

Employing the CRISPR/Cas9 system for improvement of plant defense against pathogens

M. Galli, Dr. J. Imani & Prof. Dr. K. H. Kogel

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Targeted genome engineering

It's a technological approach which allows **to determine the function of specific genes** via modification of their expression.

Technologies:

- I. Gene overexpression
- II. Antisense RNA
- III. RNA interference (RNAi)



Limitations → incomplete/temporary gene knock-down (KD) and poor specificity

- IV. Site-Specific Nucleases (SSNs)

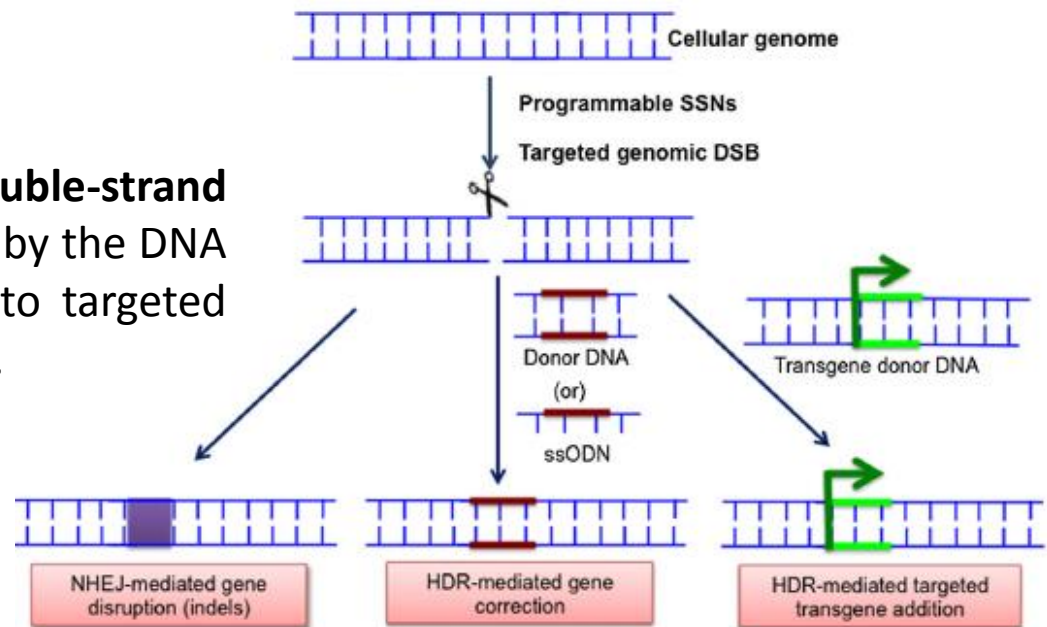
Advantages → complete knock-out (KO), higher sequence fidelity and possibility of transgene-free plants in next generations

Site-Specific Nucleases

- I. Zinc finger nucleases (Kim *et al.*, 1996)
- II. Transcription activator-like effector nucleases (Boch *et al.*, 2009)
- III. RNA-guided engineered nucleases (Sapranaukas *et al.*, 2011)

How do they achieve gene KO?

Introducing a site-specific **double-strand break (DSB)**, which is **corrected** by the DNA repair cell machinery, leading to targeted **genetic modifications** (Kim *et al.*, 2014).



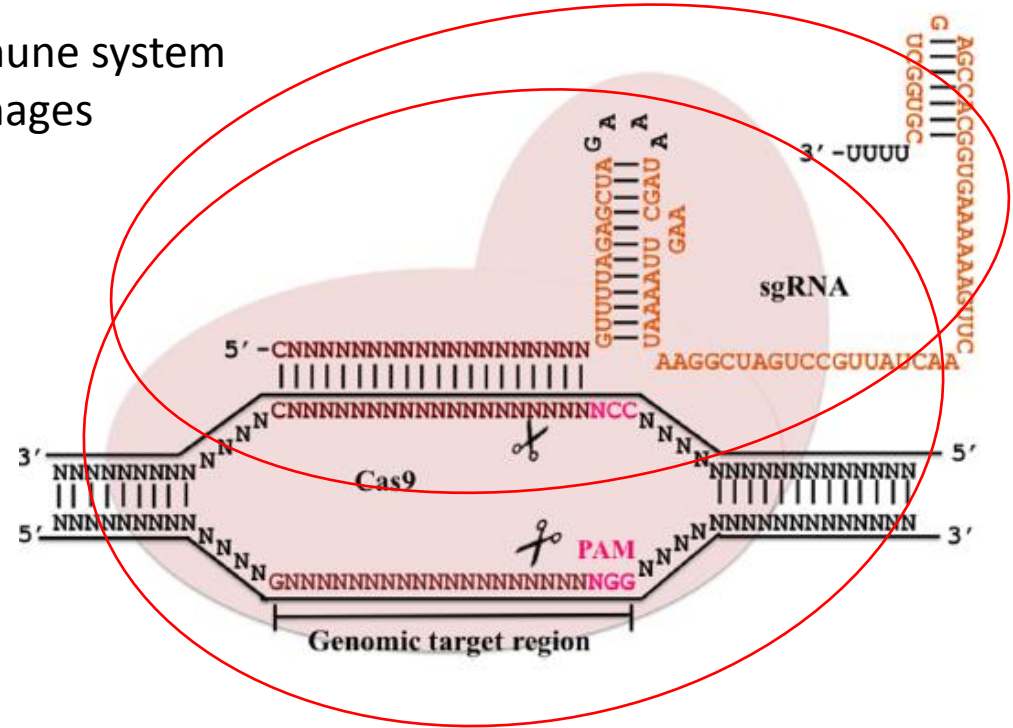
SpCas9 type II system

Discovered as part of the adaptive immune system of bacteria (*S. pyogenes*) vs. bacteriophages

The CRISPR/Cas type II system requires only two components:

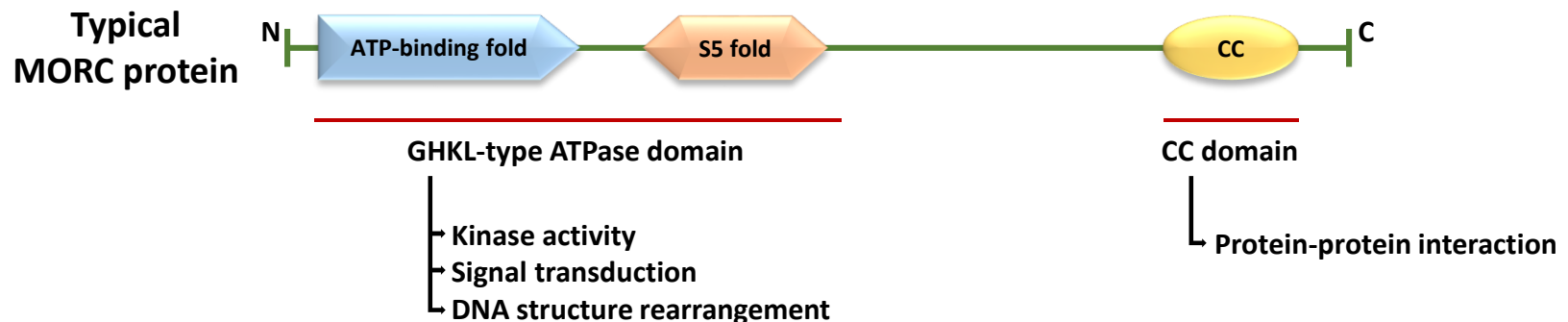
- I. single RNA chimera or single guide RNA (sgRNA)
- II. CRISPR associated protein (Cas9)

SpCas9 cleaves in a 20bp DNA sequence targeted, 3-nt upstream of the PAM site



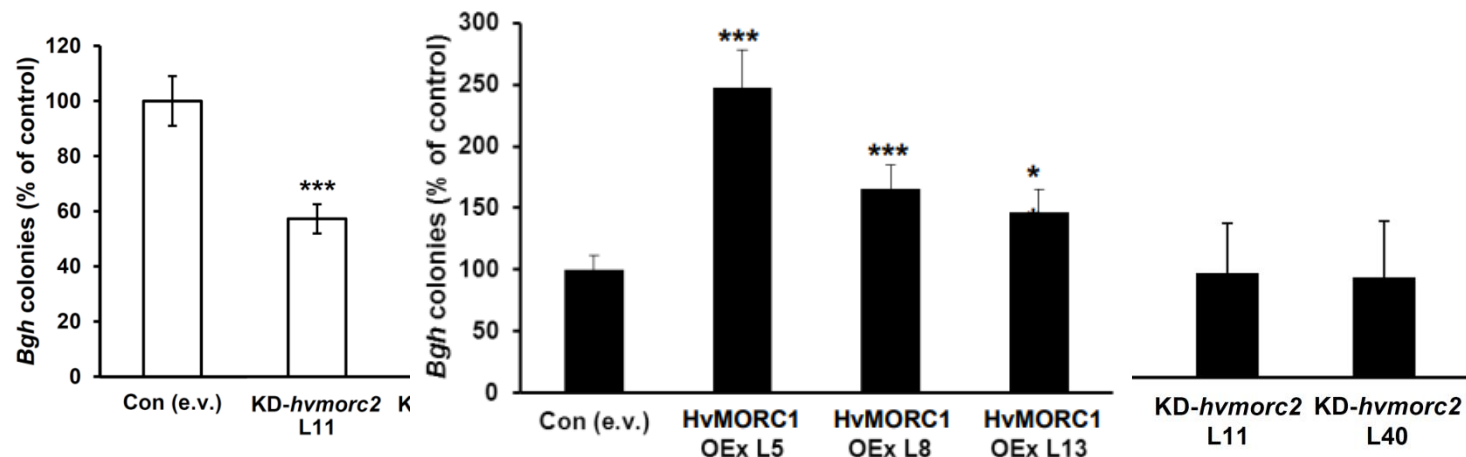
Microrchidia (MORC) ATPases

- ❖ Discovered as critical modulators of mice spermatogenesis (Watson et al., 1998), in both eukaryotes and prokaryotes they have characteristic conserved domains: a GHKL and S5 fold domains and a coiled-coil domain (Dutta and Inouye, 2000). MORC proteins are involved in cell cycle regulation, DNA methylation and repair and transcriptional gene silencing (Moissiard et al., 2012; Kock et al., 2017).
- ❖ In plants MORCs participate in multiple layers of plant immunity: in *Arabidopsis* and potatoes, they are positive regulators, whereas in tobacco and tomato they are negative ones (Kang et al., 2008; Manosalva et al. 2015).



Microrchidia (MORC) ATPases in barley

- ❖ In the monocot barley, seven *HvMORCs* are present and they act as positive regulators of plant immunity (Koch et al., 2017).
- ❖ RNAi knock-down (KD) of *HvMORC2* resulted in enhanced resistance vs. *Blumeria graminis* f.sp. *Hordei* and *Fusarium graminearum*, while plants constitutively overexpressing *HvMORC1* under control of the *CMV35S* promoter were compromised for resistance (Langen et al., 2014).

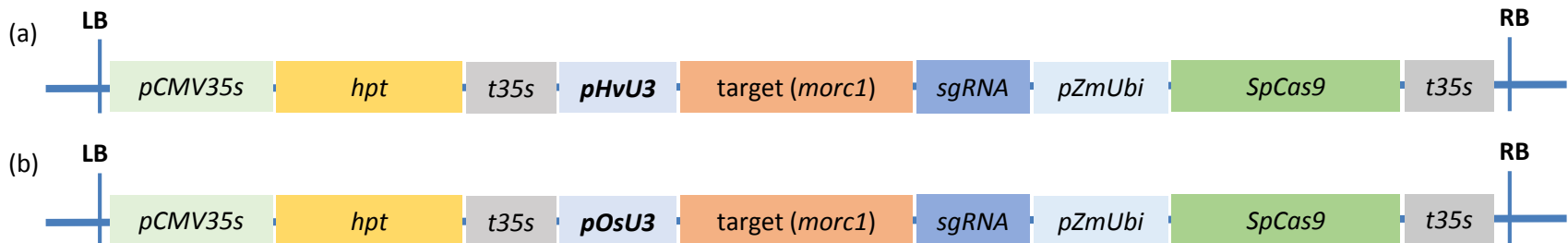


Employing CRISPR/Cas9 system to KO *HvMORC1*

Construction of the T-DNA

- ❖ Several monocot and dicot RNA Pol III promoters from snRNA genes have been used to express sgRNA for genome editing.

In this study, barley and rice (RNA Pol III dependent) *U3* promoters were used for active transcription of sgRNA in barley cells.

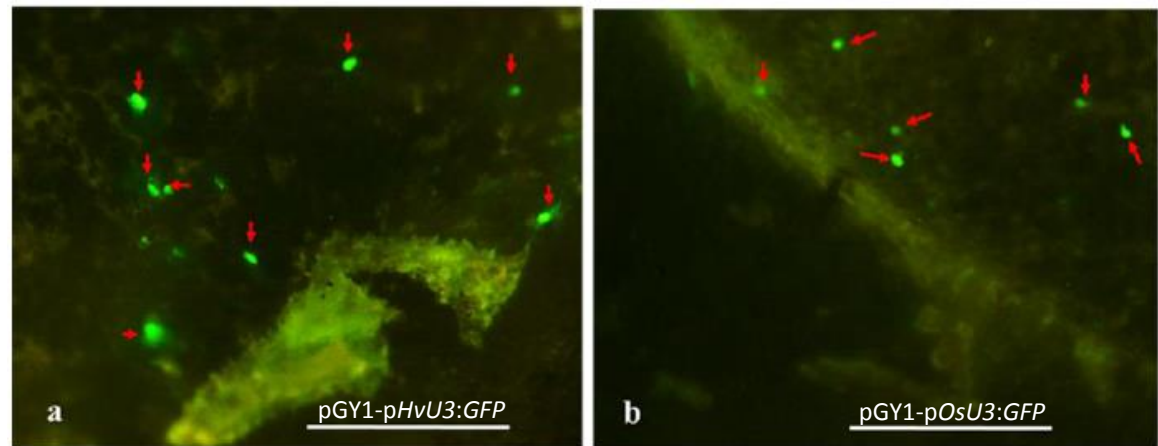
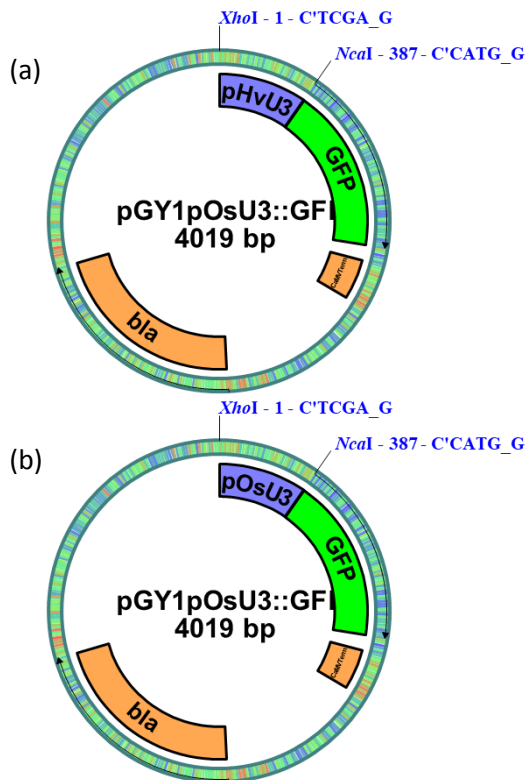


The final *SpCas9* construct, with sgRNA under the control of *HvU3* (a)/*OsU3* (b) promoter and *Cas9* gene under the maize *ubiquitin* promoter, was used for *A. tumefaciens* mediated-transformation of barley embryos.

Employing CRISPR/Cas9 system to KO *HvMORC1*

Activity of *HvU3* and *OsU3* promoters in barley

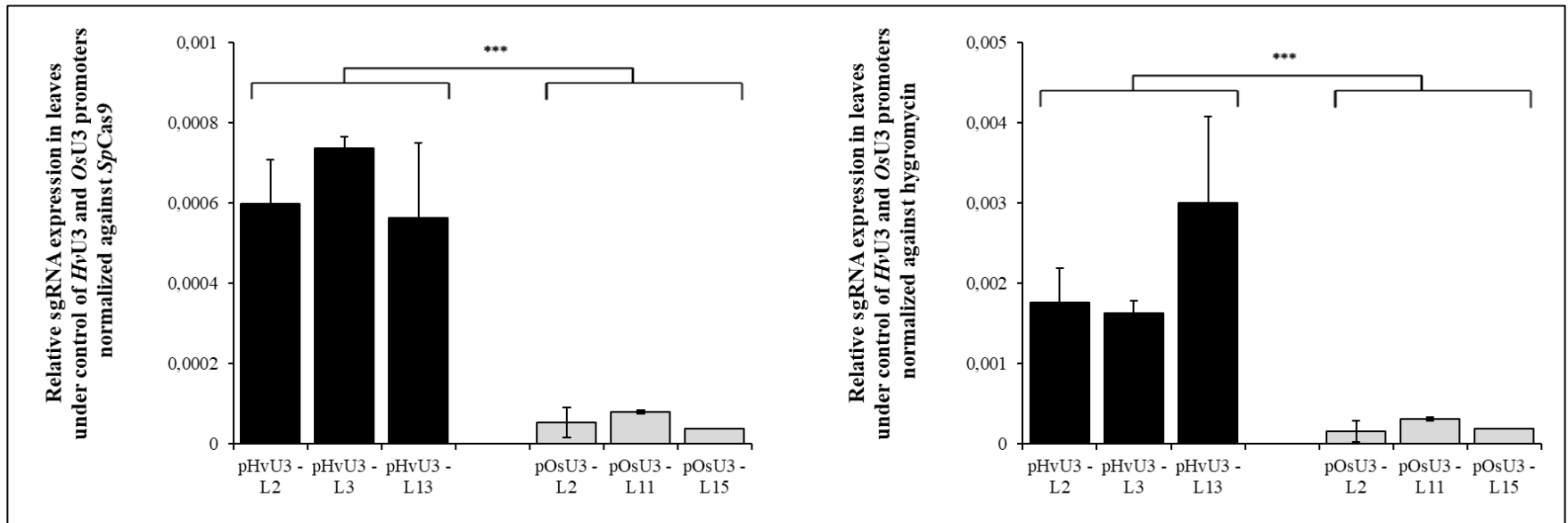
HvU3 and *OsU3* promoters were cloned in pGY1-35s::GFP (Schweizer et al., 1999) and their activity tested in immature barley embryos via biolistic particle delivery system.



Employing CRISPR/Cas9 system to KO *HvMORC1*

Activity of *HvU3* and *OsU3* promoters in barley

Expression of sgRNA under control of either the *HvU3* or *OsU3* promoter.

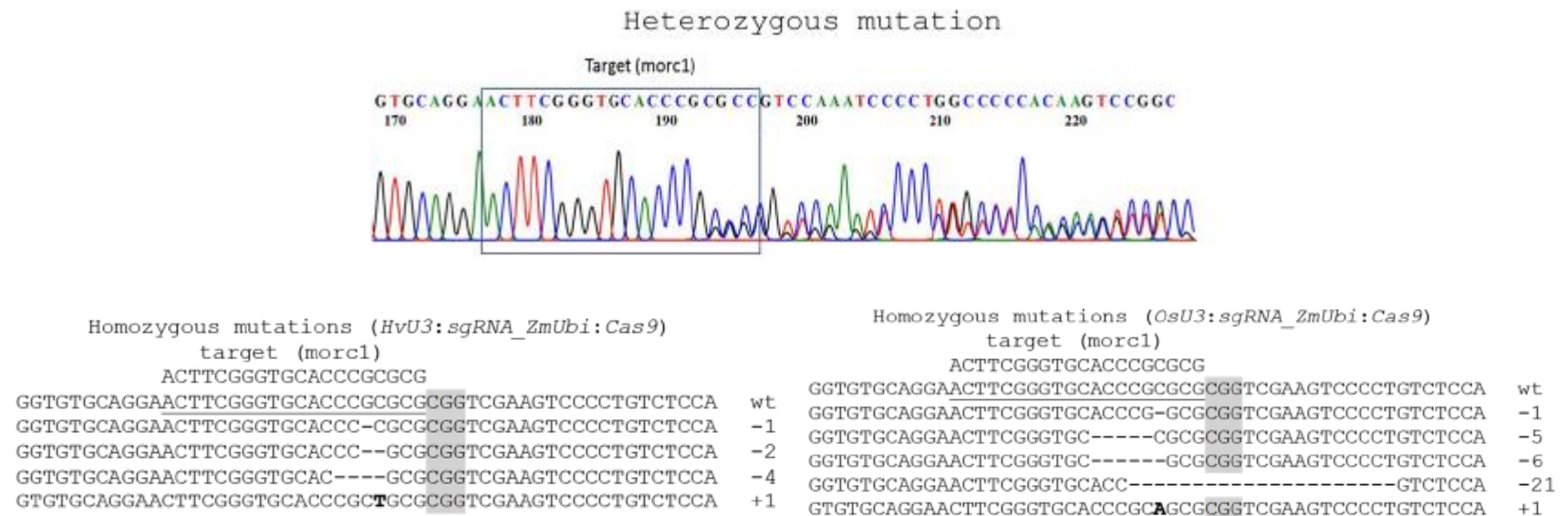


➤ *HvU3* driven sgRNA showed highest transcript accumulation as compared to *OsU3*.

Employing CRISPR/Cas9 system to KO *HvMORC1*

SpCas9 induce mutation in T1 barley plants

Mutation frequency in To *calli* for construct *HvU3:sgRNA* was 77%. In T1 plants was 100% and 70% using *pHvU3* and *pOsU3*, respectively.

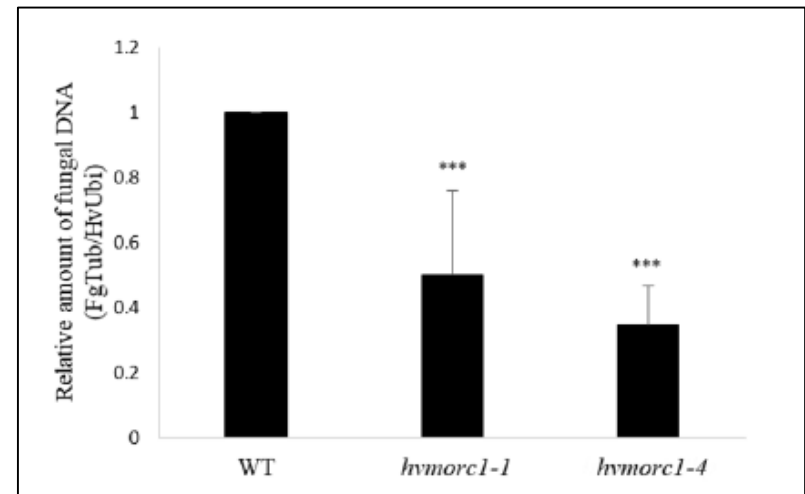
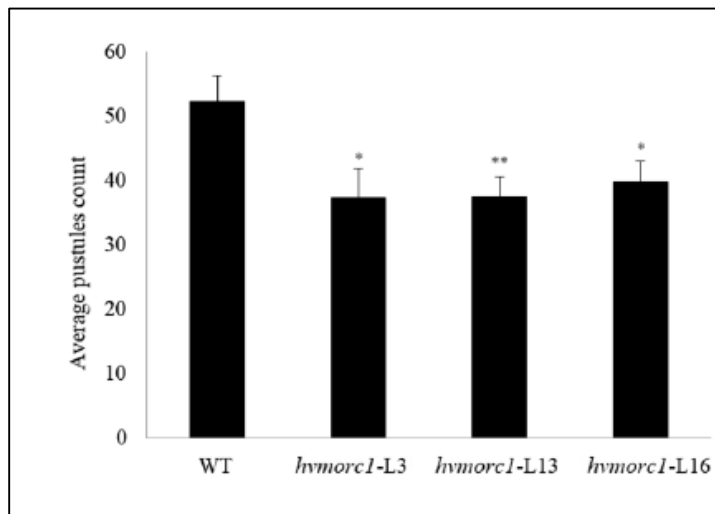


➤ *SpCas9* technique produces high frequency mutation events in barley.

Employing CRISPR/Cas9 system to KO *HvMORC1*

Barley MORC1 modulates plant immunity

Mutated *hvmorc1*-KO T1 plants from *pHvU3:sgRNA_pZmUbi:Cas9* construct were tested for powdery mildew and *F. graminearum* resistance.

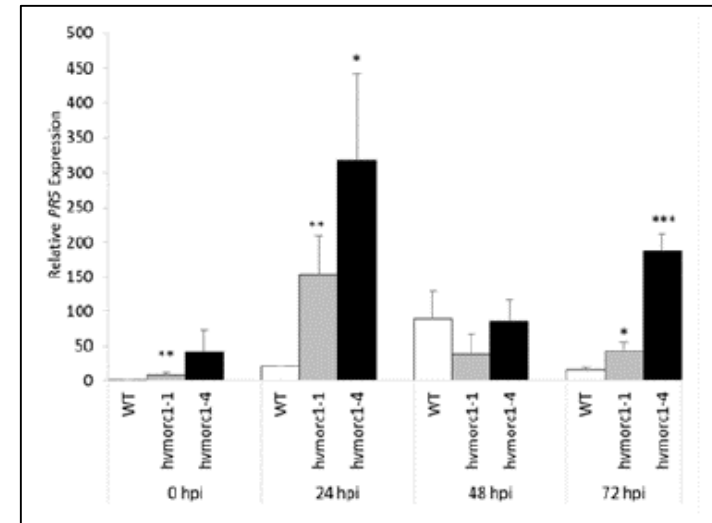
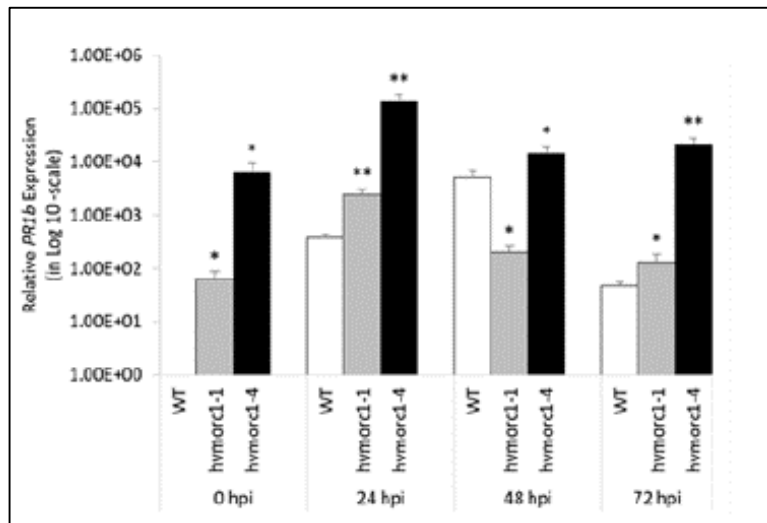


- Complete KO of *HvMORC1* enhances plant immunity against fungal pathogens *Blumeria graminis* and *F. graminearum*

Employing CRISPR/Cas9 system to KO *HvMORC1*

Barley MORC1 modulates plant immunity

Enhanced resistance of *hvmorc1*-KO lines is associated with constitutive activation of defense responses. *HvPR1b* and *HvPR5* were tested by RT-qPCR at 0, 24, 48, and 72 hpi with *Bgh*.



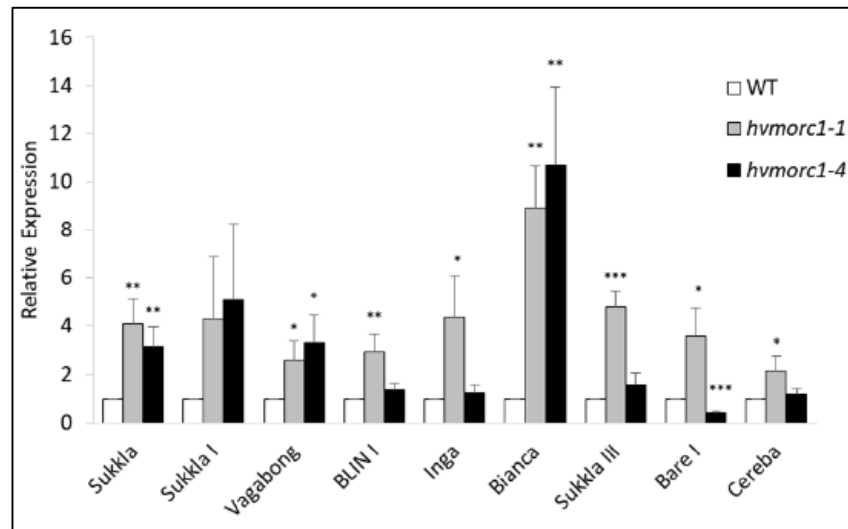
- *PR* expression is enhanced in response to *Bgh*, particularly during initial phase of fungal colonization, providing *hvmorc1*-KO mutants an early advantage.

Employing CRISPR/Cas9 system to KO *HvMORC1*

Barley *MORC1* regulates TE expression

- ❖ Arabidopsis mutants *atmorc1* and *atmorc6* are defective for transcriptional gene silencing (TGS), which plays an important role in repressing TEs (Moissiard et al., 2012).

Barley *morc1*-KO T1 plants were tested for transposable elements de-repression.

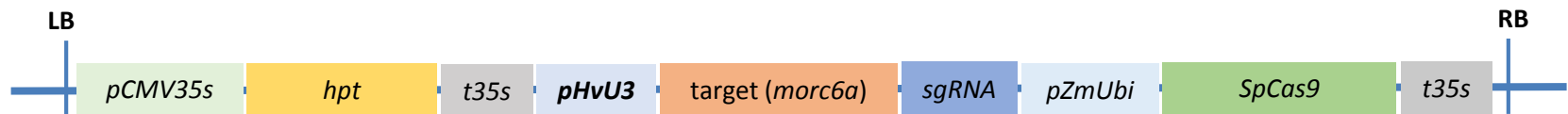


- Barley *MORC1* has a role in genome stabilization, the loss of which results in higher expression of TEs and concomitantly *PR* gene expression.

Employing CRISPR/Cas9 system to KO *HvMORC6a*

Preliminary results (I)

Barley (RNA Pol III dependent) *U3* promoters was used for active transcription of sgRNA in barley cells.



Mutation frequency in To plants was 73% using *pHvU3*, with a total of 27% bi-allelic homozygous mutated plants.

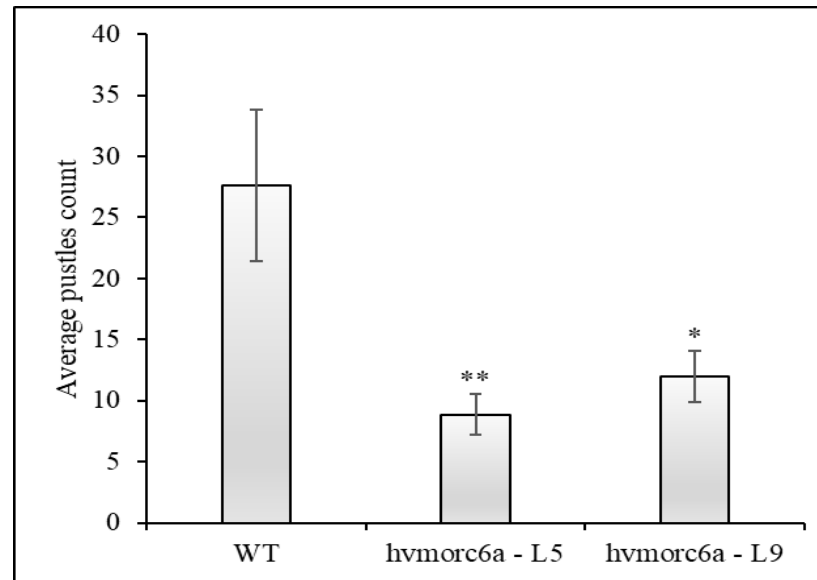
Homozygous mutations (*HvU3:sgRNA_ZmUbi:Cas9*)

	target (<i>morc6a</i>)
	GTACGGCTTGACATCGCGGG
WT	GCTCGTACGGCTTGACATCGCGGGGGG-GGGAGGGGGCGCTGGTAACGGCGCTGGTGCTGGGAAAGGGGAGGGGCTCCTCGTCGTCGCTCGCTTGAGAGAT
1bp+	GCTCGTACGGCTTGACATCGCTGGGGGGGGGGAGGGGGCGCTGGTAACGGCGCTGGTGCTGGGAAAGGGGAGGGGCTCCTCGTCGTCGCTCGCTTGAGAGAT
2bp-	GCTCGTACGGCTTGACATC--GGGGGGG-GGGAGGGGGCGCTGGTAACGGCGCTGGTGCTGGGAAAGGGGAGGGGCTCCTCGTCGTCGCTCGCTTGAGAGAT
25bp-	GCTCG-----AGGGGGCGCTGGTAACGGCGCTGGTGCTGGGAAAGGGGAGGGGCTCCTCGTCGTCGCTCGCTTGAGAGAT
60bp-	GCTCGTACGGCTTGACATCG-----TCGTCGTCGCTTGAGAGAT

Employing CRISPR/Cas9 system to KO *HvMORC6a*

Preliminary results (II)

Mutated *hvmorc6a*-KO T1 plants from *pHvU3:sgRNA_pZmUbi:Cas9* construct were tested for powdery mildew resistance.

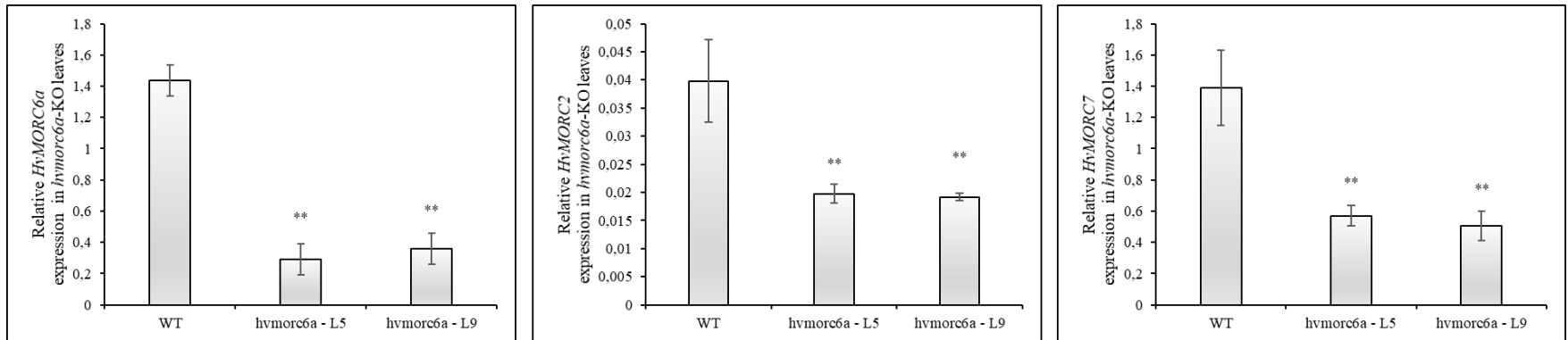


- Complete KO of *HvMORC6a* enhances plant immunity against bio-trophic fungal pathogens *Blumeria graminis*.

Employing CRISPR/Cas9 system to KO *HvMORC6a*

Preliminary results (III)

Mutated *hvmorc6a*-KO T1 plants show reduced *HvMORC2* and *HvMORC7* expression.



➤ Possibly *HvMORC6a* act as a nuclear transcriptional factor.

Outlook

Employing CRISPR/Cas9 system to KO both *HvMORC6a* and *HvMORC1*

- ❖ Three different strategies will be employed to ensure the achievement of this important step:
 - I. conventional crossing of barley homozygous *hvmorc1* and *hvmorc6a* single mutants
 - II. concomitant transformation of “wild-type” barley immature embryos with both CRISPR/Cas9 constructs
 - III. transformation of homozygous single mutants with the second construct (*hvmorc6a* KO mutants with *hvmorc1*-construct and vice versa).

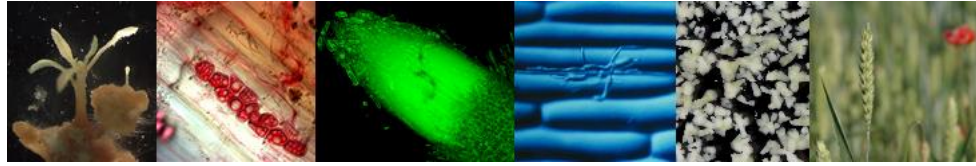
Conclusions

U3 promoters are highly suitable for sgRNA expression in barley genome editing applications, especially barley *U3* promoter.

CRISPR/Cas9 genome editing technology is an efficient tool to modify gene families in cereal crops with potential agronomic applications.

Knock-out *HvMORC1*, as well as *HvMORC6a*, produce a positive impact on fungal pathogen resistance.

Genes expression analysis may indicate that *HvMORC1* and *HvMORC6a*, like *AtMORC1* and *AtMORC6*, are involved in genome stabilization.



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and all JLU Phytopatogloy team...

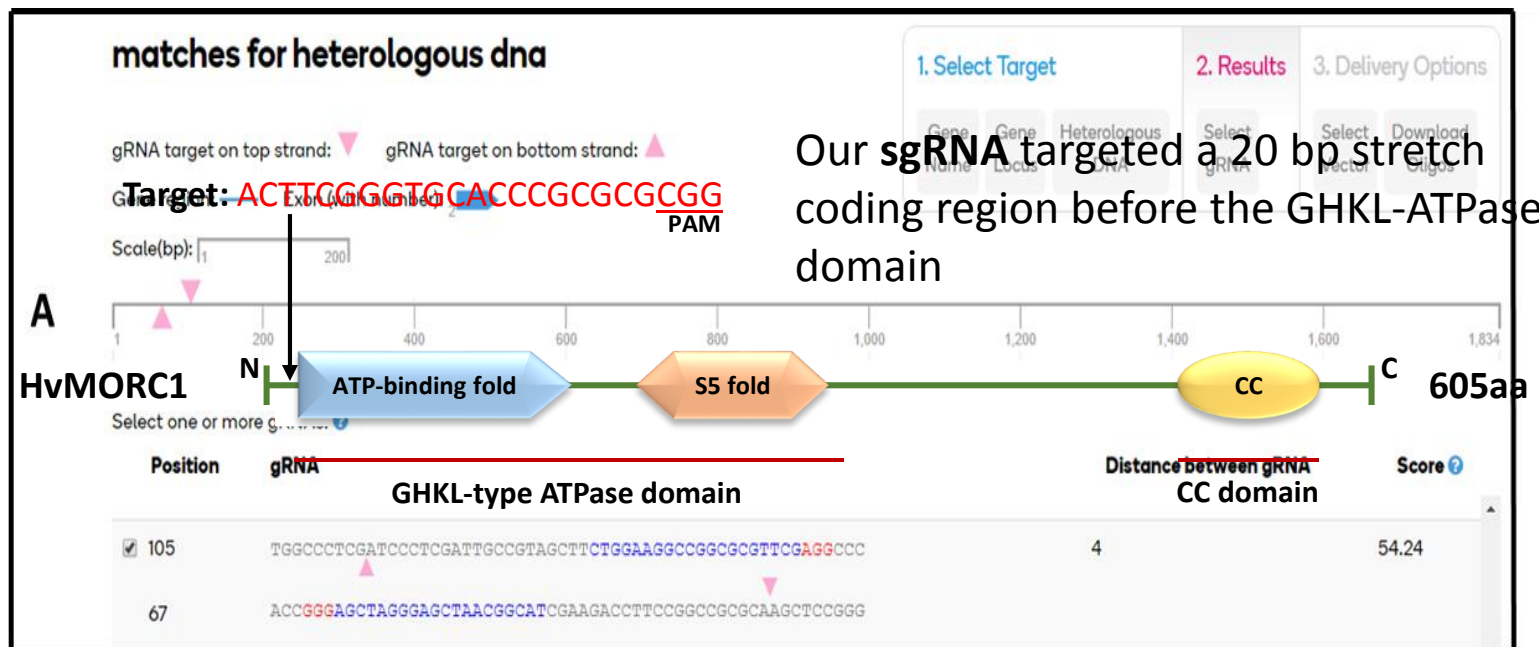
Thank you all for your attention...



Employing CRISPR/Cas9 system to KO *HvMORC1*

Choosing *HvMORC1* 20bp target region

20bp target sequences with NGG (PAM) at 3' end were selected using CRISPR sgRNA design online tool (<https://atum.bio/eCommerce/cas9/input>)



Our sgRNA targeted a 20 bp stretch coding region before the GHKL-ATPase domain