Scientific assessment of publication by *Podevin and du Jardin (2012)* (*http://www.es.landesbioscience.com/journals/gmcrops/article/21406/?nocache=1759778285*)

A recent paper by Podevin and du Jardin with the title; "Possible consequences of the overlap between the CaMV 35S promoter regions in plant transformation vectors used and the viral gene VI in transgenic plants", was recently published in *GM Crops and Food 3: 1-5.* This paper has created a discussion related to if past approvals of GM events have overlooked key safety questions related to the use of the Cauliflower mosaic virus 35S promoter (P35S) in GM plants.

P35S

Cauliflower mosaic virus (CaMV) is a DNA-containing para-retrovirus replicating by means of reverse transcription. One of the viral promoters, the 35S promoter is generally considered to be a strong constitutive promoter, and it drives high levels of RNA production in a wide variety of plants. It has been used to secure expression of the transgene in most of the GM plants commercialized so far. In the USA alone, 54 of the 86 single GM plants that have been authorized contain one or more copies of this promoter (including Roundup Ready soybeans (40-3-2), MON810 and NK603 maize). Besides studies in E. coli and in different types of yeasts, there are also reports indicating that the 35S promoter might have potential for transcriptional activation in mammalian cell systems.

P35S variants

The P35S variants used in the constructs investigated by Podevin and du Jardin have different sizes and the longest two have an open reading frame (ORF), the shortest one did not contain an ORF. The authors tested the DNA sequences of the two ORFs and concluded, "*no significant hits were obtained to the toxins and allergens database using the DNA sequences of the two 35S promoters…"* This conclusion was reached by using BLASTx of the translated sequences of two P35S against a toxin database. This approach ignores the potential availability of protein domains of toxins and allergens in the linear translated sequences. Domains are the functional portions of proteins and consist of at least 25 amino acids. If a domain search shows no hit against known toxic proteins, it should not be concluded that potential toxins might not be found in the future because the domain databases as collections of protein domains are constantly updated.

Conclusions

- The shortest functional P35S variant should be used in GM plants to avoid new ORFs.
- A potential change in the plant phenotype in new GM plants can be identified by transcriptomics, proteomics, or other profiling technology.
- Applicants or producers of GM plants should provide the genetic information concerning new ORFs to the regulators.

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