

During (shi et al.
2016). sequence-
specific designer
crispr cas9



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During the last five years, enormous excitement has been witnessed with the discovery of genome editing approaches involving sequence-specific designer nucleases (ZFN, TALEN, CRISPR/Cas), which create double strand breaks in DNA (for a Review, see Gaaj et al.

, 2013). However, of the three nucleases, CRISPR/Cas9 attracted the maximum attention for developing several plant and animal species with desired genetic modifications through genome editing. An alternative for Cas9 in the form of Cpf1 later became available giving birth to superior system in the form of CRISPR/Cpf1, which has several advantages over CRISPR/Cas2, 3 (Zetche et al., 2015; Zaidi et al.

, 2017). ZFN//TALEN/CRISPR-mediated genome editing has been a preferred approach over transgenics, since no foreign gene is being introduced, and only an existing gene is altered, using cells own machinery involving homology-dependent repair (HDR) and non-homologous end joining (NHEJ). The preferred HDR-dependent genome editing is, however, limited by low efficiency, since NHEJ competes with it and creates high frequency of indels and off-site alterations during genome editing. Also, genome editing does not allow an alteration of a specific existing base pair in a DNA molecule in a predictable manner. In view of the fact that no foreign gene is inserted during genome editing and only an endogenous gene is altered, it has been argued that products of genome editing technologies like CRISPR/Cas9 should not be subjected to the regulatory system, which is used in case of genetically modified organisms (GMOs). This has made commercialization of genome edited products easier at least in some countries. Consequently, a strain of ‘

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mushroom' with white buttons, which will not turn brown (when stored) was developed using CRISPR and commercialized in USA without being subjected to the regulations that are commonly applied to GMOs^{5, 6} (Hall, 2016; Waltz, 2016); in these edited mushrooms, a gene for PPO (polyphenoloxidase) that is responsible for browning of mushrooms was altered, thus reducing the quantity of PPO to 30%.

A mutant corn that gave high yield under drought conditions has also been developed through genome editing by DuPont and approved for commercial cultivation, so that it may also be used for commercial cultivation by the farmers and may hit the market soon⁷ (Shi et al. 2016). Sequence-specific designer CRISPR/Cas9 system contains the following two components: (i) a guide RNA (gRNA or sgRNA), and (ii) a CRISPR-associated endonuclease (Cas protein). The gRNA is a short synthetic RNA composed of a scaffold sequence necessary for Cas-binding and a ~20 nucleotide spacer (upstream of PAM sequence) that defines the genomic target to be modified.

The gRNA is designed keeping in mind the sequence that needs to be altered, so that Cas9 binds to the desired site and creates DSBs at specific desired site. In other words, the genomic target for binding Cas protein and for creating alteration in a specific region of the genome is decided by gRNA. However, outcome of CRISPR/Cas9-mediated alteration in the genome is not precise at the individual nucleotide (base) level, and therefore it can not be used for specific alterations at the level of single specific base. In actual practice it has been noticed that a variety of products are obtained and a selection needs to be exercised to obtain the desired product, which is <https://assignbuster.com/during-shi-et-al-2016-sequence-specific-designer-crisprcas9/>

generally available at a frequency of not more than 5%. CRISPR-Cas9 also introduces random insertions, deletions, translocations and other base-to-base conversions, which is another limitation associated with CRISPR/Cas9 system.