

Base editing and its implications in herbicide tolerance

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1	Need of herbicide tolerance: A case study
2	Basic mechanism and history of CRISPR/Cas9
3	Base editing : what and why?
4	Types of base editing and case studies: Cytosine base editing, adenine base editing and dual base editing
5	Shortcomings and conclusion

Zhang et al (2019), *Nature plants*

Why herbicide tolerance ? A story... For control of Jointed Goatgrass (Weed) Imidazolinone (IMI) is used

- IMI herbicide persist in soil causing heavy loss to crops such as sugarbeet, tomato and chilli
- Its persistence may vary for 90 to 360 days as per soil conditions due to this multi harvest

from a same field in a same year is affected

- New herbicides are required with less persistence in soil and crops are required to make resistant to new low persistence herbicide
- **METSULFURON**, a Sulfonyl urea also cause harm to wheat
- What is next??

BASF warns on seeding choices for drought-hit imi-treated fields

Steer clear of non-Clearfield canola, durum, canary seed in rotations, company says

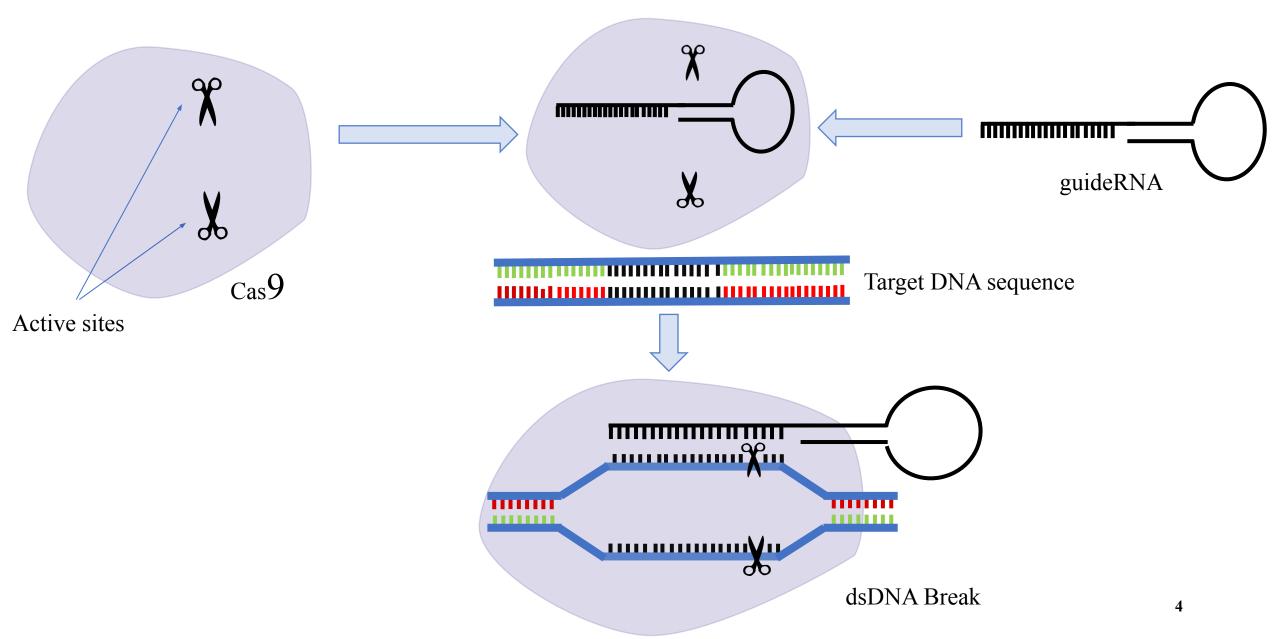
Posted Sep. 22nd, 2021 by Dave Bedard Be the first to comment







Basic mechanism of CRISPR/Cas9



Contributors of the technology

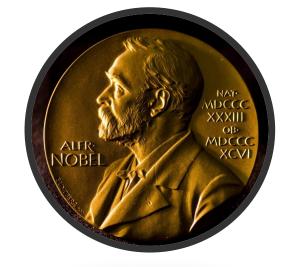


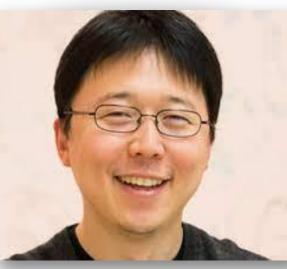
THE NOBEL PRIZE



Emmanuelle Charpentier Jennifer A. Doudna

"for the development of a method for genome editing"





Feng Zhang



Francisco Mojica





Virginijus Siksnys

Kira Makarova



John van der Oost





Philippe Horvath

Yoshizumi Ishino



Martin Jínek



Sylvain Moineau





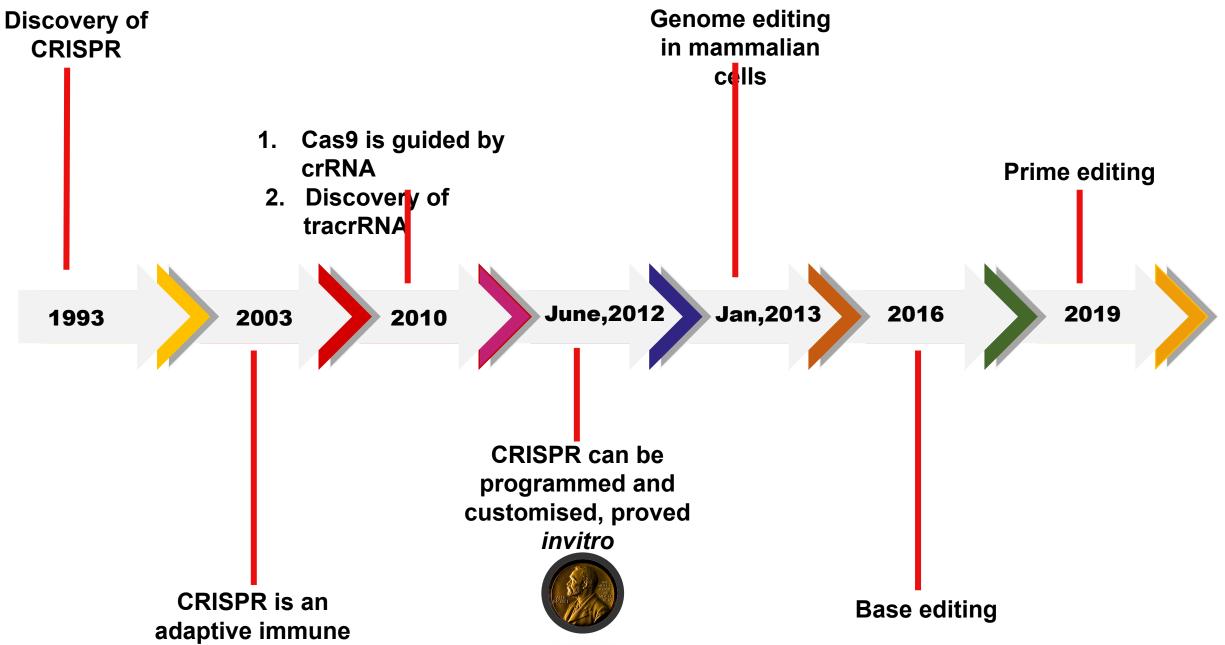
Rodolphe Barrangou





David Liu

Brief timeline



6

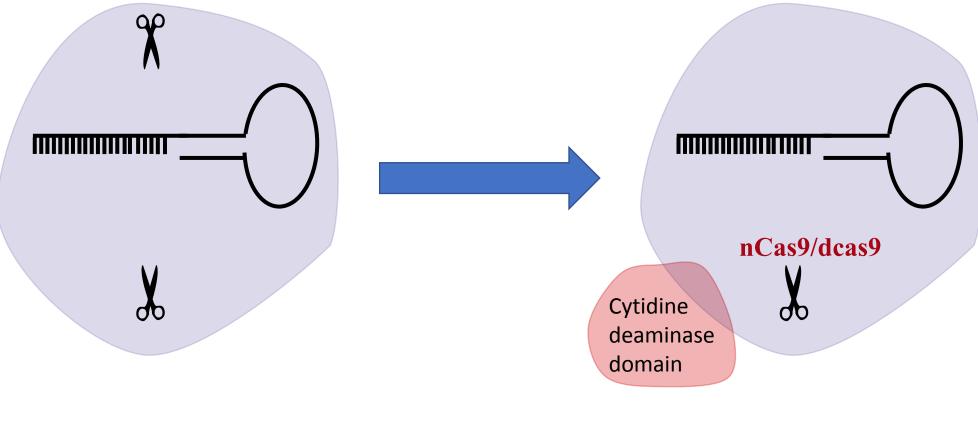
What and why base editing?

- It is capable of introducing **high frequency of substitution mutation** which is in contrast to conventional genome editing
- Base editing involves **single strand breaks** whereas conventional genome editing involve double strand breaks which generally leads to undesirable insertion and deletions
- Base editing is **more precise and error free** as compared to conventional genome editing
- Base editing does not require **donor DNA template**

CYTOSINE BASE EDITING



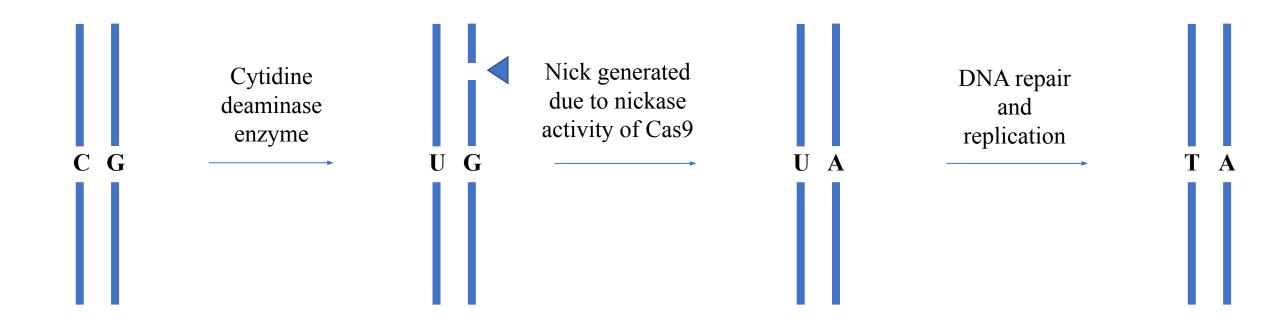
Difference between Cas9 for conventional genome editing and base editing

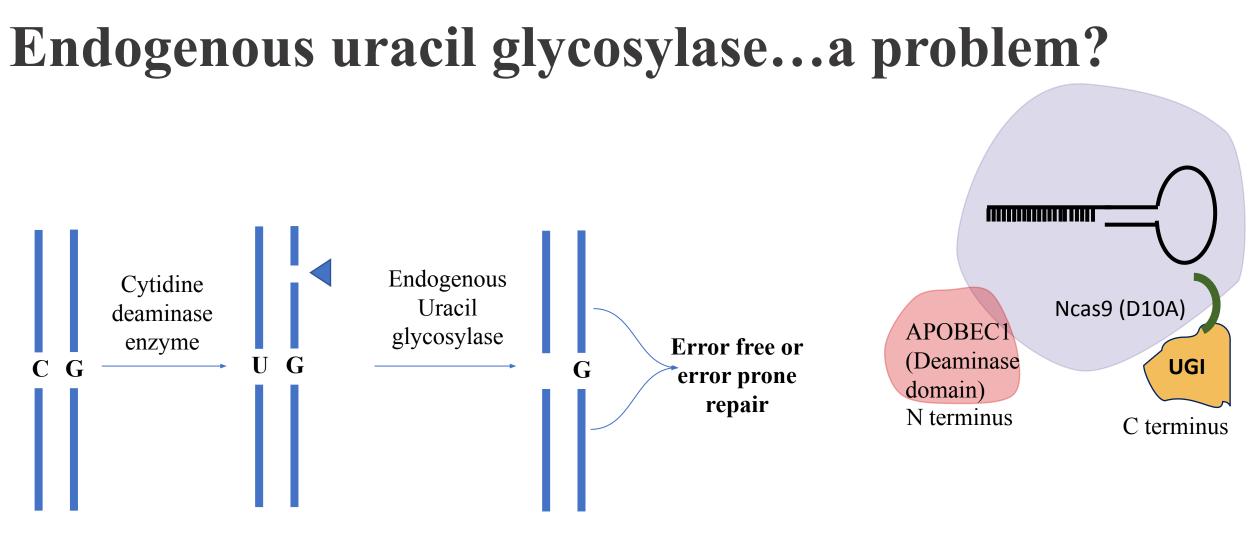


Conventional CRISPR protein

Chimeric protein

Mechanism of cytosine base editing





6 fold increase in editing efficiency

Back to story... What is next??

- ✔ Finding a low persistent herbicide
- ✓ Making wheat resistant to that particular herbicide





NICOSULFURON Zhang et al (2019), *Nature plants*



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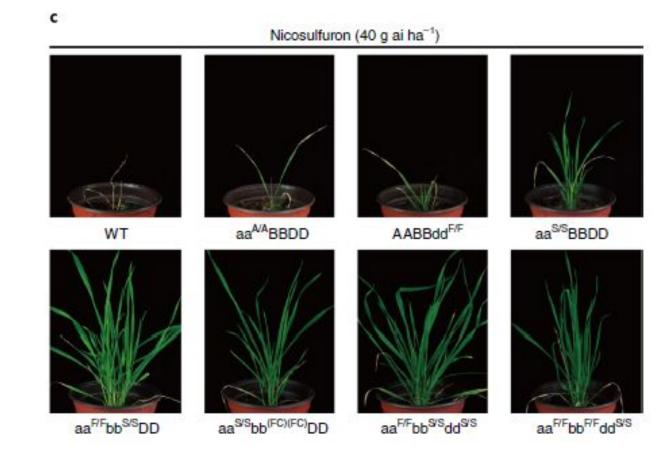




- Acetolactate synthase (ALS), a key enzyme in the biosynthesis of branched-chain amino acids.
- ALS genes can harbor point mutations that confer sufficient tolerance to herbicides
- TaALS-P174 site was edited using cytosine base editors
- Mutation efficiency was 2.5%

Number of plants	Genomes mutated
8	3
2	2
3	1
3	Silent mutations

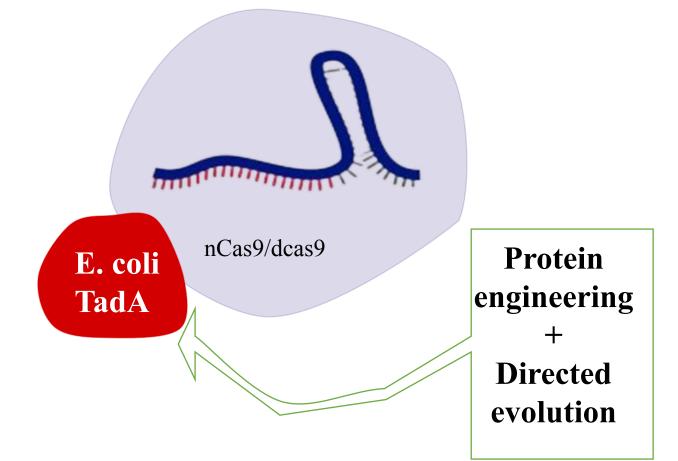
* Plant having more edited alleles were more resistant



ADENINE BASE EDITING



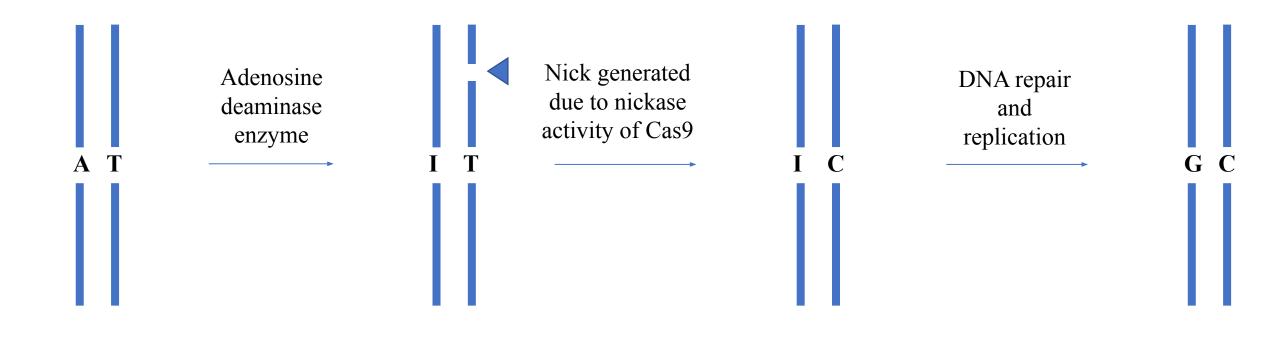
Adenine base editing



• Unlike cytidine deaminases, adenine DNA deaminases do not occur in nature.

E. coli TadA is a tRNA ADENINE DEAMINASE that converts adenine to inosine in the single stranded anticodon loop of tRNA Arg.

Mechanism of adenine base editing





Lolium rigidum A Forage Crop



medium supplemented with haloxyfop-R-methyl

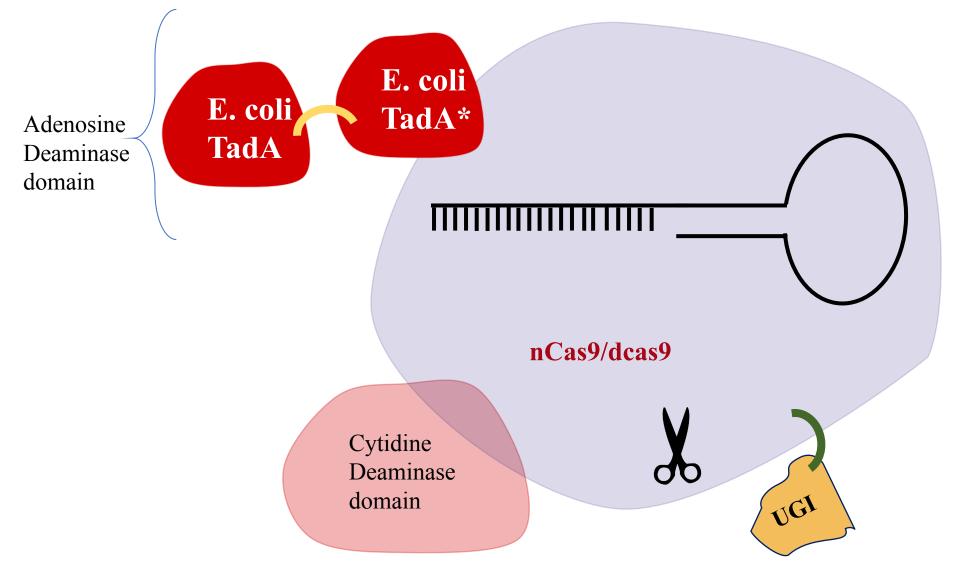
Li et al (

- The half-life of haloxyfop in the rhizosphere soil is 2.6–4.9 days (Liang et al, 2020)
- Acetyl-coenzyme A carboxylase (ACC) is an important target for herbicide tolerance
- T to C replacement (C2088R) in *Lolium rigidium* could endow plants with resistance to various herbicides
- The point mutation C2088R in *Lolium rigidum* corresponds to C2186R in rice (*Oryza sativa*), which is the target site *OsACC*-T1 in this study
- The mutant plant survived haloxyfop-R-methyl with normal phenotypes and no symptoms of damage whereas wild-type plants displayed severe stunting and withered leaves

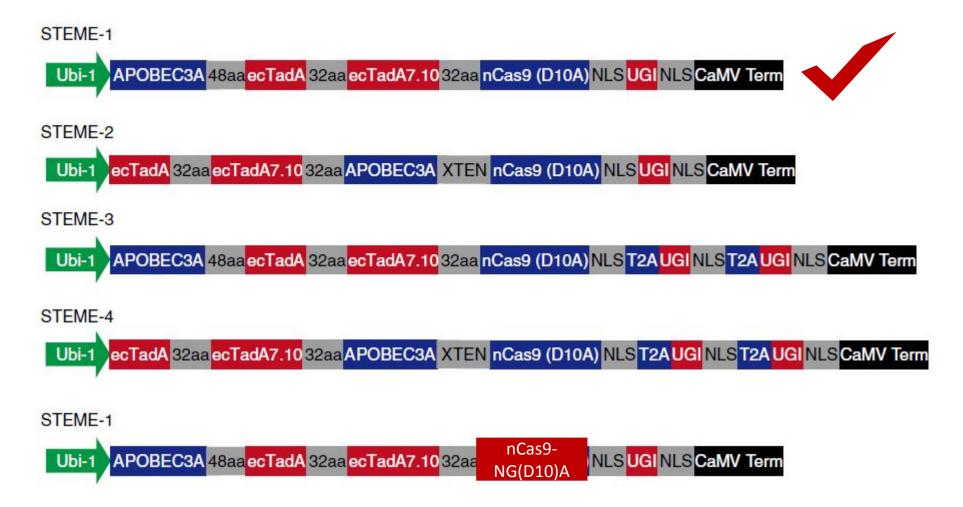
DUAL BASE EDITORS



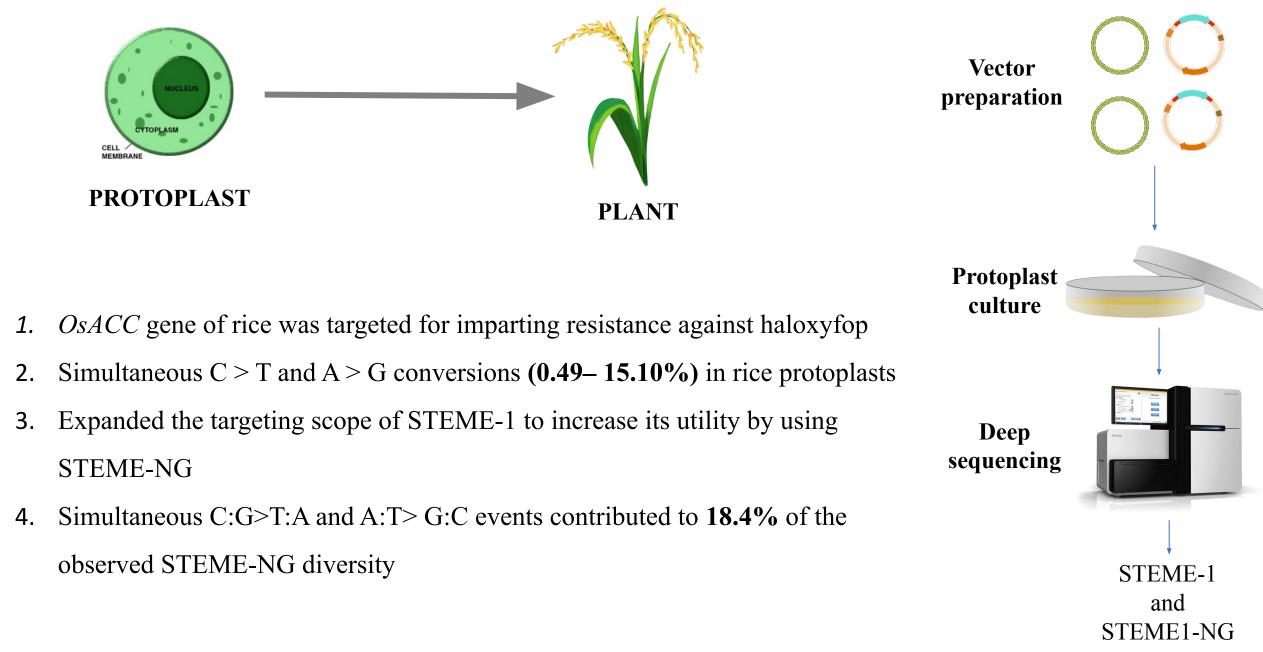
DUAL BASE EDITORS



Saturated targeted endogenous mutagenesis editors (STEME) vectors



Li et al (2020), Nature biotechnology

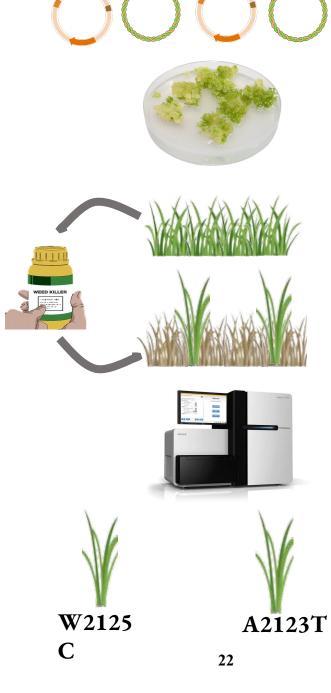


- CT domain

Description	Number
No. of sgRNAs designed	200
STEME-1	102
STEME-NG	98

Efficiency of simultaneous editing of cytosine and adenine -3.84%

Li et al (2020), Nature biotechnology



SHORTCOMINGS

Limited PAM sites

- Use of base editors are limited by presence of NGG PAM sites.
- New types of Cas protein and engineered Cas9 variants with altered PAM sequences have been introduced into base editors e.g., LbCpf1-BE0

Wide editing window

- CBEs can edit any sequence present in its catalytic window (4-5 nucleotides)
- It will pose a problem in case of continuous stretch of "C" (CCCCC).
- Base editors with narrow editing window (1-2 nts) are desirable

Off target activity

- Increased level of deaminase and UGI increases off target activity
- Sequence independent deamination was also found
- ABE also find out to cause off target activity at RNA level in mammalian cells

CONCLUSION

- Due to **increasing resistance of weeds to already available herbicides**, there is dire need of identifying new herbicides and making crops resistant to them.
- Base editing can be effectively used to generate wide array of mutations in ACC and ALS type of genes to impart herbicide tolerance to plants.
- Base editing is better than conventional breeding in terms of target specificity, increased precision and reduced unwanted variation
- Base editing can also be used to enhance **molecular diversity and directed evolution** by inducing different mutations
- Base editing cannot be used to insert specific sequences. Moreover, **prime editing** can be used for that purpose









Thanks