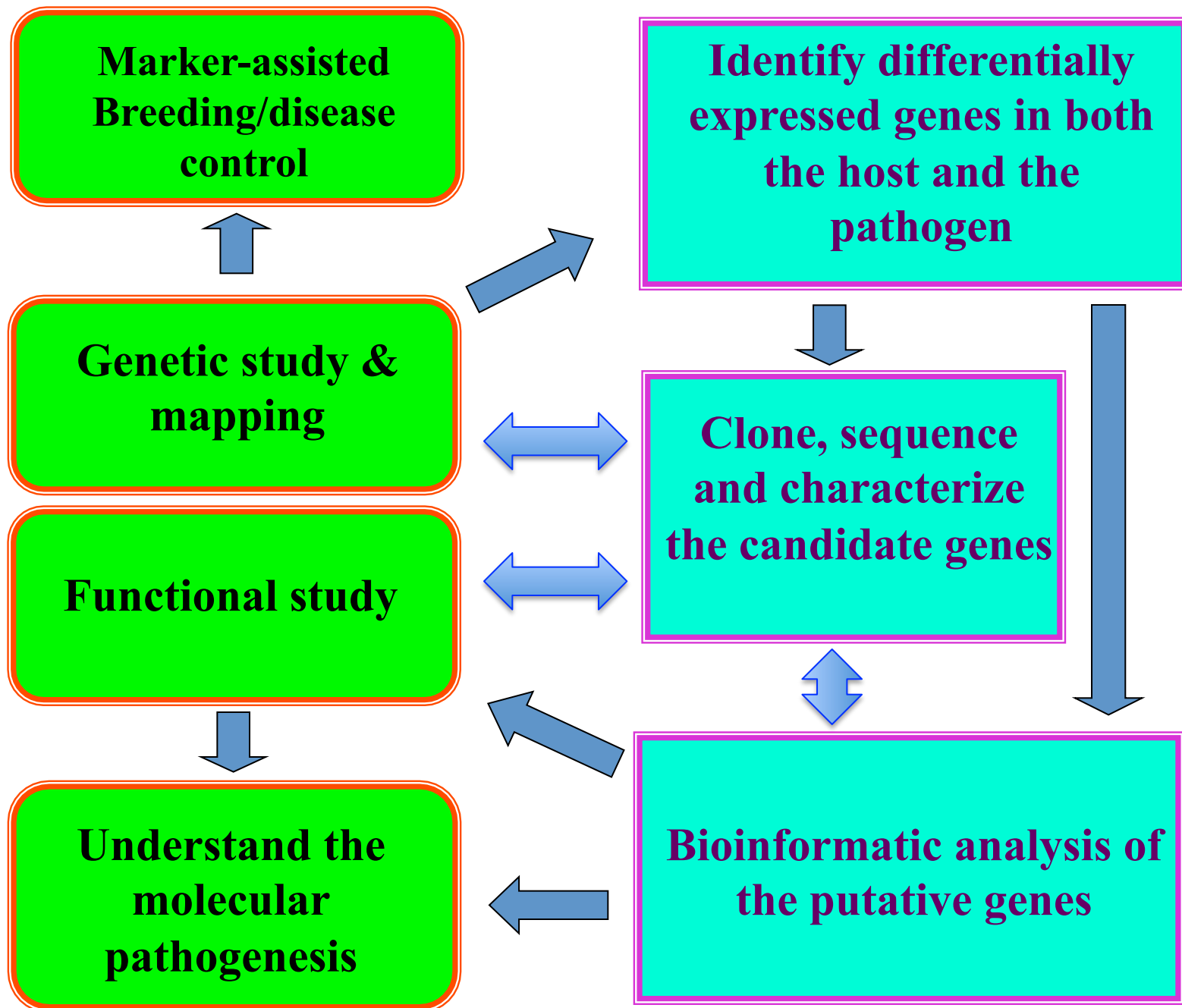




- **FHB is an extraordinary disease**
  - Several *Fusarium* species can cause FHB
  - Hemitrophic pathogens
  - Disease management is very difficult
  - Host resistance is quantitatively inherited
    - Not much resistance has been found in durum wheat and barley
    - Hundreds of QTL have been reported in bread wheat
      - All bread wheat chromosomes are involved
  - Pyramiding QTL has not worked as we've expected
  - No functional gene has been identified for any of the QTL until this study
- ***Qfhb1* (a.k.a *Fhb1*, *QFhs.ndsu-3BS*) on 3BS is the most important QTL in bread wheat**
  - Responsible for about 20-60% of the resistance variation
  - Validated under multiple genetic backgrounds in multiple environments

- FHB needs extraordinary means to control
- FHB results from interactions between *Fusarium* pathogens and their hosts
- Disrupting this interaction should help prevent the disease from happening
- This can be done by identifying, understanding and manipulating the molecular mechanisms of the pathogen-host interactions
- Therefore, it is critical to identify, clone and understand the key genetic components of major FHB resistant QTL



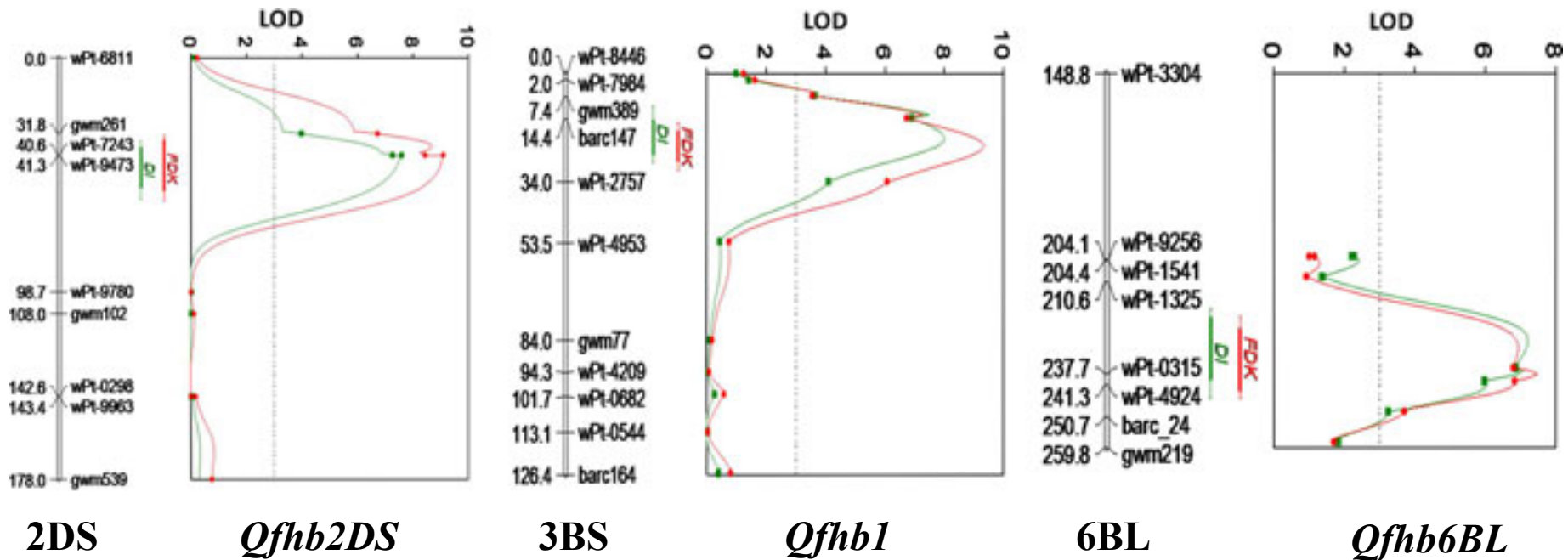


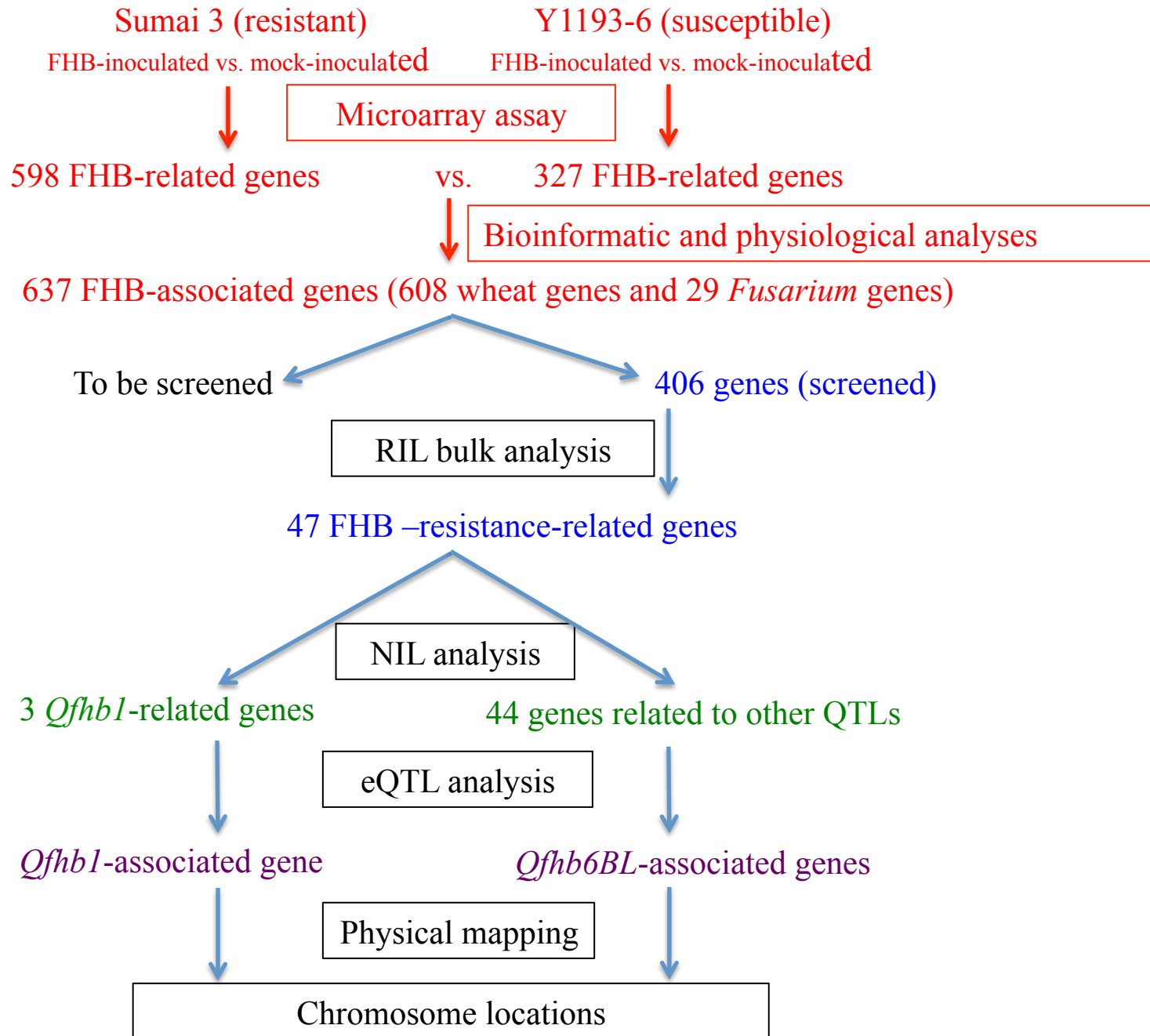




# QTL Mapping

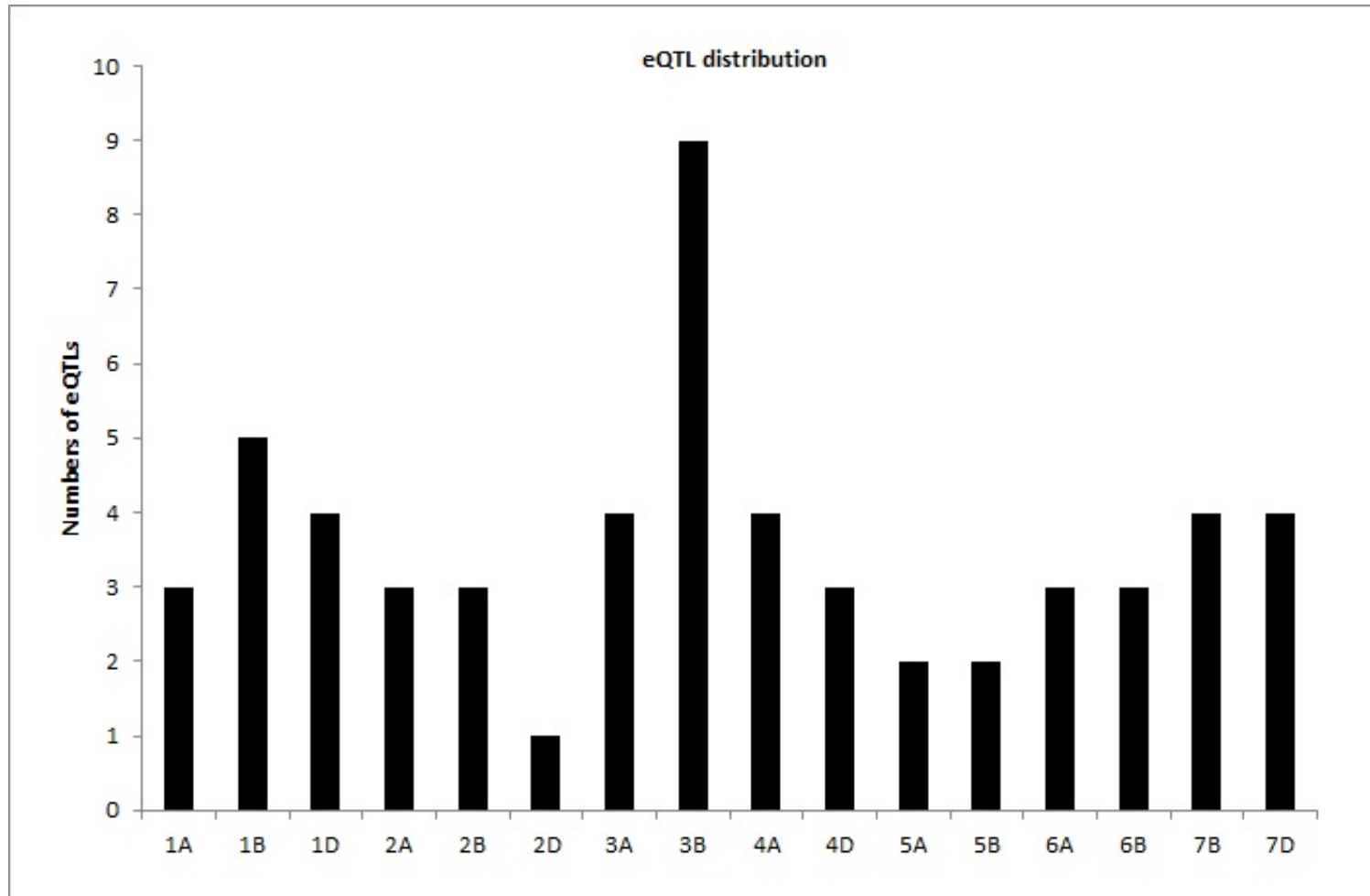
- A Sumai 3/Y1193-6 F<sub>2:6</sub> recombinant inbred line (RIL) population has been created by single-seed method for QTL mapping
- This RIL population has been genotyped with SSR and DArT markers and investigated for FHB incidence and severity for multiple years both in greenhouse and the field
- Three major FHB-resistant/susceptible QTL have been mapped with this RIL population



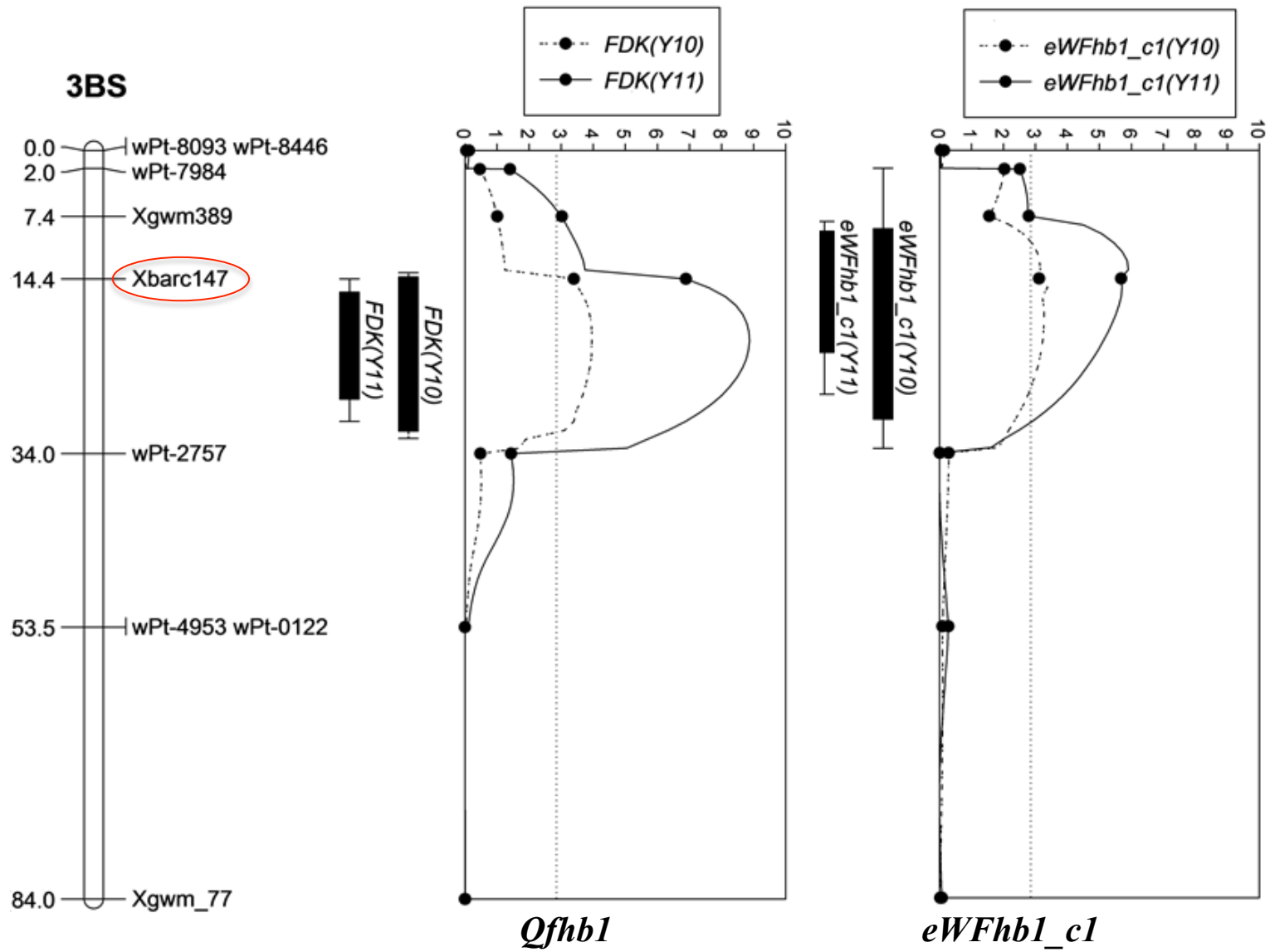




## Distribution of FHB Resistant eQTLs in Wheat Genomes

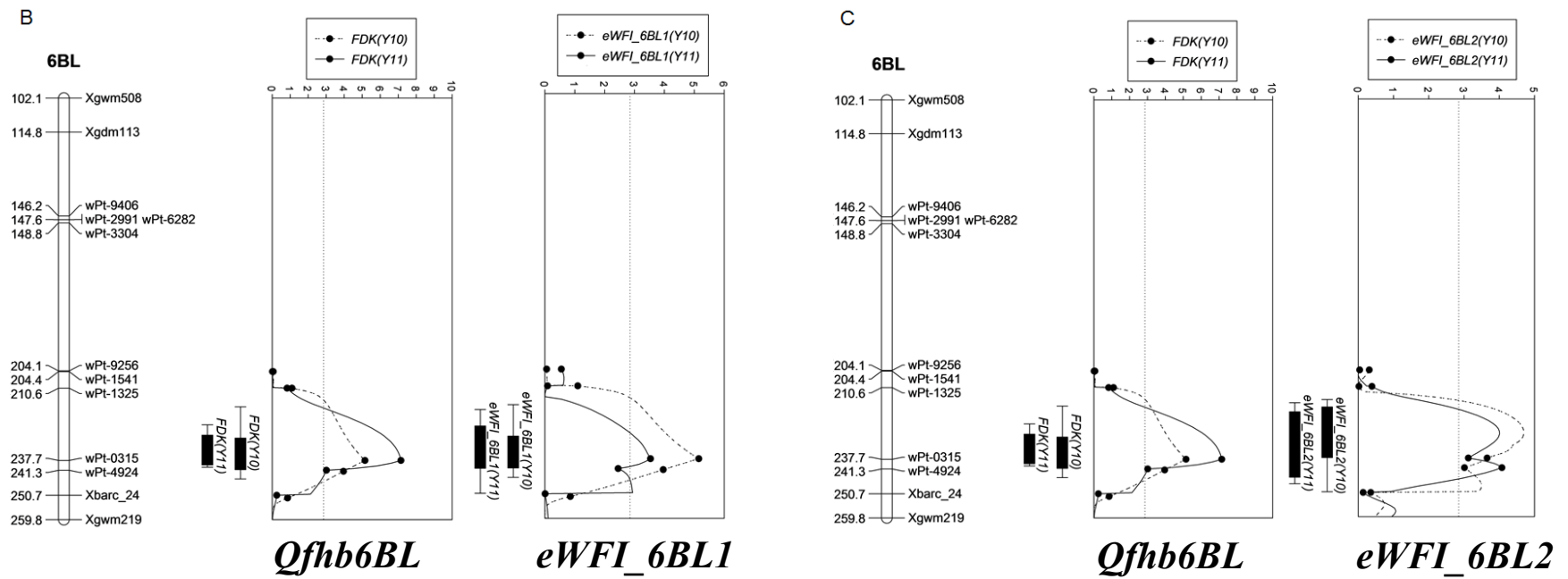


(Zhuang et al., MPMI 26:442-450, 2013)



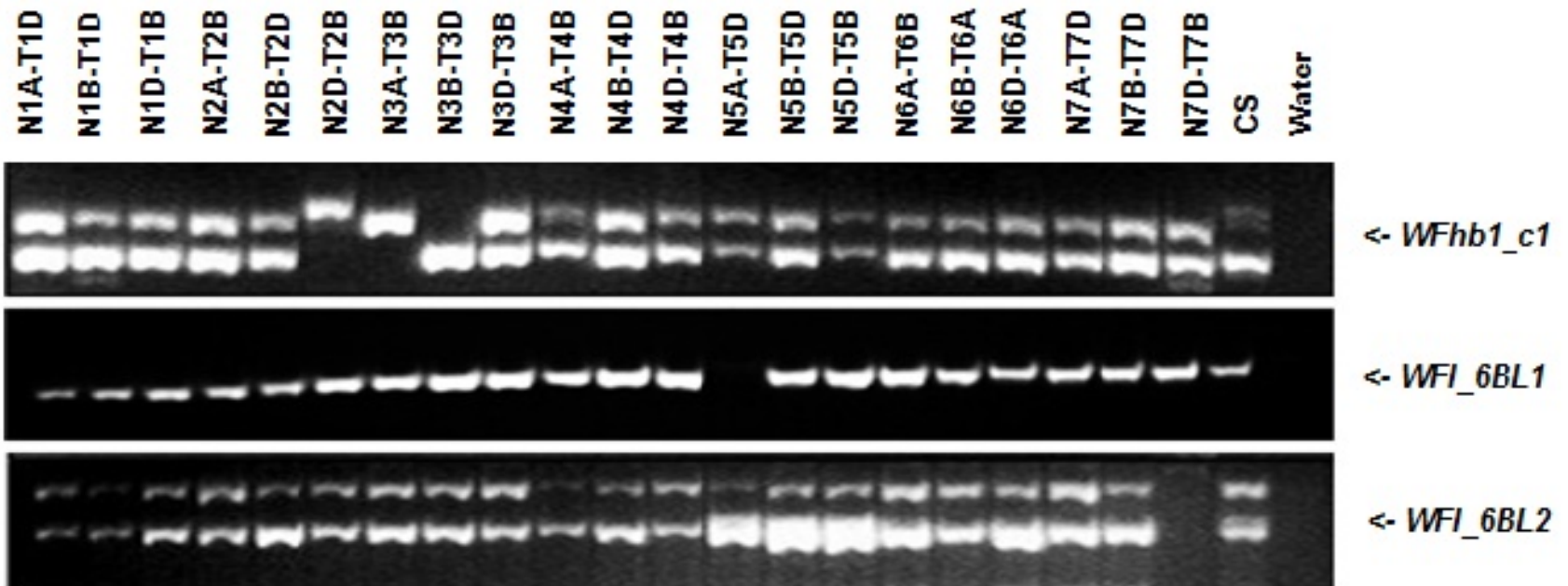
(Zhuang et al., MPMI 26:442-450 , 2013)





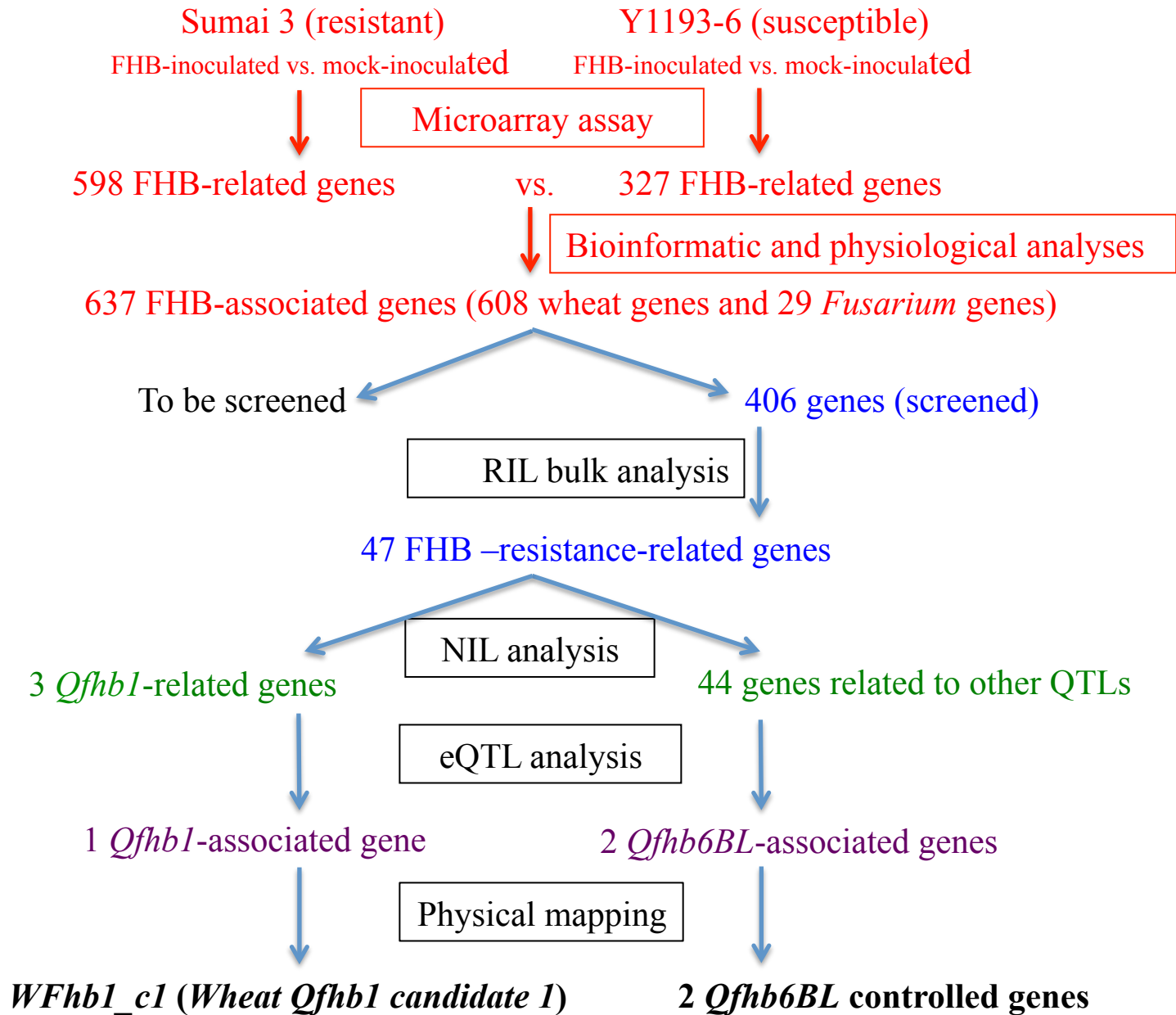
## Performance of Major FHB-resistant eQTL

Year	Chr. arm	eQTL	Flanking markers	Chromosome position	Additive effect	Variance explained (%)
2010	3BS	<i>eWFhb1_c1</i>	<i>Xbarc147-XwPt2757</i>	14.40	0.6706	24.59
	6BL	<i>eWFI_6BL1</i>	<i>XwPt1325-XwPt4924</i>	237.71	1.2912	24.91
	6BL	<i>eWFI_6BL2</i>	<i>XwPt1325-XwPt4924</i>	227.13	0.6869	11.15
2011	3BS	<i>eWFhb1_c1</i>	<i>Xgwm389-XwPt2757</i>	13.41	0.9743	38.95
	6BL	<i>eWFI_6BL1</i>	<i>XwPt1325-XwPt4924</i>	237.71	1.9251	22.23
	6BL	<i>eWFI_6BL2</i>	<i>XwPt1325-XwPt0315</i>	227.61	1.2269	31.93

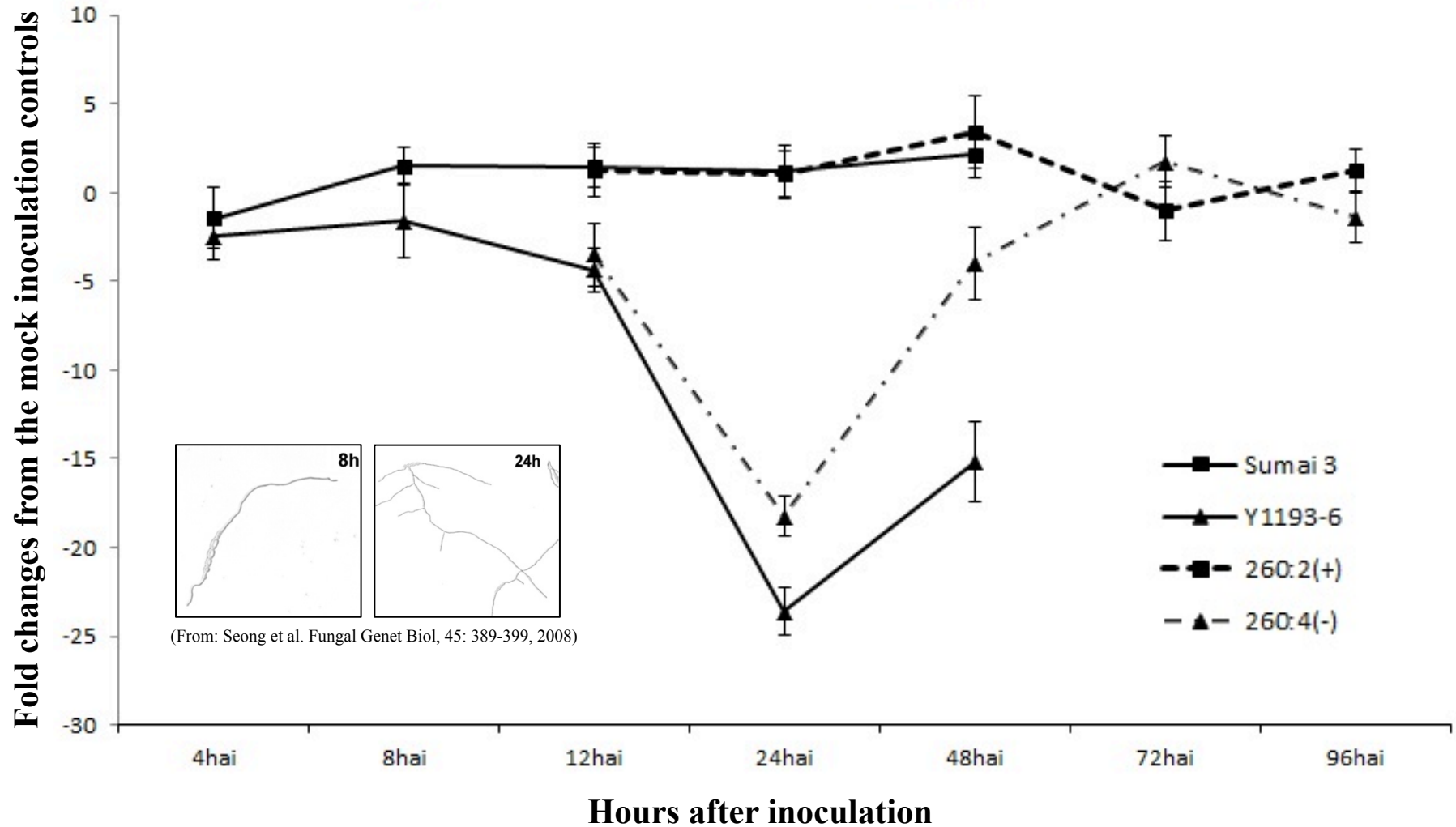


(Zhuang et al., MPMI 26:442-450, 2013)





## Expression Changes of Wheat Gene *WFhb1-1* in the Inoculated Spikelets of FHB-resistant Sumai 3 and 260-2, and of FHB-susceptible Y1193-6 and 260-4 after Infection by *Fusarium graminearum*

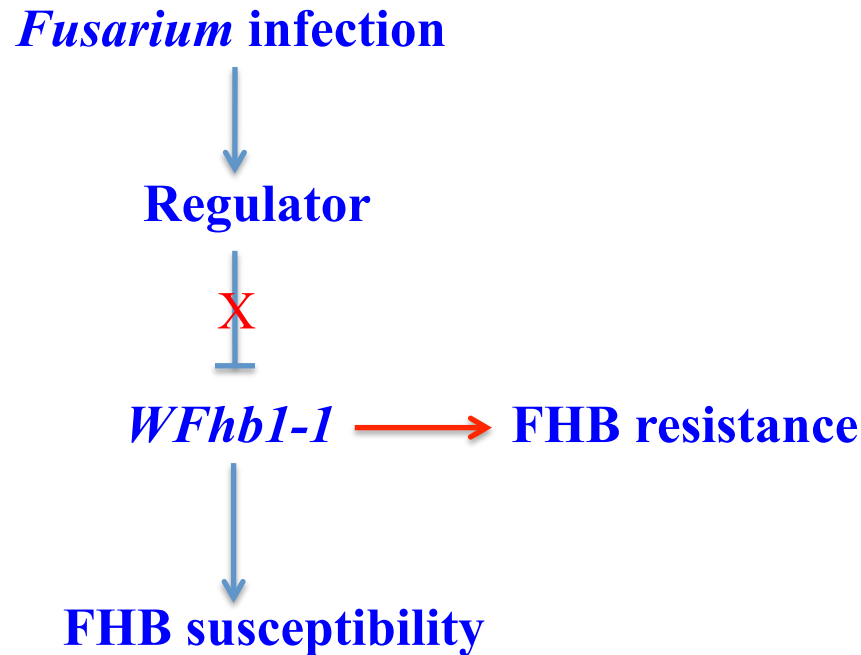


(Adapted from Zhuang et al. MPMI 26:442-450, 2013)

(Unpublished data has been removed)



# The way that FHB-resistant gene *WFhb1-1* may contribute to FHB resistance/susceptibility



It is the regulatory sequence(s) of *WFhb1-1* that decide if a plant is resistant or susceptible to FHB in wheat

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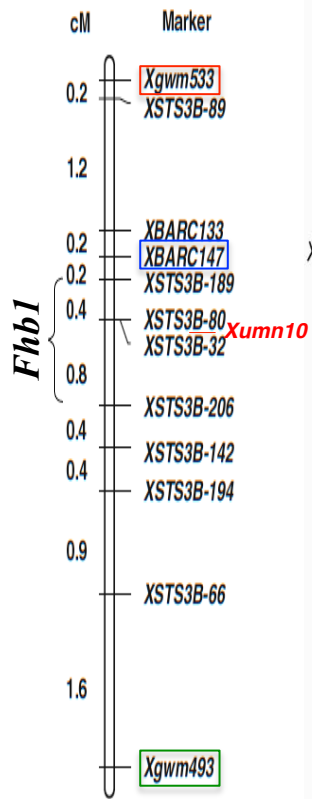
# Summary

- *WFhb1-1* is a functional genic component of *Qfhb1* with an unknown function
  - very weakly similar to Arabidopsis MYB79 or PME1 gene
- *WFhb1-1* plays a key role in FHB resistance of wheat
- *WFhb1-1* exists and functions in every wheat varieties
- Suppression of *WFhb1-1* due to pathogen infection early in the pathogenesis leads to FHB development in bread wheat
- Regulatory sequences of *WFhb1-1* are apparently much more important than the encoding sequence for determining FHB resistance/susceptibility
- *WFhb1-1* seems to be negatively regulated by actions of pathogen siRNAs

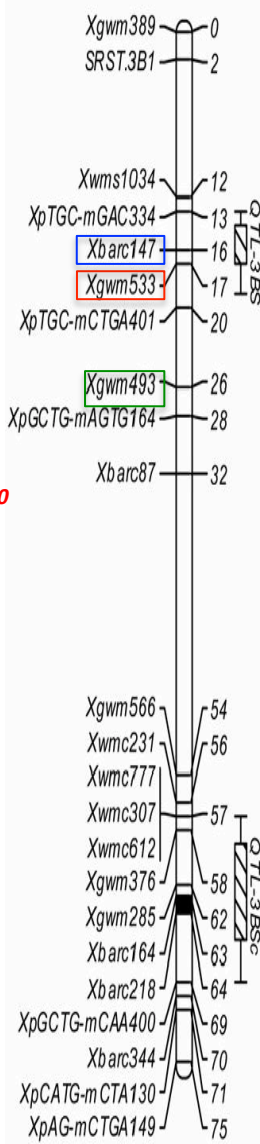
# Mapped positions of *Qfhb1* and *WFhb1-1*

Wangshuibai/Wheaton CS-SM3-3B/Annong8455

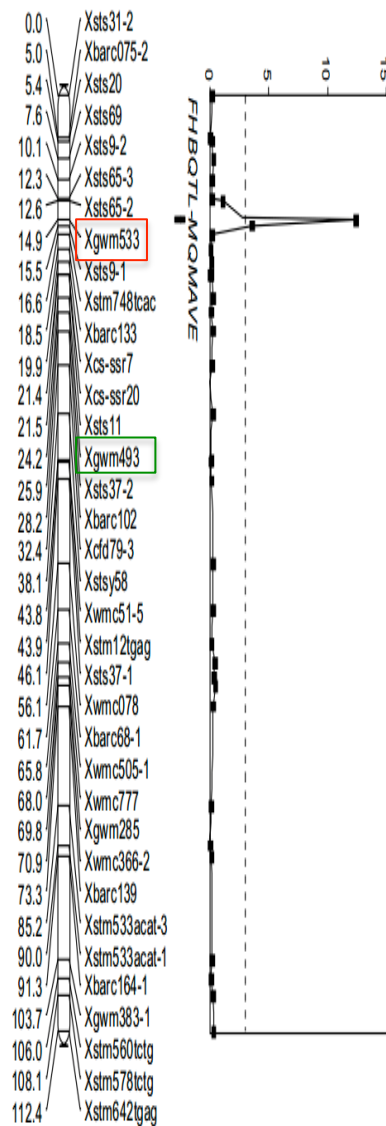
Sumai 3/Stoa



Liu et al. 2006

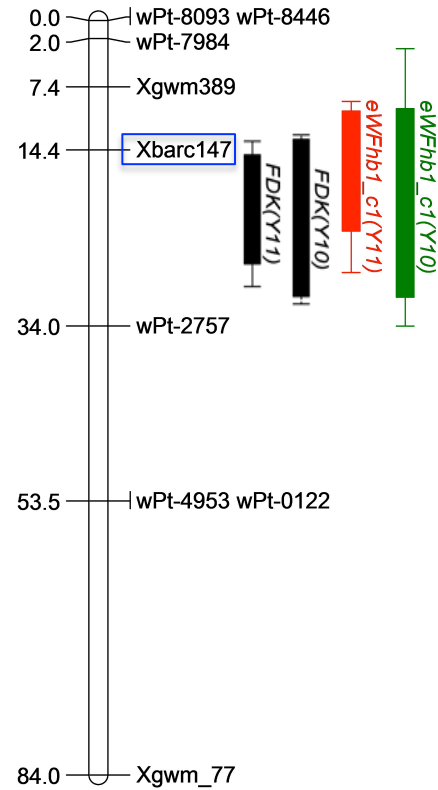


Yu et al. 2008



Zhou et al. 2010

Sumai 3/Y1193-6



Basnet et al. 2012  
Zhuang et al. 2013

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# Acknowledgement

## **Yen's lab:**

### Former members:

Denghui Xing  
Lanfang Bai  
Guangle Li  
Noah Wiedel  
Dengcai Liu  
Yuejin Weng  
Lixin Wang

### Current members:

Yongbin Zhuang  
Aravind Galla  
Yinjie Qiu  
Subha Dahal  
Anjun Ma

## **South Dakota State University:**

Karl Glover                      Yue Jin (now at USDA-ARS)  
Shauket Ali                      Yajun Wu                      Jackie Rudd (now at TAMU)  
Wanlong Li                      Xijin Ge                      Amir Ibrahim (now at TAMU)  
William Berzonsky (now at Bayer CropScience)

## **University of Minnesota:**

James Anderson  
Yanhong Dong

## **Cornell University:**

Gillian Turgeon

## **University of Wisconsin:**

Nancy Keller

## **Montana State University:**

Li Huang

## **University of Nebraska:**

P. Stephen Baenziger

## **USDA-ARS:**

Shiaoman Chao

## **This research is partially funded by the following:**

South Dakota Wheat Commission  
USDA-NIFA-AFRI Award (2014-67013-21567)  
SDSU Scholar and Research Initiative Fund  
South Dakota Agricultural Experiment Station  
USDA-ARS-USWBSI