**Genomics approach for PHS in rice**

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 cross hybrid, and double haploidy.  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**).

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 the hormonal 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 and maturation, transcriptome studies ([Huh et al., 2013]( https://www.sciencedirect.com/science/article/abs/pii/S0176161713001053),[Xie et al., 2019](https://bp.ueb.cas.cz/pdfs/bpl/2019/01/35.pdf), [Park et al., 2021](https://www.frontiersin.org/articles/10.3389/fpls.2021.727302/full)) using contrasting rice materials has been performed. Interestingly, candidate genes regulating hormones including ABA, GA and IAA have been highlighted including transcription factors such as DREB (dehydration-responsive element-binding protein), Basic Helix-Loop-Helix Transcription Factor (bHLH), late embryogenesis abundant protein (LEA), NAC transcription factor, and CCAAT-HAP3 transcription factor. This emphasizes the contributions of TFs as one of the key players mediating of the hormonal expression.

Meanwhile microRNAs (miRNAs) are well known to be dependent of hormonal regulation *in planta* [(Reyes et al., 2007)](https://onlinelibrary.wiley.com/doi/10.1111/j.1365-313X.2006.02980.x)). Recently, [Park et al. (2021)]( https://www.frontiersin.org/articles/10.3389/fpls.2021.727302/full#h4) identified two candidate miRNAs (osa-miR5827 and osa-miR1862h) associated with two PHS-related genes OsFbox594 and OsbHLH084 respectively.

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, few 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 [(Singh et al. 2013)](<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0077009>), [Lujan-Soto et al 2021](<https://www.mdpi.com/2223-7747/10/2/236>). The role of the ARGONAUTE4\_9, a DNA methylation RNA-dependent gene has been proved in wheat PHS. However, the epigenetic framework of PHS in rice is still elusive. 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.  Moreover, an intensive validation of the existing candidate genes should be processed via Crispr-Cas9, RNAi, *Agrobacterium tumefaciens* mediated transformation for example. This will surely boost the design of PHS resistant rice.

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.

**References**