Is the Hidden Viral Gene Safe? GMO Regulators Fail to Convince

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Having unwittingly allowed a viral gene into the food chain, the response of regulators so far has been to release statements intended to allay public concerns. These statements, however, are inadequate to meet a potentially major food crisis. Not only do they fail to address important issues but they are also scientifically questionable even within their chosen frame of reference.

The GMO regulators involved are the European Food Safety Authority (EFSA) and Food Standards Australia New Zealand (FSANZ). These two agencies have separately released statements (see complete texts EFSA and FSANZ) defending their risk assessments and conclusions in response to our recent article "Regulators Discover a Hidden Viral Gene in GMO crops".

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This article, published by *Independent Science News* (*ISN*), addressed a recent scientific publication that showed GMO regulators have repeatedly approved crops carrying a transgenic viral sequence they did not realize also encoded part of a viral gene (Podevin and du Jardin 2012). The 'hidden' viral gene in question is called Gene VI and it resides within a DNA sequence called the cauliflower mosaic virus (CaMV) 35S promoter. The CaMV 35S promoter is important for the reason that it is almost ubiquitously used in commercial GMOs. In the *ISN* article we further proposed that Gene VI of CaMV represents a potential threat to crop health and human health.

In this second article we now question the two statements being offered to the public and journalists by EFSA and FSANZ. The credibility and effectiveness of regulators rests on their actions being based on 1) scientific knowledge, 2) scientific integrity, and 3) the public interest. We assess the EFSA and FSANZ statements and find them to be both scientifically misleading and also inadequate to meet the public interest concerns raised by the discovery of Gene VI. This is due to their reliance on scientifically unverifiable assertions and logical fallacies. We also here draw attention to important scientific questions raised by the recognition of Gene VI within the CaMV promoter that regulators have yet to address.

Regulators Misrepresent the State of Scientific Knowledge

The following six quotes are extracted from the statements by EFSA and FSANZ

1) "*Human exposure to DNA from the cauliflower mosaic virus and all its protein products through consumption of conventional foods is common and there is no evidence of any adverse health effects.*" (FSANZ)

In order for this statement to be supported by scientific data there would have to exist controlled experiments feeding CaMV DNA, or its viral proteins, to experimental subjects (animal or human). In addition, there would also have to be epidemiological data linking CaMV consumption (which as FSANZ notes appears to be common enough for this to be done) with human health status. To our knowledge, experiments have not been done in either area, and we challenge FSANZ to provide scientific references for this statement. Without relevant experiments absence of evidence is not evidence of absence. It is especially inappropriate given the high and sometimes increasing rates of diet-related chronic illness in countries consuming the most GMOs.

FSANZ's conclusion also contradicts that of Podevin and du Jardin, who first discovered the problem. These authors specifically do not state that there is *"no evidence of any adverse health effects."* On the contrary, their analysis implied Gene VI might be both an allergen and a source of harm as a viral gene. They found that Gene VI "*is a potential allergen*" (this finding, perhaps because their results were contradictory, was in the conclusions amended to "*is most likely not a potential allergen*") and further, they stated that some versions of Gene VI "*might result in unintended phenotypic changes*" (Podevin and du Jardin 2012).

Whether one looks at the larger picture, or the details, there is no scientific case for the strong reassurance offered by FSANZ.

2) "*Genes from the virus in question have been used safely in transgenic plants for almost 30 years*" (FSANZ)

The safe history of transgenic plant use is a matter of speculation. Direct animal feeding studies are contradictory and epidemiological studies on actual human populations are lacking. The scientific literature contains multiple reports of harm towards animals from transgenic crops which could have been acknowledged, including recently a paper by the group of Seralini (2012). These reports go back to the 1999 *Lancet* publication of Ewen and Pusztai which attributed some of the intestinal abnormalities they observed in rats fed GM potatoes to something other than the transgenic protein itself. At the time they speculated, to widespread disbelief, that part of the DNA construct (which included the CaMV 35S promoter) was potentially the cause (Ewen and Pusztai 1999). It is possible that what Ewen and Pusztai observed is explained by the presence of Gene VI fragments.

The strong and repeated impression created by GMO regulators in general is that they believe experiments reporting harm do not merit citation, nor require repeating. This is despite the fact that recognition of alternative hypotheses and repeated experimental testing are the accepted methods of resolving scientific differences and advancing scientific understanding. In sharp contrast, the attitude of regulators appears to be that the presumption of safety is as good as the demonstration of it.

3) "*Genes from the virus in question have been extensively characterised*" (FSANZ)

Characterization of CaMV and its genome is an active scientific field in which research is ongoing. As we pointed out (in Regulators Discover), a new function for Gene VI was identified even while Podevin and du Jardin's publication was in press (Love et al. 2012). To imply that sufficient and definitive knowledge has emerged about a scientific subject is to contradict a basic premise of scientific enquiry.

4) "*There is no credible scientific evidence suggesting its (Gene VI) use poses a risk to human health or safety*" (FSANZ)

As we discussed (in Regulators Discover), a body of scientific work spanning twenty years describes Gene VI as a plant toxin; as interfering with host plant defenses; as interfering with the basic mechanism of protein production (which is common to humans, animals, and plants); and lastly as a disruptor of RNA silencing (also a conserved biological mechanism shared by plants, animals, and humans) (e.g. Park et al. 2001; Love et al. 2012). These facts are clearly established in the scientific literature, even to the point of some of these specific functions being attributed to distinct regions of Gene VI. Thus, in the scientific literature they are not in dispute. Regulators should make clear how the scientific understanding of viral Gene VI is consistent with their allowing it (or a fragment of it) to be present in the food supply. [For a discussion of gene fragments and their significance to Gene VI see footnote (1)].

5) "*The viral gene (Gene VI) belongs to a plant virus (Cauliflower Mosaic virus) that cannot infect animals or humans*" (EFSA)

This is a misleading statement. We agree that CaMV is not a normal human pathogen; however, the more relevant scientific question is whether CaMV can reproduce itself inside individual human cells and interfere with their normal functioning. To our knowledge, there have been no attempts made to infect animal cells or human cells with CaMV in a scientific experiment. Without such specific experiments EFSA's statement is scientifically unverifiable and unsupported. We are not surprised, therefore, that when asked to provide supporting data for this statement EFSA failed to do so (2). It is known, however, that parts of CaMV are functional in mammals. The CaMV 35S promoter is active in hamster and human cell lines (Tepfer et al. 2004; Myhre et al. 2006). Thus the only pertinent scientific evidence casts active doubt on the accuracy of EFSA's statement.

6) "*(Gene VI) therefore presents no threat to human or animal health*" (EFSA)

This statement is formally linked by EFSA to the one above (Point 5). Even were its premise (that CaMV is not itself harmful) to be scientifically established, it is nevertheless false to equate the hazards of a living, replicating viral infection with the hazards from a gene fragment found (and potentially highly expressed) in every cell of a GMO food plant. A partial list of the situations in which they potentially (or actually) are dissimilar would include:

a) As discussed (in Regulators Discover), depending on the specifics of its genome integration into commercial GMOs, Gene VI DNA may produce either a simple viral protein fragment or a chimeric (part-viral) protein. In either case the result will not be equivalent in structure, cellular

location, or quantity, to any protein produced by the virus.

b) The natural hosts of CaMV are plants in the brassica family (Schoelz 2008). Gene VI in GMO crops is found commercially mainly in soybeans, cotton, maize and canola. Only the latter is a brassica. Therefore, the genetic and physiological context of transgenic Gene VI is typically not equivalent to a natural viral infection.

c) Gene VI in nature is produced in the context of an active viral infection process. If Gene VI is expressed in a transgenic plant this will mostly occur in uninfected cells where it will not be interacting with other CaMV proteins. Many potentially important differences arise from this fact. Viral proteins are commonly modified by viral infection (Hellen 1989), are differently active in the presence of other viral proteins (Asai et al. 2006), or transport each other to different cellular compartments (Sanderfoot and Lazarowitz 1995).

A simple hypothetical example illustrates the potential implications. Gene VI is known to disrupt protein production, but if it requires other viral components to transport it to where protein production occurs, then it could be harmless while inside a transgenic plant but could still be toxic to humans when cells are broken open during consumption. This series of events is far from implausible. Some of the most common plant toxins are the cyanogenic glycosides, and they work in just this way to release cyanide when tissues are chewed (Poulton 1990).

Thus one can reasonably propose, that in the presence of the virus itself, intact Gene VI may behave even radically differently compared to a transgenic protein fragment encoded in a CaMV promoter. It may therefore present a substantially different risk. For both EFSA and FSANZ to use the implied safety of CaMV (which as mentioned has never been established) to infer the inherent safety of Gene VI fragments is therefore misleading. Such arguments are irrelevant distractions from the much less reassuring actual scientific information that does exist about Gene VI and which was discussed in detail in our previous article.

In summary, in their statements, EFSA and FSANZ assemble arguments that are either irrelevant (such as that CaMV is a normal part of the diet or that CaMV is toxicologically equivalent to Gene VI) or are based on unsubstantiated assertions. Consequently, through a series of logical flaws and assumptions, EFSA and FSANZ misrepresent both the state and the certainty of scientific knowledge regarding Gene VI. It is potentially acceptable for regulators to condense or simplify complex scientific information to educate or inform a lay public. What is not acceptable, however, is to 'inform' the public with misinformation.

The truly important safety concern is that the weaknesses of regulators' arguments stem from a fundamental cause. In comparison to the evidence showing potential for serious harm, there are no solid experimental or epidemiological data supporting the proposition that Gene VI, or fragments thereof, are harmless.

Regulators Fail to Address Key Findings

An important scientific question was left unanswered by regulators' official statements. Once the CaMV 35S promoter was identified as encoding a viral gene, regulators should have

investigated whether related promoters approved by them also encoded viral genes (3). Our previous article showed that they do. The FMV 35S promoter of figwort mosaic virus overlaps its cognate Gene VI. Various versions of the FMV 35S promoter have been incorporated into numerous GMO crops produced by Monsanto, including maize (**MON89034**), soybean (**MON89778** and **MON87705**), sugar beet (**H7-1**), cotton (**MON88913**), and canola (**GT73**). The longest of these FMV promoters has been commercialized in the EU, Australia, New Zealand, as well as the US, and is described in applications as being 562 base pairs in length, which is close to half the length of the entire Gene VI. Nevertheless, the FMV Gene VI has not so far been acknowledged by EFSA, FSANZ, or Podevin and du Jardin.

This additional discovery has many regulatory and biosafety implications, but the one most relevant here is that the reassurances offered so far by EFSA and FSANZ, while scientifically inadequate, are also primarily specific to Gene VI of CaMV. They do not apply to FMV which was isolated from figwort (*Scrophularia californica*) a wild species native to the southwestern US. Figwort and FMV have neither a history of widespread consumption, nor positive scientific evidence for safety.

For public safety reasons we ask why have regulators not acknowledged that FMV 35S promoters pose the same (or greater) risk of harm? What attempts are EFSA and FSANZ making to address the public safety issues with FMV Gene VI in the food supply (4)?

Conclusions

There are presently three distinct assessments of the hazards arising from the presence of Gene VI sequences in GMOs. Regulators FSANZ and EFSA are offering categorical reassurances that, with respect to Gene VI in CaMV, "*there is no evidence of adverse health effects*" (FSANZ), that "*there are no scientific grounds for reviewing approvals*" (FSANZ) and "*no safety concerns were identified*" (EFSA).

In contrast, Podevin and du Jardin wrote that, depending on the length of Gene VI inserted, Gene VI "*might result in unintended phenotypic changes*", that "*unintended effects*" were "*unlikely*", that "*unintended effects*" had a "*low likelihood*". Moreover, their data show that (in addition to its viral functions) the protein product of Gene VI, according to a standard algorithm "*is a potential allergen*". These conclusions, though imprecisely defined, are distinguishable from zero risk and appear incompatible with the categorical reassurances of EFSA and FSANZ. This is a noteworthy discrepancy in that it clearly appears to contradict the supposed reliance of regulators on the peer-reviewed scientific literature.

Our own analysis takes a third position. Based on a review of known functions of Gene VI we went further and stated that Gene VI "*might not be safe for human consumption*" and "*may disturb the normal functioning of crops*". We also noted, unlike EFSA, FSANZ, and Podevin and du Jardin, that FMV promoters also overlap FMV Gene VI. Therefore, we recommended a recall of Gene VI-containing GMO crops.

This recommendation for a recall, which we reiterate here, was based on transparent reasoning and clear scientific evidence of (i) Gene VI plant toxicity and potential human toxicity, (ii) that

Gene VI is an incompletely-characterized gene derived from a pathogen, (iii) that transgenic Gene VI can cause infection of crops by novel pathogens and, (iv) there exists a clear possibility that Gene VI could become expressed in commercial GMOs. We believe that, if these facts had been known to regulators in advance, such a gene would never have been approved.

We also note some additional facts in this case:
(1) By approving transgenes containing viral sequences, regulators have placed the public in an entirely *unnecessary* position of risk (since non-viral promoters were available).
(2) The failure of regulators to identify Gene VI in initial assessments occurred in spite of a "*detailed examination of the inserted sequence*" (EFSA), and even though Gene VI was described in the scientific literature as long ago as 1980.
(3) As a consequence regulators have been forced to enter into a retrospective discussion of the hazards of Gene VI of CaMV (and have apparently yet to do so for Gene VI of FMV).
(4) Regulators have failed to implement the GMO monitoring procedures that might have offered protection against such regulatory failures. Monitoring would have allowed regulators to definitively place scientific limits on the extent of the harm from Gene VI in commercial crops and in the food chain.

These four reasons alone define this episode as a categorical and systemic failure of risk assessment. But the cumulative errors are now substantively increased by the evasions, the misrepresentations of scientific knowledge, and the logical flaws contained in regulators' 'reassurances'.

Combined with other recent scientific reversals and repeated questions over conflicts of interest, EFSA's credibility is at a low point. Three immediate actions would begin to restore confidence that EFSA is now acting in accordance with the scientific evidence and the public interest. The first would be to ban the future use of viral sequences in commercial GMOs; the second would be to recall transgenic events containing CaMV and FMV 35S promoters; the third would be to implement meaningful GMO monitoring. These actions will have the further benefit of sending a clear signal to GMO developers that safety needs to be built into GMOs and that regulators will not tolerate unnecessary hazards and risks.

Footnotes
1) *The scientific literature describes numerous functional gene and protein fragments.* They include many transgenic proteins. For example, most insecticidal Bt toxins (the Cry proteins) in commercial GMOs are fragments and do not produce the full length native protein. In the case of the Cry protein in MON810 (a GMO maize event in commercial use) sequences are missing from both ends of the native protein as the result of an accident during transgene insertion (Freese and Schubert 2004).

EFSA and FSANZ could also have noted that viral proteins, presumably because they are often multifunctional, can even gain extra functions when expressed as fragments (Nagano et al. 2001).

And finally, the infamous US corn failures of 1971 and 1972, which were the most widespread genetic failures of a crop plant ever recorded, resulted from a spontaneous genetic

rearrangement that created a novel gene called T-urf13 (Ullstrup 1972). T-urf13 produced a protein fragment comparable in size to the smallest Gene VI sequence identified by Podevin and du Jardin. It is a fusion protein created from at least three separate genes (Levings 1990), and confers almost total susceptibility to the maize pathogen southern corn leaf blight (*Bipolaris maydis*; race T). The result, since T-urf13 was in almost universal use, was the substantial destruction of the US corn crop two years in succession. The T-urf13 incident is a highly relevant model for how Gene VI could be expressed as a fusion protein in a widely grown transgenic event and cause widespread harm.

The above are only a few of many examples.

2) *When asked for supporting data, EFSA declined to identify specific experiments*. The following is from an exchange of letters between EFSA and Fran Murrell of MADGE, Australia (Feb 2013):

Dear EFSA
In your "FAQ on inserted fragment of viral gene in GM plant"
you say:

"*The viral gene (Gene VI) belongs to a plant virus (Cauliflower Mosaic virus) that cannot infect animals or humans and therefore presents no threat to human or animal health. This virus naturally infects many plants with no recorded health effects.*"

Can you please send me references to support:
a) the claim that the CaMV virus can't infect humans/animals.
b) research into the health effects of CaMV

Many thanks, Fran Murrell
EFSA's Answer:

Dear Mr Murell,
Thank you for your email and interest in the European Food Safety Authority (EFSA).

a) It is generally accepted by the scientific community that plant viruses cannot infect animals and vice-versa. To date, there are no known cases of a plant viruses which can infect vertebrates or humans(1,2). This is also the case of CaMV, for which the only described hosts are plants (3).

b) There are no reported health effects on the CaMV, in spite that it is estimated that ca 10% of the cauliflowers and cabbages are infected with CaMV (4). With respect to the gene VI of CaMV, recent investigations did not find any similarity to known toxins or allergens (5).

References
1. Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA, editors (2005). Virus Taxonomy, VIIIth Report of the ICTV. London, UK: Elsevier. 1259 p.
2. Jones RA (2009). Plant virus emergence and evolution: Origins, new encounter scenarios, factors driving emergence, effects of changing world conditions, and prospects for control.

Virus Research 141: 113-130.
3. Brunt AA, Crabtree K, Dallwitz MJ, Gibbs AJ, Watson L, Zurcher EJ, editors (1996). Plant Viruses Online: Descriptions and Lists from the VIDE Database. (http://pvo.bio-mirror.cn /descr184.htm)
4. Hull R, Covey SN, Dale P, (2000). Genetically modified plants and the 35S promoter: assessing the risks and enhancing the debate. Microbial Ecology in Health and Disease 12: 1-5
5. Podevin N, and du Jardin P, (2012). Possible consequences of the overlap between the CaMV 35S promoter regions in plant transformation vectors used and the viral gene VI in transgenic plants. GM Crops and Food 3: 1-5

Conclusion: EFSA again failed to provide specific evidence of feeding studies or epidemiological studies of CaMV toxicity.

3) *There is a wealth of evidence that regulators had no prior knowledge of Gene VI*. FSANZ, for example, wrote in its 2005 "Final Assessment Report" to approve Monsanto's **MON88913** cotton:

"*Although CaMV is a known plant pathogen, only a single fragment of the CaMV genome corresponding to a promoter, has been transferred into cotton (Odell et al 1985). No other DNA fragments, including genes that code for pathogenicity of the virus, has been transferred into cotton line* ***MON88913***."

FSANZ describes it here as "*only*" a "*promoter*". As in other regulatory documents, there is no recognition or mention of Gene VI. Thus the Podevin and du Jardin publication is the first public document produced by regulators to expressly mention Gene VI by name.

4) *Why further experiments are unlikely to promptly and adequately resolve the safety issues surrounding Gene VI*: A frequently asked question has been whether further experiments can resolve the safety issues surrounding Gene VI. Two distinct issues seem relevant. The first is that further experiments take time. It will be many years before they yield answers, during which time the public will continue to be exposed to any hazards arising from expression of Gene VI sequences. That is the simple reason why such experiments are normally done before commercialization. In this case, if the existence of a gene that is toxic to plants, that enhances pathogen vulnerability, that derails protein production and inhibits RNA silencing, had been known to regulators beforehand it seems inconceivable that they would have approved it. Therefore, a recall decision is appropriate and can be made with the data available now.

The second issue relates to the practical limitations of science itself. The limitations of science are rarely discussed, in part because they often only come to the fore in issues such as this, when risk assessment or drug development require laboratory-based science to be tested in the real world. The general form of these limitations is that experiments, either on the functions (or toxicity) of Gene VI itself, or its expression from individual transgenic events, are unlikely to give results that are definitive. There are several reasons for this.

i) Any single experimental methodology, or even set of experiments, that could be proposed, from transcriptomics to proteomics (to quantify Gene VI expression); or animal feeding

experiments to determine toxicity; or even including DNA sequence analysis of individual insertion events (to look for open reading frames), necessarily have numerous and significant limitations. These quickly become evident in high-stakes discussions of any scientific subject. Thus, for example, proteomics experiments can in theory detect the presence (or absence) of proteins but their sensitivity is inevitably limited.

In one experiment relevant to the present case proteomics failed to detect a transgenic enzyme conferring antibiotic resistance even though it was confirmed to have been present and active (Corpillo et al. 2004). As another example, sequencing of transgenic events is widely regarded (unlike proteomics) as definitive, but to determine the *meaning* of that sequence, e.g. whether an open reading frame is functional or expressed, is a hard problem since the sequence requires interpretation. Moreover, there are additional complicating factors, such as splicing of mRNAs, that make DNA sequencing an imperfect predictor of gene expression (Rang et al. 2005). Thus EFSA claims to have conducted a "*detailed examination of the inserted sequence*" but they still missed Gene VI.

ii) Scientific findings are normally considered in the abstract. It is rarely acknowledged that, especially in biology, experiments are specific to a particular time and location. This limitation comes to the fore in risk assessments that require specific and detailed information about a complex real-world situation.

Thus each transgenic Gene VI fragment is a novel sequence in a unique genomic location in a specific crop variety that will be grown in variable field and soil conditions. This series of unique parameters means that any data collected under one or a few sets of conditions may be invalid under others. For this same reason, data from any one Gene VI transgene insertion event have only limited relevance to any other event. Regulatory science typically depends on ignoring such problems, but they are very real.

iii) A third complication is that even successful and rigorous experiments, performed under the most relevant conditions, do not necessarily yield more certainty. Sometimes, such as when they overturn widely held assumptions, they yield less. This may seem counterintuitive because science is often conceptualized as 'progress' towards a definitive or single truth, but actually this progress is largely an illusion caused by a limited frame of reference.

These three points are not meant as obscurantism. We believe that experiments are the key to furthering understanding, but we also recognize that their meaning can be obscure and that worthwhile risk assessment is slow. A scientific reductionism that imagines safety issues can be dealt with quickly and definitively by a few experiments fails to take into account the nature of biology and the nature of scientific understanding. We might have learned by now to not have unreasonable expectations of science, especially in biology. If, forty years after it started, the war on cancer is still not won, it is because there are good reasons for that.

The consequence of all this is that a broad perspective includes respecting the fact that the highest purpose of risk assessment is to protect the public. A recall, therefore, should be the priority. Experiments can be done later, or in parallel.

References

Asai R, A Kato, K Kato, M Kanamori-Koyama, K Sugimoto, T Sairenji, Y Nishiyama and Kawaguchi Y (2006) Epstein-Barr Virus Protein Kinase BGLF4 Is a Virion Tegument Protein That Dissociates from Virions in a Phosphorylation-Dependent Process and Phosphorylates the Viral Immediate-Early Protein BZLF1. J Virol. 80: 5125–5134.

Corpillo D, G Gardini1, AM Vaira, M Basso, S Aime, GP Accotto, M Fasano (2004) Proteomics as a tool to improve investigation of substantial equivalence in genetically modified organisms: The case of a virus-resistant tomato. Proteomics 4: 193-200.

Ewen S and Pusztai A (1999) Effect of diets containing genetically modified potatoes expressing *Galanthus nivalis* lectin on rat small intestine. The Lancet 354 1353-54.

Freese W and Schubert D (2004) Safety Testing and Regulation of Genetically Engineered Foods. (2004), Biotechnology and Genetic Engineering Reviews 21: 299-324.

Hellen CUT, HG Kraeusslich, E Wimmer (1989) Proteolytic processing of polyproteins in the replication of RNA viruses. Biochemistry 28: 9881–9890.

Ioannidis JPA (2005) Why Most Published Research Findings Are False. PLoS Med 2(8): e124. doi:10.1371/journal.pmed.0020124

Levings CS (1990) The Texas cytoplasm of maize: Cytoplasmic Male Sterility and Disease Susceptibility Science 250: 942-947.

Love AJ, C Geri, J Laird, C Carr, BW Yun, GJ Loake et al. (2012) Cauliflower mosaic virus Protein P6 Inhibits Signaling Responses to Salicylic Acid and Regulates Innate Immunity. PLoS One. 7(10): e47535.

Myhre MR, Fenton KA, Eggert J, Nielsen KM, Traavik T (2006) The 35S CaMV plant virus promoter is active in human enterocyte-like cells. Eur Food Res and Technology 222: 185-193.

Nagano H, K Mise, I Furusawa, T Okuno (2001) Conversion in the Requirement of Coat Protein in Cell-to-Cell Movement Mediated by the Cucumber Mosaic Virus Movement Protein. Journal of Virology 75: 8045–8053.

Odell JT, F Nagy, NH Chua (1985) Identification of DNA sequences required for activity of the cauliflower mosaic virus 35S promoter. Nature 313: 810-812.

Park H-S, Himmelbach A, Browning KS, Hohn T, and Ryabova LA (2001). A plant viral 'reinitiation' factor interacts with the host translational machinery. Cell 106: 723–733.

Podevin N and du Jardin P (2012) Possible consequences of the overlap between the CaMV 35S promoter regions in plant transformation vectors used and the viral gene VI in transgenic plants. GM Crops and Food 3: 1-5.

Poulton J (1990) Cyanogenesis in Plants. Plant Physiology 94: 401-405.

Rang A, B Linke, B Jansen (2005) Detection of RNA variants transcribed from the transgene in

Roundup Ready soybean. European Food Research and Technology 220: 438-443.

Sanderfoot AA, SG Lazarowitz (1995) Cooperation in Viral Movement: The Geminivirus BL1 Movement Protein Interacts with BR1 and Redirects It from the Nucleus to the Cell Periphery. The Plant Cell 7: 1185-1194.

Schoelz JE (2008) Caulimoviruses: General Features. 457-464. Encyclopedia of Virology 3rd Edition (Elsevier, Oxford).

Séralini, G-E., E. Clair, R. Mesnage, S. Gress, N. Defarge, M. Malatesta, D. Hennequin, J. Spiroux de Vendômois. 2012. Long term toxicity of a Roundup herbicide and a Roundup-tolerant genetically modified maize. Food Chem. Toxicol. 50: 4221–4231.

Tepfer M, Gaubert S, Leroux-Coyau M, Prince S, Houdebine L-M (2004) Transient expression in mammalian cells of transgenes transcribed from the Cauliflower mosaic virus 35S promoter. Environmental Biosafety Research 3: 91-97.

Ullstrup AJ (1972) The impacts of the southern corn leaf blight epidemics of 1970-1971. Annual Review of Phytopathology 10: 37-50.

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