Swiss Foundation
for Cultural and
Genetic Diversity of
Plants and Animals

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To the Third Party Beneficiary under the Multilateral System of the ITPGRFA
c/o The Secretariat of the ITPGRFA
FAO Viale delle Terme di Caracalla
Rome, Italy
Sent by email to: PGRFA-Treaty@fao.org
cc: Dr Kent Nnadozie, Secretary of the ITPGRFA
cc: Mr. Alwin Kopše, Chair of the eleventh session of the Governing Body of the ITPGRFA

17 November 2025

Ladies and Gentlemen,

Based on Art. 4.2 of the procedures for the Third Party Beneficiary[1], we request the Third Party Beneficiary to initiate dispute settlement procedures on the four cases (involving five companies) described in the Annex to this letter.

We are of the opinion that in all the cases mentioned, the patents filed constitute a violation of Article 6.2[2] of the SMTA by the recipient.

We base our opinion on the following facts:

1. All described Patents claim a native trait, based on gene sequences occurring in the accession received from the Multilateral System. Various experts have confirmed that such patents on native traits are in conflict with Art. 6.2. of the SMTA. The most recent and comprehensive report on this topic is the 'Patent Landscape Report on Inventions Based on Plant Genetic Resources for Food and Agriculture (PGRFA) and Related Digital Sequence Information/Genetic Sequence Data (DSI/GSD)', published by the CGIAR Genebank Accelerator. It states that:

   Patents with the potential to limit the use of the PGRFA on which an invention is based are usually patents involving so called "native traits", *i.e., naturally occurring characteristics observable in existing plants. [...]*

1 4.2. The Third Party Beneficiary may receive information on possible non-compliance with the obligations of the provider and recipient under a Standard Material Transfer Agreement from the parties under the Standard Material Transfer Agreement or any other natural or legal persons. The information shall only be used for the purposes of initiating dispute settlement procedures under the Standard Material Transfer Agreement. Link to the Procedures: www.fao.org/3/be066e/be066e.pdf

2 6.2 The Recipient shall not claim any intellectual property or other rights that limit the facilitated access to the Material provided under this Agreement, or its genetic parts or components, in the form received from the Multilateral System.

“High impact” claims are those that practically completely limit the utilization of the PGRFA that underpin the claimed invention *or other PGRFA that include equivalent elements and characteristics such as homologous naturally occurring genes and traits.*

And they mention following claim as a “High impact” claim:
“Cultivated” plant with a trait obtainable (or introgressed) from the original material, its parts (including seeds, and fruits)

The patents involved in the cases described all include such a kind of “High impact” claim and are listed in the core patent dataset of the report, called the ‘gold set’, comprising a globally representative number of patent documents that limit, or have the potential to limit the use of PGRFA materials from which the inventions were derived.

2. Obviously, there’s only a conflict with the SMTA if an SMTA has been signed. In all the cases shown, it’s clear from the patent descriptions that the native trait was obtained from an accession in the Dutch gene bank (CGN). CGN has confirmed to us that since 6 March 2007, all access to their gene bank has been via the SMTA and that in all cases mentioned, the recipients /patent holders also had at least once access to the mentioned CGN accession by signing (or click-wrap) an SMTA.

Thus, all conditions for a breach of contract with the SMTA appear to be met: users had access to the material in the Multilateral System through an SMTA, and the recipients claimed intellectual property rights that limit the facilitated access to the material or its genetic parts or components in the Multilateral System.

It is of utmost importance to us (and to many other providers) that these dispute settlement processes clearly clarify that the patents on native traits referred to in the Annex are in conflict with the obligations of recipients who have signed an SMTA. This issue goes to the heart of the Multilateral System, which aims to facilitate access to plant genetic resources for food and agriculture. If these patents remain in place, the facilitated access granted by the SMTA will be undeniably hampered. This is because it would be used, via patents, to deny other users of the Multilateral System such facilitated access. And it was precisely to prevent this outcome that Article 12.3(d) was enshrined in the Plant Treaty text and incorporated into the SMTA as Article 6.2. If these patents remain in place, they will likely also deter many providers from integrating new plant genetic resources into the Multilateral System. After all, why should a country grant access to its resources if it may risk losing the ability to use freely these resources due to the subsequent patenting of native traits?

In addition, if such patents create the risk that the use of gene bank material — and the introgression of gene sequences into newly developed varieties from this material — may lead to patent infringement, this reduces legal certainty for all future potential users. Consequently, gene banks will no longer be able to fulfil their obligation to make the material freely available, with a sufficient degree of legal certainty.

We therefore call on the Third Party Beneficiary to initiate dispute settlement in accordance with Article 8 of the SMTA to ensure that the Recipients referred to, or affiliated with, the patent applicants named in the Annex, withdraw the pending patent applications and abandon granted patents, and to seek additional remedial action or compensation, as appropriate, for the violation of recipient’s obligations under the SMTA. Only in this way will the spirit and letter of the Treaty and the SMTA be fulfilled.

As these cases are of great importance for the implementation of the Plant Treaty and the SMTA, we ask the Third Party Beneficiary to inform us, the Contracting Parties, and other interested stakeholders, about the further process and opportunities to provide additional information based on any clarifications submitted by Recipients, and the decisions made on these cases, in a timely and transparent manner.

We are available at any time to provide further information and to exchange views.

Kind regards

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Annex

The data was taken from the Google Patents database. The cases mentioned relate to the entire patent family; individual patents from the respective patent families are cited as examples below. The patent claims may differ in the various jurisdictions.

Case 1

WO2011003783A1 —
Plant resistant to bremia

2010-06-30 Application filed by Syngenta Participations AG

Patent granted in Europe (EPO), Spain, USA, Japan, Australia

Claim 1 (EP3603384B1).
Lactuca sativa plant resistant to *Bremia lactucae,* wherein the *Bremia* resistance locus is obtainable from the genome of a wild *Lactuca* plant, particularly from the genome of *Lactuca saligna,* and wherein the *Bremia* resistance locus is a qualitative resistance locus located on chromosome 8 […]

Description (link to the CGN Accession):
In a particular embodiment of the invention, a downy mildew resistance gene has been identified in the wild lettuce *L. saligna* accession IVT1306(=CGN05315), which confers full resistance to all known *Bremia* races to date. It was introgressed by embryo rescue in cultivated *L. sativa.* […]

In one specific embodiment of the invention, the wild ancestor, from which the *Bremia* resistance trait may be obtained, is wild *Lactuca saligna,* particularly wild *Lactuca saligna* IVT1306(=CGN05315), or from a progeny or an ancestor thereof comprising said qualitative trait locus. […]

Lactuca sativa line LSA-(1306/SAT×SAT)-37-1-3:1 resulted from a cross of a wild *Lactuca saligna* accession IVT1306 (=CGN05315), as the donor of the resistance trait with a *Lactuca sativa* inbred line.

Case 2

WO2022008422A1 — Bremia lactucae resistance sg01

2021-07-05 Application filed by Syngenta Crop Protection AG Switzerland

Pending in Australia, USA, Japan and other states, granted in Europe (EPO) and in China with different claims

Claim AU2021303718A1:
That Which is Claimed is: 1. A *Lactuca sativa* plant with enhanced resistance to *Bremia lactucae* comprising an introgressed sequence from *Lactuca serriola* that confers a qualitative and dominant resistance to *Bremia lactucae,* wherein said introgressed sequence is comprised in *Lactuca serriola* accession CGN23091 […]

Description (Link to CGN Accession):
In particular embodiments, the invention discloses a novel source of resistance to *Bremia:* CGN23091, a wild *Lactuca serriola* accession. By introgressing the *Bremia* resistance conferring sequences from the

wild source into cultivated lettuce plants (e.g., *L. sativa*), a qualitative *Bremia* resistance was conferred to the cultivated lettuce plant […]

In a first aspect, the disclosure provides a lettuce plant (e.g., a cultivated lettuce plant, such as a *Lactuca sativa* plant) resistant to *Bremia lactucae* comprising an introgressed sequence from *Lactuca serriola* that confers a qualitative and dominant resistance to *Bremia lactucae,* wherein said introgressed sequence is comprised in *Lactuca serriola* accession CGN2309 […]

The inventors determined that wild Lactuca serriola accession CGN23091 has a broad spectrum resistance to *Bremia lactucae,* designated as the «SG01» resistance. A first backcrossing cycle was made to introduce the SG01 *Bremia* resistance from the wild *L. serriola* accession into a susceptible *Lactuca sativa.* […]

Case 3

EP4338585A1 — Spinach plant having novel downy mildew-resistant gene

2022-05-12 Application filed by Sakata Seed Corporation

Pending in Canada, Japan, Europe (EPO), South Korea, China, Australia

Claim 1 (CA3218397A1):
A downy mildew resistant spinach plant (excluding Spinacia tetrandra) having a downy mildew resistance RTM-1 gene, which is located on chromosome 4 of the Spinacia tetrandra line CGN25466: MGK 01.

Description (link to the CGN Accession):
The downy mildew resistant spinach plant according to [1] above, wherein the RTM-1 gene is a gene that exists in a range from chr4_7962907 to chr4_8617232 on chromosome 4 of the Spinacia tetrandra line CGN25466:MGK 01 […]

This introduction of the RTM-1 gene into the genomic DNA can be achieved, for example, by introducing a chromosome fragment that includes the site where the RTM-1 gene is located (the RTM-1 gene locus) in chromosome 4 of the Spinacia tetrandra line CGN25466:MGK 01. […]

Using the wild species Spinacia tetrandra line CGN25466:MGK 01 acquired from CGN of Holland in 2013 as a parent, a novel downy mildew resistant line was developed […]

Case 4

WO2015136085A1 — Bremia lactucae resistant plants

2015-03-13 Application filed by Rijk Zwaan Zaadteelt En Zaadhandel B.V., Nunhems B.V., Vilmorin & Cie

Granted in Mexico, Australia, Spain, Europe (EPO), USA

Claim 1 (EP3116304B1):
A cultivated lettuce plant (*Lactuca sativa L.*) comprising an introgression from *L. saligna* on the bottom of chromosome 9 comprising a dominant resistance allele from *L. saligna* which confers a broad spectrum resistance to *Bremia lactucae,* […]

Description (link to the CGN Accession):
The said resistance of the invention is controlled by a resistance allele on the bottom of linkage group 9, the inheritance of which is consistent with that of a monogenic dominant trait. The term “dominant” is

to mean in this context that the fully achievable resistance is observable in plants comprising the resistance allele in the homozygous or heterozygous state. The resistance allele according to the invention or an introgression fragment comprising the resistance allele, is obtainable from the genome of a distantly related wild species, in particular from the genome of wild accessions of *Lactuca saligna* containing the bott_C9 resistance allele which confers broad spectrum *Bremia lactucae* resistance, including but not limited to, CGN 15705.

"Introgression from *Lactuca saligna"* or "introgression fragment from *Lactuca saligna"* herein refers to a fragment of a linkage group (or part of, or region of, a linkage group) which has been introduced from *Lactuca saligna* into cultivated lettuce *(Lactuca sativa)* by crossing or traditional breeding techniques, such as backcrossing e.g. the introgressed fragments is the result of breeding methods referred to by the verb "to introgress" (such as backcrossing). Such a cultivated lettuce plant thus has a "genome of cultivated *Lactuca sativa",* but comprises in the genome a fragment of a wild lettuce e.g. an introgression fragment of a related wild *Lactuca genome,* such as *Lactuca saligna* e.g. the bott_C9 resistance allele, from CGN 15705 […]

Identification of the resistance allele on linkage group 9: Lactuca saligna CGN 15705 was found according to the invention to have a broad spectrum resistance to *Bremia lactucae.* An initial crossing was made between plants of *Lactuca saligna* CGN 15705, and Lactuca sativa cv. Olof. Resulting F1 plants were backcrossed to the recurrent *Lactuca sativa* parent and/or selfed to generate BC1sativa and F2 segregating populations, respectively. […]