**Genomics approach for PHS**

Genomics assisted breeding for PHS has retained the attention of the scientific community the last two decades. Tremendous advances were carried out with the identification of useful PHS resistance genes. A glance of the diverse strategies employed for PHS resistance detection is summarized in the figure 1. The first and foremost stage in this process relied on the characterization of germplasm for the identification of promising genetics resources. Meanwhile several parental lines were released including IR24, Asominori, Jinsang, and Gopum. Besides the detection of contrasting materials regarding PHS resistance, the resistance gene pool from wild relatives including *O. rufipogon* [(Phan et al., 2021)](https://link.springer.com/article/10.1007/s42976-021-00162-0#ref-CR20) and *O. nivara* [(Li et al., 2006)]( https://nph.onlinelibrary.wiley.com/doi/full/10.1111/j.1469-8137.2005.01647.x) and weedy rice [Gu et al 2004] (<https://academic.oup.com/genetics/article/166/3/1503/6050471?login=true#236962316>) was investigated. Several mapping populations were generated following RILs, BILs, CSSLs, Three-way hybridization, and double haploid.  The earlier detection of QTLs relied mostly on RFLP and SSRs markers. However, whole genome sequencing approach with a high resolution mapping at SNP level has been initiated.

A total of xxxx QTLs have been detected within all chromosomes of the rice genome (Table 1).

***Comment a little the table***

At early stage of PHS gene detection, comparative genomics has been tested. Orthologous genes identification by comparing with well characterized PHS genes in barley and wheat exhibited the presence of GA20-oxidase encoding gene [Li et al. 2004]( https://link.springer.com/article/10.1007%2Fs10142-004-0104-3).

In order to find out genes involved in PHS and subsequent related biological processes including seed dormancy, transcriptomic studies using contrasting rice materials has been performed. Worker et al pinpointed 2222 genes associated with ......biological process. MicroRNA and small RNAs also played a critical role in the gene expression in seed dormancy, germination, maturation.

***The impact of those RNA on the key hormone regulation ie ABA and gibberellin in rice might be an area of new discoveries for the management of PHS.***

High quality genome resource enabled the detection of PHS related-genes via genome wide association analysis and genome-wide identification approaches. [Zhu et al. (2021)](https://www.mdpi.com/1422-0067/22/4/1661) pinpointed the role of a bZIP transcription factor OsbZIP09 which expression is induced by ABA. The mutation of this gene inhibited PHS in rice. By mining GWAS and transcriptome data, [Shi et al. (2021)](<https://link.springer.com/article/10.1007/s00122-021-03911-1>) found a significant effect of the variation of SNPs in the promoter region of the Os9BGlu33 gene regarding germination index.

From those huge genetic and genomic resources, some major genes have been functionally validated. [(Sugimoto et al., 2010)](https://www.pnas.org/content/107/13/5792.short) identified the Sdr4 gene as responsible of seed dormancy control. Interestingly, OsVP1 exhibited a regulatory effect on Sdr4 gene via ABA signaling pathway [Chen et al., 2021](https://www.sciencedirect.com/science/article/pii/S2214514120301045). Transcription factor also play a crucial role for regulating the hormonal expression in rice. [Hobo et al. (1999)](<https://www.pnas.org/content/96/26/15348.short>), [Wu et al. (2021)](https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbr.12848) and [Wang et al. 2020](<https://pubs.acs.org/doi/abs/10.1021/acs.jafc.0c04748>) demonstrated the interaction between VP1 and TRAP1 (bZIP transcription factor) and Rc (basic helix–loop–helix (bHLH) transcription factor) genes for ABA regulation.

Considering the importance of environmental effect on seed dormancy and germination, we suggest an investigation of the epigenome on rice. In fact, an increasing evidence has been in favor of DNA and histone methylation in regards with PHS resistance genetic mechanism (Genetic and epigenetic factors may be behind why some wheat strains begin to sprout prematurely under high humidity and rainfall conditions & Time to Wake Up: Epigenetic and Small-RNA-Mediated Regulation during Seed Germination & Post-transcriptional regulation of seed dormancy and germination: Current understanding and future directions). The ARGONAUTE4\_9, a DNA methylation RNA-dependent gene has been found to be involved in the sprouting of wheat. Therefore, deciphering the epigenetic factors contributing to the PHS resistance regulation in rice will lay a foundation for a deep understanding of the full machinery in real climate impacted conditions.

Altogether, post-transcriptional regulation encompassing, splicing RNA and epigenetics offer a new avenue for unravelling of the mechanism of resistance of PHS in rice. Ultimately, a deeper comprehension of the whole machinery will provide a gain for designing better rice with added value.