Collaborative Campaigning for Food Sovereignty & Environmental Justice

June 23, 2021

Comments submitted by the Canadian Biotechnology Action Network to Bureau of Microbial Hazards, Food Directorate, Health Canada

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RE: Consultation: Proposed new guidance pieces for the Novel Foods Regulations, focused on plant breeding

Response to "A Primer on Gene editing technology in relation to Health Canada's product-based regulatory framework for Novel Foods"

The Canadian Biotechnology Action Network (CBAN) is writing to provide comment on Health Canada's "A Primer on Gene editing technology in relation to Health Canada's product-based regulatory framework for Novel Foods" which appears as Annex 2 to the consultation document "Proposed Changes to Health Canada Guidance on the interpretation of Division 28 of Part B of the *Food and Drug Regulations (the Novel Food Regulations*): When is a food that was derived from a plant developed through breeding a "novel food"?)"

This response is in addition to comments on the proposed new regulatory guidance submitted by CBAN on May 11, 2021.

The Canadian Biotechnology Action Network (CBAN) brings together 16 groups to research, monitor and raise awareness about issues relating to genetic engineering in food and farming. CBAN members include farmer associations, environmental and social justice organizations, and regional coalitions of grassroots groups across Canada: Canadian Organic Growers, Check Your Head, Council of Canadians, Ecology Action Centre (NS), Ecological Farmers Association of Ontario, GE Free BC Network, Greenpeace Canada, Growers or Organic Food Yukon, Inter Pares, National Farmers Union, No More GMOs Toronto, GMO-Free PEI, Organic Agriculture Protection Fund of SaskOrganics, Union Paysanne, SeedChange, Vigilance OGM. CBAN is a project on the shared platform of MakeWay Charitable Society. **www.cban.ca**

CBAN thanks Dr Ricarda Steinbrecher for assistance with scientific aspects of this response. Please see the Annex for Dr Steinbrecher's biography.

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Notes on terminology

The term genome editing is commonly used in the scientific literature to refer to the new genetic engineering techniques that are here referred to by Health Canada as "gene editing."

As discussed in Kawall et al. (2020), using the term gene editing would not include the alterations of multiple genes or regulatory genomic elements like enhancers or noncoding RNAs that are possible with these techniques. The term, for example, does not recognise that whole gene families (like all gluten genes) can be modified at one time (by multiplexing).

Additionally, gene sequences and their role and actions are dependent on context and interaction with other sequences. They cannot be fully understood outside their context or in isolation from the rest of the genome. The term gene editing may imply that only a single gene is altered or affected, out of context of the genome and irrespective of the impact on the genome. Therefore, the use of the term genome editing is preferred over gene editing and used throughout our response.

The term genome editing is also widely used in processes of the UN Convention on Biological Diversity and the term "new genomic techniques" is used by the European Commission and the European Food Safety Authority.

A. Overview

The Canadian Biotechnology Action Network is deeply concerned by the presentation of "A Primer on Gene editing technology in relation to Health Canada's product-based regulatory framework for Novel Foods" to the Canadian public as part of Health Canada's public consultation on new regulatory guidance for the products of genetic engineering.

The primer was provided to the public as an annex to one of Health Canada's two consultation documents and Health Canada says it "informs the Department's proposed position on how foods derived from gene-edited plants are to be regulated." However, **the primer does not provide a scientific rationale for the regulatory guidance proposals**, nor does it provide a description of the technology and regulatory issues for the public. The primer does not reflect the "**review of the current scientific knowledge** regarding the use of gene editing technologies" [emphasis added] that is mentioned in the primer summary. On the contrary, **the primer provides little information and little science**.

The primer provides no evidence of a "thorough scientific literature review," the "details" of which were, according to a March 2021 letter from Health Canada to CBAN, to be "included as part of Health Canada's consultation" (McIntyre 2021). (Please see the below Introduction for a discussion of this correspondence between CBAN and The Minister of Health.)

The primer is insubstantial, incomplete, imprecise, and inappropriate.

The proposal to allow some genetically engineered foods (genetically modified organisms or GMOs) - produced through new techniques - onto the market with no government oversight demands that Health Canada provide a solid science-based justification. The onus for stating the case rests with Health Canada. However, the primer does not argue the case as to why some foods from genome edited plants that have no foreign DNA could safely be exempt from government safety assessment. Rather than provide a scientific rationale for the proposals, the primer repeats many of the statements about genome editing that are made in the consultation documents, without discussing the science behind them. The primer is lacking depth and scientific rigour. This amounts to **a shallow and uneven summary of the assumptions that underlie the approach behind Health Canada's regulatory guidance proposals**. The primer is a poorly designed basis for public consultation.

In our estimation, there is only one section of the primer – Section 4: "Gene editing technologies – unintended off-target edits" – that discusses issues with any depth or relevance. However, this section is narrowly focused on "off-target edits" which is just one sub-category of unintended effects that can result from genome editing. **The primer omits discussion of a range of unintended effects that should be central to discussing the science behind the regulatory guidance proposals. In this respect, Health Canada's presentation of the science is negligent and appears biased**.

We are genuinely concerned that the lack of scientific information, analysis and questioning in the primer, and the state of this presentation, may reflect a cavalier attitude towards:

- the science,
- the regulatory guidance proposals and related public consultation,
- public transparency and accountability in relation to the regulation of genetic engineering,
- the responsibilities of the regulator, and/or
- the safety of genetically engineered foods.

The Canadian Biotechnology Action Network reiterates our good faith engagement in this consultation process and the depth of our interest in the issue of genetic engineering to improve democratic governance and the sustainability of our food system. CBAN is a network of 16 groups, representing diverse communities and a wide range of interests across Canada. We have written numerous reports that document issues of concern with the use of genetic engineering in food and farming and with government regulation and policy. We have most recently published a report on genome editing that highlights many of the issues and science missing from Health Canada's primer (Canadian Biotechnology Action Network 2020). As the regulators responsible for the safety of genetic engineering in our food supply, **we ask Health Canada to demonstrate due diligence in examining the risks of genome editing and to display an appropriate interest in evidence-based decision-making and public transparency**.

B. Introduction

Health Canada's "primer" does not reflect a rigorous scientific literature review nor the most current scientific knowledge, and it does not allow for Health Canada's conclusion that "the use of gene editing technologies does not present any unique safety concerns compared to other methods of plant breeding."

In advance of Health Canada's March 25, 2021 consultation launch and publication of the primer, in response to a letter of concern from CBAN to the Minister of Health on March 3, Health Canada wrote on March 17 to CBAN to say that,

> *"Health Canada has undertaken a comprehensive effort to develop a proposed policy that is **informed by the most current scientific information** about modern plant breeding and gene editing techniques. This includes discussions with academics, public sector plant breeders, private sector breeders, and reviews of the scientific literature."* *[emphasis added]*

The letter from Health Canada to CBAN also stated that,

> *"In the summer of 2020, **Health Canada conducted a thorough scientific literature review** regarding gene-edited plants used for food. In addition, the Department **engaged various scientific experts in the field of plant breeding and gene editing to validate the scientific review. Details of this review will be included as part of Health Canada's consultation**, which will be launched shortly...Health Canada has reviewed all information obtained through its scientific review, the information sessions and the expert panel to inform its proposed guidance."* *[emphasis added]*

The Canadian Biotechnology Action Network is therefore surprised by the publication of a type of summary in the form of a "primer" which fails to provide information that reflects a rigorous scientific literature review and that does not allow for the conclusion stated by Health Canada in their letter to CBAN, that,

> *"Current findings show that gene-edited plants are as safe as their conventionally bred counterparts. Gene editing allows for improved precision when developing new plants and is subject to the same rigorous breeding practices as conventionally bred plants."*

The primer does not provide a scientific rationale for Health Canada's regulatory guidance proposals that would exempt many genome-edited GMOs from government oversight. The summary of the primer says,

> *"Through **a review of the current scientific knowledge** regarding the use of gene editing technologies to develop new plant varieties, Health Canada concludes that the use of gene editing technologies does not present any unique safety concerns compared to other methods of plant breeding. By consequence, foods derived from gene-edited plants are subject to the same considerations that determine the novelty status of all products of plant breeding, including the new elements of guidance presented in this consultation document."* *[emphasis added]*

However, the primer does not reflect such a review and does not reflect the current scientific knowledge. Furthermore, the primer does not provide the information and analysis to allow for this stated conclusion and to justify the proposal to exempt many foods from genome edited plants from a Health Canada safety assessment.

By any measure, the primer is insubstantial and insufficient.

C. The Primer

The purpose of the primer is not clear because the document does not provide a scientific rationale for the proposals, nor does it offer the public or product developers clear information about genome editing or the issues relating to regulation. The content and format, including the lack of comprehensive scientific background information regarding safety claims or lack of risk, make this primer inappropriate and inadequate for a scientific or lay audience.

Our specific response to the primer content focuses on section 4 “Gene editing technologies – unintentional off-target edits” as the only section of the document that discusses the science with any specificity and coherence to invite such a response. However, the section discusses the science in a restricted and selective manner such that it does not engage in a full discussion of unintended effects.

The content and presentation of the primer does not mirror the significance of Health Canada’s regulatory guidance proposals. In our view, it provides a lot of irrelevant and inadequate information and little pertinent analysis. The primer appears as a four-page document that cites 18 scientific papers. The brevity of the document and paucity of references may not have been problematic if the summary was clearly written. Instead, we observe a cursory and careless treatment of the scientific literature, including of the references cited. The primer does not meet CBAN’s expectations as raised by Health Canada in their letter of March 17.

The primer content is insubstantial

The content of the primer is not informative, and it does provide a clear discussion or summary of the regulatory issues and/or the science of genome editing for regulation. **With the exception of section 4, the primer sections are short and, in our view, largely pointless because of the lack of information, clarity and scientific rigour**.

Primer section 1 “What is gene editing technology?” does not describe the technology itself nor provide the public with useful information about genome editing. Instead, this section makes general, cursory statements about the character of the techniques and makes the assertion – a statement with no data presented to corroborate it - that genome editing results in “no more unintentional effects” than other technologies.

In reality, the number of unintended effects resulting from any technology can vary significantly due to factors such as experimental conditions, exposure rates and experimental design, and indeed the experience and knowledge of the product developer. As discussed in Eckerstorfer et al. (2019), the various techniques of genome editing are dissimilar in terms of the number of

unintended effects due to off-target activity – with some of the factors influencing the level of unintended activity having been identified. Furthermore, unintended effects are not only a question of numbers as suggested in the primer's statement. The location of unintended alterations (mutations) as well as the kind or type of unintended alterations will largely determine their impacts and severity, and require specific attention. In brief, there are three aspects of unintended alterations that should be fully addressed alongside each other as relevant to risk assessment:

(1) Quantity: how many (unintended) alterations are being induced;

(2) Quality: this relates to and depends on the context where a unintended alteration occurs, which genes are unintentionally altered (DNA sequence as well as epigenetic changes) and which regulatory elements and mechanisms might be altered;

(3) The type of the (unintended) induced alterations: are they point mutations, small insertions or deletions (InDels), larger structural changes such as inversions, translocations, deletions duplications, etc.

Numbers on their own, especially when viewed as an average for the whole set of different genome editing technologies, have little relevance for case-by-case safety assessments.

Primer section 2 "How can gene editing technology be applied to plant breeding?" is one paragraph that makes general statements about what plant developers say about how genome editing could be applied and how the techniques could achieve such changes.

Primer section 3 "Gene editing techniques – creating genetic variation in plants" makes a statement about the ability of genome editing to target locations in the genome for change (referred to in the primer as precision but more accurately referred to as specificity and efficiency) with the concluding sentence, "The precision aspect of gene editing can simplify the food safety evaluation of a new, gene-edited crop and therefore offers the possibility for new products to be developed and commercialized in a timely and efficient manner." This is an example of one of the many throw-away sentences in the primer that provide no objective information of significance in relation to genome editing and the regulatory questions at hand, but repeat assumptions without discussion of the science.

Please see below for a discussion of the primer section 4 "Gene editing technologies – unintentional off-target edits".

Primer section 5 "Gene editing technologies – delivering the gene editing tools to living cells" refers to the role of foreign DNA in genome editing. It merely indicates that many genome edited products may not have foreign DNA remaining in the GMO and reminds the public and product developers that, in the proposals for regulatory guidance, for those GMOs with foreign DNA, "the safety of this new characteristic would have to be substantiated as part of a pre-market safety assessment" while others may not be subject to government oversight. It fails to fully address the issue of delivery systems and their consequences, including a spectrum of unintended alterations (see Unintended Effects below). Instead, it reduces concerns to only the presence of foreign DNA, whilst this is often not easily detected and has been missed even when it is complete genes derived from the bacterial delivery system (Norris et al. 2020).

Primer section 6 "Gene editing technologies – one of many tools plant developers use together to create new plants" makes general statements about plant breeding and field testing to conclude with the sweeping statement that "these unique characteristics [off-target edits and the transfer of DNA sequences encoding the genome editing tools] of gene editing technology will be eliminated from most products."

Primer section 7 "Gene editing – pre-market and post-market product safety" starts with a statement that is irresponsible from a food safety regulatory perspective, even in a product-based system: "The food derived from gene-edited plants is what consumers will be exposed to, not the technology used to create these plants."

The primer either does not fully reflect the scientific review conducted by Health Canada or is reflective of a shallow, incomplete review.

The reference list and the use of the references in the primer indicates a cursory treatment of the issues and of the science. The reference list adds to our concern that we are critiquing a primer that either does not fully reflect the scientific review conducted by Health Canada or reflects a shallow, incomplete review:

- **Five of the 18 scientific papers cited in the primer were missing from the reference list in the consultation document** until CBAN requested a full list of references, prompting Health Canada to publish a corrected consultation document. While we would not want to overstate the consequence of such mistakes that can be made in any institution, this treatment of referencing adds to our concern that the primer reflects an inattention to the scientific literature and a cavalier attitude towards public discussion of the science.
- In some cases, the content of the primer does not accurately reflect the associated referenced paper, for example the use of Wolt et al. (2016) in discussion of "off-target edits" (mentioned below).
- Section 1 of the primer relies heavily on the conclusion of Graham et al. (2020) and explicitly refers the reader to the references of Graham et al. in an apparent attempt to indirectly add more references to the primer. This is an inappropriate referral because the content of Graham et al. was not discussed in any detail. We note that 12 of the 14 authors of that paper disclosed conflicts of interest.
- The reference list includes a 2019 article from the Canadian Grocer, a retailer industry magazine, which we cannot see referred to in the primer or consultation document text and whose purpose is therefore unknown.

D. Unintended Effects: A discussion of section 4 "Gene editing technologies – unintentional off-target edits"

Section 4 of the primer - "Gene editing technologies – unintentional off-target edits" - does not provide sufficient science, analysis or openness. An important range of unintended effects is unacknowledged and omitted from this discussion. **The scope of inquiry is limited to a narrow band of off-target effects that Health Canada refers to as "off-target edits"**.

The primer refers to unintentional "off-target edits", but this is not a widely used term. The primer defines "off-target edits" as "genetic changes that result from the gene editing tools working at genomic sites other than the intended edit site (Wolt et al. 2016)", though Wolt et al. 2016 do not

use the term “off-target edits”. Others using the term tend to be referring to a very limited range of off-target effects that occur at “a site with sequence similarity to the targeted edit region” (Graham et al. 2020). In this respect, the primer focusses on a narrow set of off-target effects, neglecting other off-target effects and a range of other unintended effects. The term “off-target effects” is commonly used when investigating the unintended effects arising from the use of genome editing techniques but has a range of interpretations and excludes, for example, unintended on-target effects.

The appropriate term for the necessary discussion would be “unintended effects”, which can be sub-categorised as laid out below.

Unintended effects: comprising unintended on-target, off-target or non-target effects, and near-target (or on-target) structural effects.

In order to avoid being guided by assumptions and in order to evaluate the available evidence (or lack of it), there is a broad spectrum of potential unintended effects arising from genome editing and the processes involved that should be presented and investigated.

The unintended effects that we expect to be discussed should include:

1. Unintended **on-target** effects

    i. Unintended and unpredicted effects due to the intended loss of function of the targeted gene(s) and all its (their) copies. This would in particular be the case if a gene and/or its products are involved in more than one trait or action.

    The occurrence of such pleiotropic effects is well known and probably common, but often little understood and nearly impossible to predict unless the function and interaction of a gene as well as the consequences of the loss-of-function of this gene have been fully investigated. For example, a range of pleiotropic effects have so far been identified with loss-of-function of certain *‘Mildew resistance locus’ (Mlo)* genes, which on one hand results in increased resistance to mildew, yet will also result in increased susceptibility to other fungal pathogens, yield decrease, display of early leaf senescence and discolouring (chlorosis) etc. In fact, there is a correlation between engineered powdery mildew resistance and unintended pleiotropic phenotypes (Kusch & Panstruga 2017). Strong pleiotropic effects were also described for the inactivation of specific fatty acid desaturase *(FAD2)* genes in the oilseed plant *Camelina sativa*, thought to possibly also enhance its sensitivity to environmental conditions (Morineau et al. 2017). See also Eckerstorfer et al. (2019) for discussion.

    ii. Production of novel RNAs, peptide fragments or proteins due to unintended frameshift mutations or exon-skipping as an unintended result of the intended on-target knock-out mutations (loss-of-function) (Tuladhar et al. 2019, Lalonde et al. 2017, Mou et al. 2017, Kapahnke et al. 2016).

    iii. It is important to assess each of the incapacitated (“knocked-out”) gene copies for frameshift mutations and exon-skipping, as knock-out mutations will usually all have a differently repaired DNA sequence.

    iv. Larger DNA insertions, deletions or inversions have also been observed in target sites.

Whilst assessments of on-target effects are frequently reported for genome editing of mammalian cells, there are only a few reports for plants, for example in rice, where the authors underline the importance of such assessments (Biswas et al. 2020).

2. Unintended **off-target** or **non-target** effects

   Off-target effects are often described as any change that occurs due to the activity of the site-directed nuclease and the resulting consequences, including larger structural chromosomal rearrangements; non-target effects are seen as being due to any of the processes involved, including earlier genetic engineering (when required to insert the gene for the site directed nuclease, e.g. CRISPR/Cas), or protoplast techniques, tissue culture involved etc. Yet at present - when a number of different processes are being used in order to obtain a genome edited plant - a clear distinction between off-target and non-target effects cannot readily be made. As genome editing is a multistep process, the potential unintended effects from every stage need to be considered in safety assessment, with effects including:

   i. Small alterations (deletions, alterations or insertions) of DNA sequences other than the target site due to unspecific off-target cuts by a site directed nuclease (SDN).

      As detailed below (see Genome Editing as Novel), off-target alterations will include genome areas and sequences that are otherwise 'protected' from mutations and would therefore not easily take place with any other method. They would also include mutations at copies of the same off-target gene, which, again, would be highly unlikely to occur with any other methodology. Furthermore, it will also induce different repair mechanisms from those induced by other technologies used thus far. Together, these results demonstrate genome editing as a novel process and technology.

   ii. Small alterations (deletions, alterations or insertions) of DNA sequences other than at the target site due to additional processes involved, e.g. tissue culture, transformation of the plant with an SDN construct (e.g. for CRISPR/Cas) (Wilson et. al 2006).

      The argument that "on average" (Graham et al. 2020, as referenced in the primer) there are "no more" unintended mutations due to genome editing than due to any other methodology or technique is irrelevant for a case-by-case risk assessment because it will not be true for many cases, and it does not take into account the quality or type of mutation. Consequently, these unintended alterations will need to be considered and assessed.

   iii. Larger structural changes of the genome, such as larger translocations, deletions, duplications, inversions, scrambling - anywhere in the genome due to the processes involved, including due to the off-target cutting by an SDN.

      See comment under 2.ii. above.

   iv. As (1.i) above: Unintended and unpredicted effects due to the unintended loss or change of function of an "edited" non-targeted gene and possibly all its copies/alleles.

   v. As (1.ii) above: Unintended and unpredictable effects due to e.g. frameshift mutations in the unintentionally 'edited' and possibly knocked out non-target gene that may give rise to novel RNAs or possibly novel proteins (Tuladhar et al. 2019, Lalonde et al. 2017, Mou et al. 2017, Kapahnke et al. 2016).

vi. Unintended presence of foreign DNA sequences in the genome such as vector DNA or DNA present in the growth medium.

DNA double strand cuts (breakages) allow for the unintentional integration of any DNA present, which was shown in plants for vector DNA derived from transformation processes as well as from transient expression vector, where bacterial DNA was integrated (e.g. Andersson et al. 2017, Zhang et al. 2018). In animal cells, it was found that unintentional inserted foreign DNA fragments can not only be derived from the vector construct (Norris et al. 2020), but may also be derived from the genome of the bacteria used to multiply the vector DNA (e.g. Escherichia coli) or, surprisingly, taken up from the source of the growth medium, such as bovine or goat DNA, or retrotransposon (Ono et al. 2015, 2019).

vii. Presence of extra DNA fragments in the genome derived from the 'transient' provision/ addition of short DNA templates to alter one or two nuclear base pairs at a target site in the process of homology repair of a targeted double-strand break (SDN-2 category).

3. Unintended **near-target (or on-target) structural effects**:

Larger structural genomic changes such as translocations, deletions, duplications, inversions and scrambling of chromosomal sequences near the SDN target site (as well as at the SDN target site).

Whilst this is much better researched for mammalian cells, and may well occur more frequently in mammalian cells, it has been shown to also occur in genome edited plants (Hahn & Nekrasov 2019). Yet no systematic research on this has taken place and it has been recognised that current high-throughput whole genome sequencing methodology is unlikely to detect larger structural rearrangement due to the sequenced DNA fragments being too short.

This list indicates some of what should have been presented and argued in the primer. Instead, the primer does not present any details and avoids possibilities for deliberations and scientific argumentation regarding unintended effects and risks. Instead, the primer claims that all off-target effects are the same as those that may arise with the use of any other technique and concludes that these could and should therefore be discounted as significant for product safety assessment.

E. Genome Editing as Novel

Genome editing is novel technology, with novel capacities and consequences.

An underlying assumption of Health Canada's primer is that naturally occurring or intentionally introduced random mutations are randomly distributed across the whole genome to an equal extent, i.e. "randomly in terms of location within the plant genome (Schnell et al., 2015)", as is expressed in section 3 of the primer and reaffirmed in section 4. However, this understanding is not supported by scientific evidence. On the contrary, **recent publications show that the distribution of mutations is not random across the genome**, but rather that the de novo mutation rate is lower for gene sequences than for non-gene sequences and that particular genes are more protected against de novo mutations than others by the activation of DNA mismatch repair (Belfield et al. 2018, Huang et al. 2018, Monroe et al. 2020).

For example, studies in *Arabidopsis thaliana* have shown that the DNA mismatch repair will particularly check and correct those sequences that are part of genes, thus leading to a lower natural or induced mutation rate for those sequences (Belfield et al. 2018). Monroe et al. (2020) find that a combination of different features provide a higher protective status for certain genes and gene sequences, namely: (a) a combination of the DNA sequence and its epigenetic status, together termed cytogenetic features, which relate to the packaging and methylation state of a sequence, related to histone modifications, and chromatin accessibility; (b) the physical distancing of coding sequences away from mutational hotspots with the help of introns (non-coding spacers within a gene) and longer untranslated regions (UTRs) (genes lacking introns were found to have a 90 percent higher mutation rate); and (c) if a gene is an essential or highly conserved gene where mutations would have a deleterious or strongly damaging effect, their coding sequences are highly protected, i.e. have a low mutation rate. Whilst many of the processes and components involved are not yet understood or identified, the role of specific repair mechanisms in conjunction with cytogenetic features seems to be at the centre of it.

These and other recent findings are challenging the classical evolutionary theory that mutations occur randomly irrespective of their consequences for the organism (e.g. fitness costs). This also has consequences for genome editing. For the first time, genome editing makes the whole genome accessible for changes (via targeted mutations), including those sections that otherwise would be protected (Kawall 2019). As a site directed nuclease (e.g. CRISPR/Cas9 or TALENs) is designed to cut a specific DNA sequence, it will cut the same sequence again should the repair mechanism have repaired it correctly. Such a nuclease will likely continue to do so until no more target sequence is available due to incorrect repair (Brinkman et al. 2018). Whilst this will result in high efficiency of cutting and mutating/changing of target sites, the same may be true for non-target sites with similar DNA sequences. **These would be unlike any other random mutations, as they would also override the cell's own protective mechanisms as well as potentially alter, not just a single copy of a non-target gene but several or all copies** (depending on plant species and degree of ploidy) - something that would not happen with other comparable technologies, such as chemical or radiation-induced mutagenesis.

This persistence and overriding of the cell's own protective mechanisms makes genome editing a novel technology with novel capacities and consequences unlike any other.

Equally, the feature of altering more than one copy of the same gene is unique to this technology, with consequences thus far little understood or investigated.

F. Conclusion

Health Canada's inclusion of the primer in the consultation documents suggests an openness to discuss the science behind the regulatory guidance proposals and to provide information to the public in the interests of transparency and accountability. However, the primer in its present form is a negligent treatment of the scientific literature and the state of the current scientific inquiry. The presentation of such an inconsequential document risks portraying Health Canada as indifferent to robust scientific inquiry and dismissive of the public's interest in this issue. **The primer undermines the authority of Health Canada to propose new regulatory guidance**.

G. Key Recommendations

Genome editing should be understood to be novel and regulated as such. The processes of genome editing have novel capacities and consequences. Furthermore, new techniques are in development: We do not know what techniques will be developed and applied in the near or long term, and the regulatory system needs to be prepared to ensure any foods produced with new genomic techniques are safe.

Health Canada should subject all genetically engineered foods including those produced by genome editing techniques to government safety assessments. Health Canada should retain regulatory authority over all genetically engineered products and ensure government oversight over all GMOs entering the food system.

The federal government should create an independent, arm's length scientific risk assessment authority in order to provide scientific guidance on regulatory decision-making concerning genome-edited and other genetically engineered products. This authority should be established to implement recommendation 9.3 of 2001 The Royal Society of Canada's Expert Panel on the Future of Food Biotechnology: "The Panel recommends that the Canadian regulatory agencies implement a system of regular peer review of the risk assessments upon which the approvals of genetically engineered products are based. This peer review should be conducted by an external (non-governmental) and independent panel of experts. The data and the rationales upon which the risk assessment and the regulatory decision are based should be available to public review." (Royal Society of Canada 2001)

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Annex

Biography: Dr Ricarda Steinbrecher

Dr Ricarda Steinbrecher is a biologist and molecular geneticist based in Oxford, UK, educated at the University of London and the University of Kiel, Germany. First specialising in gene regulation and gene modification, she worked in the field of mutational analysis, gene identification and gene therapy. Since 1995 her focus has been on biosafety aspects of genetically modified organisms. More recently, she has been concentrating on synthetic biology, new genetic engineering techniques such as CRISPR-Cas9, and gene drive organisms. Dr Steinbrecher is co-director of EcoNexus, a public interest research organisation focusing on new technologies and their impacts on biodiversity, ecosystems, food security and agriculture.

Dr. Steinbrecher has been actively involved in UN-led processes since 1996, especially of the Convention on Biological Diversity (CBD) and its Cartagena Protocol on Biosafety. Since 2015 she has served on the Technical Expert Group on Synthetic Biology of the CBD, also covering gene drives. She is a member of the Federation of German Scientists (FGS/VDW) whom she represents at the international UN negotiations, and is a founding and board member of the European Network of Scientists for Social and Environmental Responsibility (ENSSER).

Recent publications as co-author include:

Chapters 1 and 2 in ‘Gene Drives: A report on their science, applications, social aspects, ethics and regulation’ - published in 2019 by Critical Scientists Switzerland (CSS), ENSSER and VDW.

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