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)

July 2025

A draft version of this report was prepared and presented for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025. The patent landscape analysis and other technical information is updated as of March 2025.

Abstract

This report provides an overview of the patent landscape in relation to PGRFA-based inventions involving naturally occurring ('native') traits and related DSI/GSD. In particular, the report focuses on the potential of patent claims to limit (or not) others' uses of PGRFA and related DSI/GSD on which the protected invention is based and/or other PGRFA in which equivalent or very similar traits and related DSI features are naturally present. We identified 399 patent documents (first filings) – representing a relatively small percentage of the overall global patent activity as captured through the most relevant PGRFA indicators – that have the potential to limit the use of PGRFA materials from which these inventions were derived in further research and breeding. Based on the analysis of the claims in these patent families, we identified twelve types of claims that have medium to high potential to affect the relevant restrictions. However, we were unable to assess the extent to which materials from the Multilateral System (MLS) of the FAO Plant Treaty were used in the development of these patented inventions. The current legal and technical features of the data architecture of the international patent system do not make it possible to assess how many patents have been applied and/or granted for inventions that incorporate, or are based on, PGRFA materials from the MLS. We identify options that the *Ad Hoc* Open-Ended Working Group to Enhance the Functioning of the Multilateral System could consider in order to address the issues raised in this report, including means to ensure 'findable' disclosures of MLS materials upon which patented inventions are based, and suggest further analysis and/or guidelines, to be developed by the Technical Advisory Group on the MLS and SMTA, to address the relationship of different types of patent claims to Treaty Article 12.3(d), which provides that: *"Recipients shall not claim any intellectual property or other rights that limit the facilitated access to the plant genetic resources for food and agriculture, or their genetic parts or components, in the form received from the Multilateral System."*

Descriptive outline: Following a brief introduction in Section 1, Section 2 describes the different types of intellectual property rights that are available in different jurisdictions to protect PGRFA-related innovations. Section 3 summarizes the research methods. Section 4 presents a global overview of the patent landscape for PGRFA. Section 5 proposes a typology of 17 categories of patent claims related to PGRFA-based inventions and assesses the potential of each claim type to limit the subsequent use of the PGRFA. Section 6 identifies possible options to enhance transparency and mutual supportiveness between the Plant Treaty and the International Patent System, and to address potential impacts of patents on the use of PGRFA from the Multilateral System. It concludes by suggesting possible follow-up research.

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Acronyms

CPC: Cooperative Patent Classification developed by the EPO and USPTO

DSI/GSD: digital sequence information / genetic sequence data

GB: the Governing Body of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture

EPC: European Patent Convention

EPO: European Patent Office

GM traits: genetically modified traits

IPC: International Patent Classification

IPRs: intellectual property rights

MLS: the Multilateral System of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture

NGTs: new genomic techniques

OM: original material

PBR/PVP: plant breeders' rights / plant variety protection

PCT: Patent Cooperation Treaty

PGR: plant genetic resources

PGRFA: plant genetic resources for food and agriculture

R&D: research and development

SMTA: Standard Material Transfer Agreement

UPOV: International Union for the Protection of New Varieties of Plants

USPTO: United States Patent and Trademark Office

WG-EFMLS: The *Ad Hoc* Open-Ended Working Group to Enhance the Functioning of the Multilateral System.

1. Introduction

Since the 19th century, it has been possible to obtain patents on plant-related inventions in an increasing number of countries. However, their volume only increased with the rise of modern biotechnology in the 1980s. Such plant-related inventions are based on,[1] and can comprise within the claims, plant genetic resources for food and agriculture (PGRFA), their functional traits, the encoding digital sequence information/genetic sequence data (DSI/GSD), as well as their uses in plant breeding. The negotiators of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture (hereafter the Plant Treaty) were conscious about the potential impacts that intellectual property rights (IPRs) could have on the availability of, and the facilitated access to PGRFA in the Multilateral System (MLS). Article 12.3(d) in the Plant Treaty states that *"Recipients shall not claim any intellectual property or other rights that limit the facilitated access to the plant genetic resources for food and agriculture, or their genetic parts or components, in the form received from the Multilateral System."* Article 6.2 of the Standard Material Transfer Agreement (SMTA) reproduces the same provision.

These provisions are subject to a range of interpretations. There is now a renewed focus on this issue in the context of the ongoing negotiations to enhance the functioning of the MLS, particularly regarding intellectual property rights related to DSI/GSD and products derived thereof. Meanwhile, there is no shared knowledge base among Contracting Parties and stakeholders about the kinds of patent claims that are being granted in relation to patentable subject matter based on, or comprising PGRFA, and their potential impact on the subsequent uses of such PGRFA generally – including potentially those that are accessible through the MLS.

The primary purpose of this study is to provide an overview of the relevant patent landscape in relation to PGRFA. In doing so, it analyses the different types of patent claims being granted, and the extent to which they limit (or not) others' uses of PGRFA, and related DSI/GSD on which the invention is based for research, breeding and training for food and agriculture, and commercialization of resulting products – regardless of the varying interpretations of Treaty Article 12.3(d), SMTA Article 6.2, and other relevant Plant Treaty provisions.[2] It is also important to highlight that claims to such patent protected materials and/or uses of PGRFA (and any derived embodiments) may encompass 'equivalent' features or characteristics, such as naturally occurring traits, sequences and genes that can be naturally present in other PGRFA as well.

The subsequent sections of this paper are organized as follows: Section 2 describes the different types of intellectual property rights that are available in different jurisdictions to protect PGRFA-related innovations. Section 3 summarizes the various research methods that were applied throughout this study. Section 4 presents a global overview of the patent landscape for PGRFA. Section 5 develops and proposes a typology of 17 categories of patent claims related to PGRFA-based inventions and assesses the potential of each claim type to limit the subsequent use of the PGRFA on which the invention is based (or any homologous features or characteristics in other

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[1] "Based on" means that the PGRFA and/or any DSI/GSD derived therefrom must have been necessary for the claimed invention, and that the claimed invention must depend on the specific properties of the PGRFA and/or on the said DSI/GSD.

[2] The mention of any specific patent in this report does not mean that the related PGRFA is governed under the Multilateral System of the Plant Treaty. All patents are to be understood as examples of how inventions based on PGRFA can be claimed and may limit others' uses of such PGRFA.

PGRFA) in research, breeding and training for food and agriculture (i.e., upstream effects of patent protection). Section 6 identifies options for consideration by the *Ad Hoc* Open-Ended Working Group to Enhance the Functioning of the Multilateral System (WG-EFMLS) to enhance transparency and mutual supportiveness between the Plant Treaty and the International Patent System, and to address potential impacts of patents on future use of PGRFA from the Multilateral System. It also concludes by suggesting possible follow-up research.

2. Different types of IPRs over PGRFA and their parts and components

Different intellectual property rights can be obtained in various jurisdictions to protect plant-related innovation.

Plant Breeders' Rights (PBR), also known as plant variety protection (PVP), provide an exclusive right for the commercial exploitation of a specific plant variety. They do not limit access to, or utilization of, any PGRFA which have been used in the making of the protected variety. Furthermore, under the UPOV Convention, there is a breeders' exemption that allows use of the protected variety for breeding or discovering and developing new varieties. The resulting new varieties can be freely commercialized except when they are 'essentially derived' from a protected variety (i.e., present high genetic conformity and retain the essential characteristics of the latter), in which case the breeder's permission is required. In consequence, the exclusivity granted by a UPOV-compliant PBR/PVP is essentially limited to the propagation of the specific variety or almost identical ones.

So-called '**Plant Patents**' provide protection for plant varieties of certain – usually asexually propagated – plant species. Plant patents are a *sui generis* form of intellectual property protection and should not be confused with (utility) patents on plants or plant varieties or PBRs/PVPs. They are only available in a few countries including Japan, Korea and the USA. Eligibility for protection and scope differ from country to country, but generally the protection that they afford is lesser than that of utility patents. For instance, the U.S. Plant Patent Act requires for protection that the concerned *specie* is asexually (i.e., vegetative) propagated and that the variety be a "*distinct and new variety of plant, including cultivated sports, mutants, hybrids, and newly found seedlings.*"[3] The rights resulting from a plant patent are limited to asexual propagation. This means that the commercialization of plants obtained through sexual propagation of the protected variety would not infringe the plant patent. Like PBR/PVP, plant patents vest owners with rights of control over the patented plant varieties *per se*. Anyone seeking to commercialize those protected varieties is required to seek permission of the right holder. However, the protected varieties can be used by others for further research and breeding, and the protection does not extend to genetic materials or uses of genetic materials other than the asexually propagated variety as a whole.[4]

In a vast majority of countries, **Utility Patents** provide protection over plants beyond a specific variety and can also extend to plants' parts, traits and genetic characteristics. There are two primary classes of patent claims: 1) Claims to compositions such as plants, plant parts (including seed and fruits), DNA or protein sequences, and molecular markers; and 2) claims to processes

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[3] Manual of Patent Examining Procedure (2021) Chapter 1600 - Section 1601. Introduction: The Act, Scope, Type of Plants Covered [R-11.2013]. Available at https:// www.uspto.gov/web/offices/pac/mpep/s1601.html.

[4] Interestingly, the same asexually propagated plant variety may be protected under both the US Plant Variety Protection Act and the Plant Patent Act of 1930, codified as 35 U.S.C. Ch. 15 - PLANT PATENTS. Available at: https://www.law.cornell.edu/uscode/text/35/part-II/chapter-15.

such as processes for making/breeding plants (production processes), processes for identifying/analyzing plants (working processes), and processes of using plants and plant parts. While composition claims confer a direct protection for the claimed product, production processes confer an indirect protection. In all WTO countries, the scope of a process claim extends at least to the direct product of a process, and in some countries can also extend to other products (such as other biological materials derived from the directly obtained biological material through propagation or multiplication and possessing those same characteristics). In consequence, the patent may be infringed if the resulting plant of a patented process is used for the development of another product, even if the protected process itself has not been applied. Utility patents give the owners the right to prevent others from using, replicating and selling the patented invention without permission. Unlike PBR/PVP and plant patents, products and processes protected by patents cannot be used for further research and breeding without permission from the patent owner, except when national patent laws provide for specific exemptions to this rule. In addition, in a few countries (including, notably, the USA), utility patents can be granted over specific new plant varieties. In these cases, the use and incorporation of the protected variety's parts and components in other plants or varieties do not infringe a variety patent as long as the resulting plant is different from the protected variety in other essential traits.

The ensuing sections of this study presenting the patent landscape of PGRFA-related inventions focus on utility patents.

3. Summary of Research Methods

The patent system is a powerful international information system that can be instrumental in supporting policy formulation through the provision of accurate quantitative research and innovation data in different sectors.

Box 1 – Deep dive: Patent classification systems, patent and other databases, and how they were used in this study

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Patent classification systems primarily describe the content of patent documents.

The International Patent Classification (IPC) system, maintained by the World Intellectual Property Organization (WIPO), is the most widely used. Patent activity involving PGRFA is concentrated in three main areas or classes of the IPC: New Plants or Processes for Producing Them (Subclass A01H), Biochemistry and Biotechnology (Subclass C12N)[5], and Peptides (Subclass C07K). However, these are large areas of the patent system. For example, activity under A01H will include forestry and ornamental plants that are not of direct interest for activity involving PGRFA. Activity for Biochemistry and Biotechnology includes activity involving genetic resources across the full spectrum of organisms. To address this, the IPC classification system was manually reviewed to identify the main indicators of direct relevance to PGRFA.

The IPC system responds to the needs of WIPO Member States through regular revisions. For example, in the last 10 years, the IPC has introduced new patent classifiers for the taxonomy of plants used in food and agriculture (e.g.A01H6/20 for *Brassicaceae*) as well as indicators related to technological areas that are becoming more and more relevant for PGRFA research and development, such as artificial intelligence (e.g.G06N for computational models).

In addition to the IPC, the European Patent Office (the EPO) and the United States Patent and Trademark Office (USPTO) have developed the Cooperative Patent Classification (CPC). The IPC and CPC follow the same structure. Thus, subclass A01H for New Plants and Processes for Producing Them is the same in both classification systems.

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[5] In this paper we use the terms 'biotechnology' and 'genetic engineering' interchangeably to describe general activity under class C12 and in particular subclass C12N, which is described as "microorganisms or enzymes; compositions thereof; propagating, preserving, or maintaining microorganisms; mutation or genetic engineering; culture media (microbiological testing media C12Q 1/00)". The majority of patent activity involving PGRFA in the field of biotechnology is classified under subgroup C12N15/82 which includes: "Mutation or genetic engineering; DNA or RNA concerning genetic engineering, vectors, e.g. plasmids, or their isolation, preparation or purification; Use of hosts therefor… for plant cells." The full IPC can be accessed here and the CPC can be accessed here.

However, the CPC provides more detailed classification on the group and subgroup level than the IPC. In relation to the subject matter of this study, the Cooperative Patent Classification (CPC) has been further developed to include indicators for genome editing (CRISPR) and related technologies as well as more detailed indicators for Artificial Intelligence (AI) related patent activity than are currently offered by the IPC.

In this paper, we have used both the IPC and the CPC. Although it has been adopted by a growing number of patent offices, including major offices such as China, the CPC is not as widely adopted as the IPC. The advantage of using the CPC is that it is responsive to emerging developments. A disadvantage of the CPC is that its global coverage will be more limited than the IPC and it will therefore underestimate wider activity. However, this disadvantage is outweighed by the fact that its extra granularity assists with capturing emerging technologies.

The gold standard for patent statistics is provided by the EPO World Patent Statistical Database (PATSTAT), developed by the European Patent Office and used by statistical authorities such as EUROSTAT and the OECD for reporting on trends in science and technology. We used the Autumn 2024 edition of PATSTAT in the preparation of this paper. We also used the open access Lens database from the non-profit CAMBIA in Australia, which provides information on DNA and amino acid sequence listings that accompany patent filings.

From the outset, the study set out to identify a core patent dataset, 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 as well as other PGRFA that include components equivalent to those covered by those patents, for instance, naturally occurring traits and genes.

To identify the patent documents to include in the gold set, we applied a specific search profile in Patsnap[6] followed by a manual review and selection of patents that met all the following conditions:

1) Be part of IPC patent classes for Angiosperms (i.e., flowering plants) characterized by their plant parts (A01H5) or by their botanic taxonomy (A01H6) and the related subclasses.

2) The patent claims reference a deposit of the resulting biological material.[7] Without a deposit, patent claims which cover a plant with specific characteristics are usually not enabled, unless full sequence information is provided for the causative genes.

3) Their territorial scope is that of the Patent Cooperation Treaty (PCT) and the European Patent Convention (EPC), i.e., patents that have been filed in one or more countries under these treaty instruments. This criterion allowed us to filter out plant patents and utility patents on specific plant varieties, which are allowed and filled in a few (important) countries (see below *Table 2*) and which are difficult to distinguish by automatic means from patents on plants with native traits.

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[6] Patsnap is an AI-powered tool for patent searches, available at: https://analytics.patsnap.com/search/input/field. The search terms were as follows: CLASS:(A01H5* OR A01H6*) AND CLMS:(ATCC OR NCIMB OR deposit*) AND PN:(WO* OR EP*) NOT CLMS:(event*).

[7] To obtain a valid patent an invention needs to be described in way that it can be carried out by a person skilled in the art. For inventions related to certain plant characteristics, this usually requires the disclosure of a physical source from which the characteristic can be obtained. As these sources need to be publicly available over the entire time of the patent in order to meet the 'enablement' requirement, usually the required biological materials are deposited under the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure, which is a WIPO administered treaty. However, despite this and the likely implications in terms of 'enablement', many patents do not make reference to a deposit including in cases such as the "Broccoli Patent" (EP1069819B2 subject to the Broccoli I (G 2/07 – G 01/08) and Broccoli II (G 2/12 – G 2/13) decisions) and the IRRI's patent application WO2014118636A3 on the SPIKE gene originating from an Indonesian farmers' variety of rice named "Daringan" (accession code IRGC-17446).

4) They are not patents on genetically modified events (i.e., transgenic plants), because these cases entail man-made traits, and not naturally occurring ones.

5) They do not relate to plant genetic resources that are not for food and agriculture (such as cannabis, cotton or ornamental plants).

In total, an initial set of 399 core patent documents[8] meeting these criteria was identified (see Section 5.1 and *Figure 7* for details). The advantage of applying these stringent selection criteria is that it ensured a high hit rate with a very limited number of false positives (that could be easily filtered out manually from the set). At the same time, this methodology presents the limitation that it *undercounts* potentially relevant cases, such as patents that have been applied for as single national filings in one country only (e.g. USA, China), as well as a low but steadily growing number of filings that only provide sequence information and no deposit. Despite these limitations, this initial core set provided a globally representative number of relevant patents, and became our 'gold' set for further analyses.

To capture additional patent filings relevant to PGRFA (beyond those prosecuted through the EPO and PCT), we used a standard method in Natural Language Processing called Cosine Similarity. This experiment provided an empirical demonstration of the high level of similarity between, on the one side, patent documents involving claims that limit, or have the potential to limit the use of PGRFA materials from which inventions are derived, and, on the other, utility patents over varieties, particularly those filled in the USA. This signifies that it is difficult to clearly distinguish, mathematically, between these types of documents except through the use of more advanced methods. To address this gap, we manually reviewed 677 candidate documents having 80% or above similarity with the gold dataset. This allowed us to identify an additional set comprising 194 national patent filings (in the US only, which were intentionally excluded from the previous search in the gold dataset).

Box 2 – Deep dive: *Experimenting with Cosine Similarity in Natural Language Processing*

When used in Natural Language Processing cosine similarity involves transforming texts into numerical vectors, measuring their similarity based on the cosine of the angle between vectors and producing values between -1 (opposite) and 1 (identical). These values can readily be used as percentage scores. To test for similarity, we used the complete texts of the patent claims from the gold dataset. From the 56,000 patent documents in our reference set we removed the 4,717 members of the gold dataset family. We also reduced the document set to those with patent claims in English (as cosine similarity cannot simply be used as is across texts in multiple languages). This led to a set of 8,555 distinct patent documents for PGRFA with claims in English where the status of the documents as containing naturally occurring traits was 'unknown'. The available claims in the unknown set were entirely from the US, EPC (EP) and the PCT (WO). We then calculated the cosine similarity between the patent claims of the gold dataset and the patent claims of the 'unknown' set. This experiment revealed a mean of 64% similarity between the claims of the gold dataset and the 'unknown' PGRFA dataset. We chose 80% or above similarity as the threshold for manual review. At the 80% or above similarity threshold we identified a total 677 candidate documents representing 7% of the documents that were processed. Non-relevant utility patents on varieties and other non-PGRFA related documents (e.g. primarily cotton) begin to appear at the 91% similarity mark. Furthermore, beyond this mark, irrelevant documents are interspersed among other documents that involve naturally occurring traits.

In Section 5 of this study, we further analysed the 399 patent claims in the gold dataset to develop 17 distinct typologies of patent claims that have (to various degrees) the potential effect of limiting the use of the PGRFA on which these inventions are based, as well as other PGRFA comprising analogous features and characteristics, in further research and breeding. These typologies of claims with illustrative examples are presented below in *Table 1*. We also present the results of

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[8] Patent documents exist in patent families of related documents linked by shared identifiers. The earliest priority filing in a group of related documents constitutes the base of the family or the first filing. Every other document linked to that first filing is a family member (a published application or grant, etc.). A range of definitions of patent families are available and we use the EPO INPADOC patent family definition as used in PATSTAT for the identification of first filings.

experimenting with Cosine similarity which led to the identification of an additional set of 194 relevant filings in the USA in *Box 5*, Section 5.1., and in *Annex II* – Cosine Similarity Patent Dataset of US Domestic Filings (excluded from the PCT and EPC searches used to construct the Core Patent Dataset).

From a quantitative standpoint, it became apparent while conducting the research that very little was known about the overarching patent landscape surrounding the core patent dataset and the historical and emerging patent trends that have arisen in response to new technological developments such as enhanced sequencing capability and genome editing technologies,[9] new market opportunities such as those arising in growing technology markets like China, and new patent rules such as the exclusion from patentability of naturally occurring DNA in the USA.[10]

In order to provide a global overview of the patent landscape for PGRFA-related inventions and a better understanding of the wider context in which patent activity occurs, the study further identified a standard set of indicators or subclasses for patent activity involving PGRFA from the IPC system and used them together with patent data analytics to filter patent documents in PATSTAT. This allowed us to elaborate a global picture of patent activity in relevant areas of PGRFA innovation (*Figure 1*). We then selected and applied more detailed indicators from the CPC to filter patent documents involving genome editing and plant traits, and AI related applications (*Figures 2 to 6*). We present the main statistical results and their succinct analysis, as well as some forecasts in Section 4.

Box 3 – Deep dive *on forecasting methodologies*

> It is possible to forecast or model time series data using a variety of different models. The aim here is that the forecast provides useful information on likely future trends based on existing data. In essence, most forecasting models use past data points that are weighted in some way to make predictions about the future and often take into account seasonality. We decided to forecast using the data on first filings and to produce a separate forecast for the family publications. A range of models were applied to the data using the fable package in the R statistical programming language and the model with the highest performance scores across a range of standard tests was selected. This approach largely automates the selection process between models such as Error, Trend and Seasonality (ETS) and Auto Regressive Integrated Moving Average (ARIMA) models to select the results with the best fit to the data.

Finally, we also wanted to investigate how often MLS materials are being used in the development of plant-related inventions for which patent protection has been sought. We therefore focused on using a dataset of 599,000 accession numbers from CGIAR centers' genebanks to text mine for these accession numbers in over 56,000 patent texts that had been previously selected applying our selected set of indicators or subclasses from the IPC system.[11] We additionally text mined the data for reference to the CGIAR centers and related acronyms. The problem that emerged is that while CGIAR accessions identifiers may be distinctive within the internal database systems of CGIAR centers, they are not distinctive *outside* those systems, where they collide with a wide range of other more routine uses, from years (e.g. 2000, 2002) to postal codes. In consequence, we obtained a very large number of irrelevant sentences and documents that contained a

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[9] Daria Kim, Michael A. Kock, Matthias Lamping, Pedro Henrique D. Batista, Reto M. Hilty, Peter R. Slowinski and Miriam Steinhart, "New Genomic Techniques and Intellectual Property Law:Challenges and Solutions for the Plant Breeding Sector," *Max Planck Institute for Innovation and Competition Research Paper No. 23-16*(Munich 8 August 2023).

[10] U.S. Supreme Court decision in *Association for Molecular Pathology v. Myriad Genetics*, Inc. (569 U.S. 12-398) (2013).

[11] The CGIAR accession numbers were kindly provided by Mathieu Rouard from the Alliance of Bioversity International and CIAT.

candidate match for either an accession number within the CGIAR dataset or the acronym for a CGIAR Centre name.

We also text mined the patent descriptions for the 599,000 CGIAR centers' accessions' Digital Objects Identifiers (DOIs) assigned under the Global Information System of the Plant Treaty. This produced no results. As a second test, we turned to the citations table in PATSTAT. The citations table in PATSTAT includes DOIs extracted from texts in the central database of the European Patent Office. As a validation step for the text mining, we mapped the CGIAR accession DOIs across into PATSTAT and also obtained zero results.

The minting of DOIs as part of the GLIS system is relatively recent and it was therefore not surprising that there were no results. However, this highlights the importance of the use of distinctive identifiers for accession numbers in patent applications combined with guidance to applicants on the appropriate form of disclosure.

4. Global Patent Activity on Plant Genetic Resources for Food and Agriculture – A Quantitative Analysis

This section provides a global overview of the patent landscape related to plant genetic resources for food and agriculture. For policy makers seeking to evaluate the implications and potential impacts of specific patent activity involving PGRFA (in Section 5), the statical findings produced by applying a set of standard patent indicators allows for such an assessment to be conducted with an understanding of the wider context.

4.1. A *Premiere* of Global Patent Activity related to, and comprising, PGRFA-related Inventions

Figure 1 below displays the top-ranking areas of patent activity by indicators in the field of plants and agriculture of relevance to PGRFA. Because the IPC currently groups plants by taxonomic families, this data will also include some PGRs that are not used for food or feed, but figure largely in agricultural production systems (e.g. cotton under A01H6/60). This suggests a need for future refinement to disaggregate the IPC indicators. The data displays both the number of 'first filings' of patent applications globally for the period 1993-2023, and the number of published applications and patent grants (jointly referred to as 'publications') originating from those filings.

Plant Treaty & MLS Relevant Indicators Totals

	First Filings	Publications (Family Members)
A01H New Plants	74,609	194,842
C12N Genetic Engineering	47,036	175,458
Grand Total	86,488	259,399

Plant Treaty Relevant
■ True

Plant Treaty & MLS Relevant Indicators

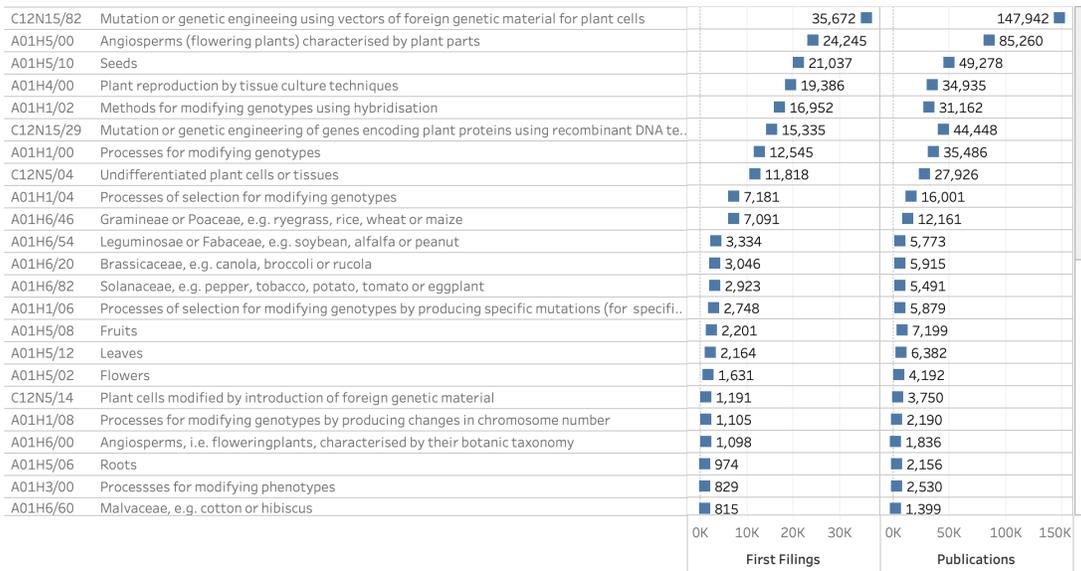| Code	Description	First Filings	Publications
C12N15/82	Mutation or genetic engineeing using vectors of foreign genetic material for plant cells	35,672	147,942
A01H5/00	Angiosperms (flowering plants) characterised by plant parts	24,245	85,260
A01H5/10	Seeds	21,037	49,278
A01H4/00	Plant reproduction by tissue culture techniques	19,386	34,935
A01H1/02	Methods for modifying genotypes using hybridisation	16,952	31,162
C12N15/29	Mutation or genetic engineering of genes encoding plant proteins using recombinant DNA te..	15,335	44,448
A01H1/00	Processes for modifying genotypes	12,545	35,486
C12N5/04	Undifferentiated plant cells or tissues	11,818	27,926
A01H1/04	Processes of selection for modifying genotypes	7,181	16,001
A01H6/46	Gramineae or Poaceae, e.g. ryegrass, rice, wheat or maize	7,091	12,161
A01H6/54	Leguminosae or Fabaceae, e.g. soybean, alfalfa or peanut	3,334	5,773
A01H6/20	Brassicaceae, e.g. canola, broccoli or rucola	3,046	5,915
A01H6/82	Solanaceae, e.g. pepper, tobacco, potato, tomato or eggplant	2,923	5,491
A01H1/06	Processes of selection for modifying genotypes by producing specific mutations (for specifi..	2,748	5,879
A01H5/08	Fruits	2,201	7,199
A01H5/12	Leaves	2,164	6,382
A01H5/02	Flowers	1,631	4,192
C12N5/14	Plant cells modified by introduction of foreign genetic material	1,191	3,750
A01H1/08	Processes for modifying genotypes by producing changes in chromosome number	1,105	2,190
A01H6/00	Angiosperms, i.e. floweringplants, characterised by their botanic taxonomy	1,098	1,836
A01H5/06	Roots	974	2,156
A01H3/00	Processses for modifying phenotypes	829	2,530
A01H6/60	Malvaceae, e.g. cotton or hibiscus	815	1,399

***Figure 1** – Overview of Core Indicators for PGRFA, 1990-2023 (PATSTAT, Autumn 2024 edition)*

Figure 1 also introduces two different ways of counting patent documents. Counts of first filings of patent applications refer to counts of the first time a patent application is filed anywhere in the world (also called the "priority" filing under the 1883 Paris Convention). First filings are used in patent statistics because they are a *proxy output indicator* for underlying investments in Research and Development (R&D).[12] In contrast, counts of publications capture applications and grants based on and linked to the same underlying invention (as the first filing) in different jurisdictions. For each claimed invention there will be just one first filing, but there may be multiple publications of the same document in different countries where protection is sought and, if granted, patents are maintained.[13] In the core indicators set we identified 86,488 first filings (INPADOC patent families) linked to 180,383 applications and 259,399 patent publications worldwide.[14]

Figure 2 below displays the rankings for the country of first filings and the top publication countries and instruments.[15] It also reveals that the origins of first filings across the period are dominated

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[12] The date of first filing is closest date to the underlying investment in R&D. See the OECD (2009) Patent Statistics Manual, and Oldham, P. (2022) The WIPO Patent Analytics Handbook.

[13] As the difference between first filings and patent publication counts suggests, the patent system has strong multiplier effects with each document published approximately 2.9 times. See Oldham, P. (2022) The WIPO Patent Analytics Handbook.

[14] These broader figures also include variety patents and utility patents on plant varieties, which are filed solely in the USA.

[15] Relevant patent instruments include the Patent Cooperation Treaty (WO) administered by WIPO as well as regional instruments such as the European Patent Convention (EP) administered by the European Patent Office.

by China (from 2012 onwards) followed by the United States, with more limited activity by other countries. Analysis of publication trends reveals a steepening demand for protection in China across this period with activity flattening in the United States at around the 3,000 publications a year mark. Data for the European Patent Convention (EP) and the Patent Cooperation Treaty (WO) is included in *Figure 2* because while activity is lower than national level data, these instruments create multiplier effects. Under these instruments applicants may submit a single application that may go on to become an application and potentially a grant in multiple countries. As such, while the counts may be lower, the impact is higher than for any single country application.

Figure 2: *Countries of First Filing and Publication Trends for Core Plant Indicators, 1990-2023 (PATSTAT, Autumn 2024 edition)*

4.2.   Applicants' Profiles

Figure 3 below shows the profiles for the top applicants for the core indicators for the period 1990-2023.[16] It reveals four main categories of applicants: Companies, Universities, Government Non-Profit Organizations and Government Non-profit University (Higher education entities). The patent landscape for PGRFA displays a mix of these entities with a handful of multinational companies leading the field in terms of global patent activity.

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[16] The data is ranked on the number of publications in order to show the relationship between first filings of a claimed invention and demand for protection (which is reflected in publication of applications and grants in one or more country). PATSTAT includes categories of applicants for use in patent statistics.

With respect to data for companies in *Figure 3*, the consolidation of the seed sector through mergers and acquisitions has been widely reported.[17] Changes of ownership are not reflected in PATSTAT data (though it should be noted currently that Monsanto is owned by Bayer; Seminis, which was part of Monsanto, also belongs to Bayer; Pioneer Hi-Bred is owned by Corteva; and Syngenta is owned by CHEMCHINA). A fuller account than is possible here could reflect the impact of these mergers and acquisitions across the patent landscape and could be a significant area for further analysis.

Applicants

	First Filings	Publications
MONSANTO TECHNOLOGY (BAYER)	5,946	16,317
PIONEER HI-BRED INTERNATIONAL (CORTEVA)	5,849	15,654
DOW AGROSCIENCES	399	5,122
SYNGENTA PARTICIPATIONS (CHEMCHINA)	1,189	4,907
DUPONT	611	4,902
BASF PLANT SCIENCE (BADISCHE ANILIN & SODA FABRIK PLANT SCIENCE)	462	4,866
CHINESE ACADEMY OF SCIENCES	2,665	3,898
BAYER CROPSCIENCE	477	3,035
SEMINIS	731	2,719
UNIVERSITY OF CALIFORNIA	371	2,045
CSIRO	196	1,837
HUAZHONG AGRICULTURAL UNIVERSITY	929	1,561
RIJK ZWAAN	382	1,531
M.S. TECHNOLOGIES	825	1,464
INSTITUTE OF CROP SCIENCE, CHINESE ACADEMY OF AGRICULTURAL SCIENCES	776	1,319
BASF (BADISCHE ANILIN & SODA FABRIK)	246	1,251
STINE SEED FARM	939	1,232
EVOGENE	199	1,225
ZHEJIANG UNIVERSITY	747	1,207
AGRIGENETICS	602	1,148
NANJING AGRICULTURAL UNIVERSITY	907	1,139
CHINA AGRICULTURAL UNIVERSITY	783	1,105
NUNHEMS	338	1,084
CROPDESIGN	100	1,062
NOVOZYMES	190	996

Psn Sector
- UNIVERSITY
- GOV NON-PROFIT
- GOV NON-PROFIT UNIVERSITY
- COMPANY

Figure 3 – *Top Ranking Applicants Core Indicators for PGRFA, 1990-2023 (PATSTAT, Autumn 2024 edition)*

It should be noted that in *Figure 3* some organizations display a relatively low number of filings, but a high number of publications that reflects the pursuit of patent protection in multiple countries.

4.3. Genome editing

Figure 4 presents the available data on trends in genome editing related activity relevant for PGRFA (and other PGR such as cannabis or cotton that are commonly used in agriculture production systems) under the Cooperative Patent Classification (CPC). To assist the reader in

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[17] Jonathan Shoham (2024), *Revisiting Seed Company Sales and Profit: Results* (S&P Global). A presentation given at WG-EFMLS-12 on 16 September 2024, p. 12, available at: https://dsi.merid.org/wp-content/uploads/sites/24/2024/12/SPGCI-Agribusiness-Presentation-FAO-September-2024.pdf.

interpreting emerging activity and purely for the purpose of illustration we also present a selection of titles from a single jurisdiction. In the case of genome editing, we have chosen Australia.[18]
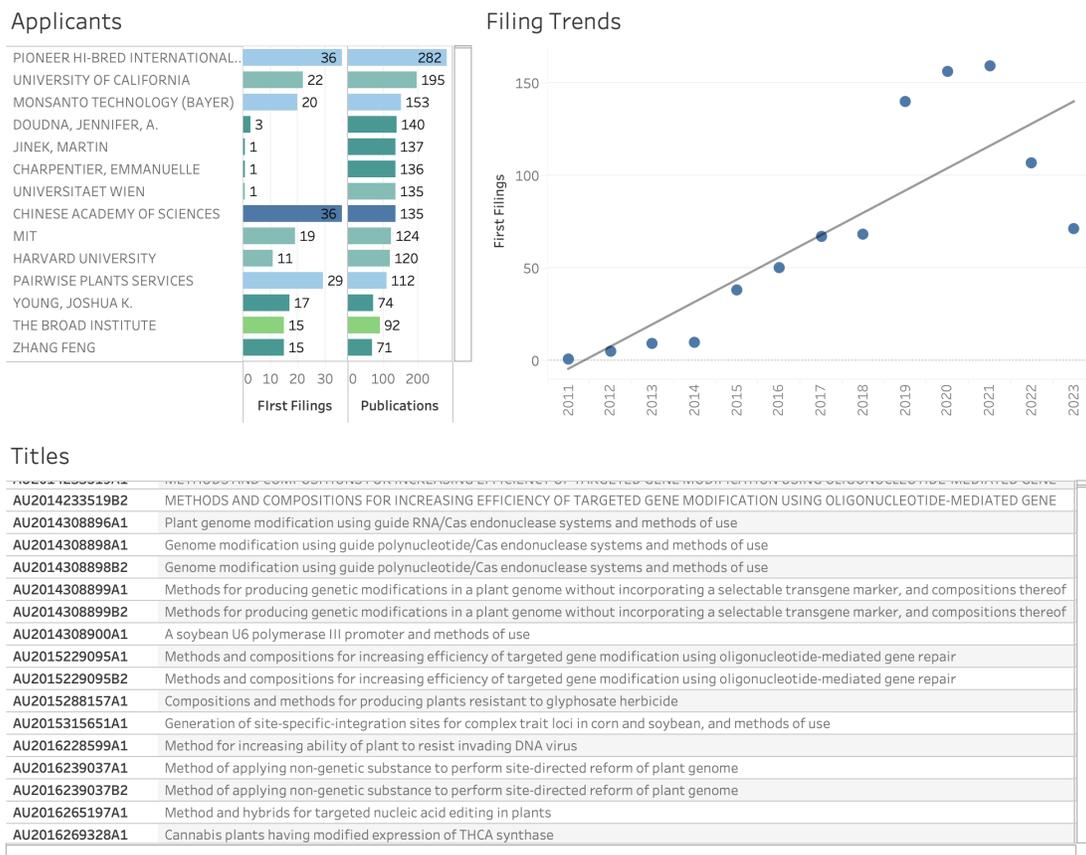

Applicants

	First Filings	Publications
PIONEER HI-BRED INTERNATIONAL..	36	282
UNIVERSITY OF CALIFORNIA	22	195
MONSANTO TECHNOLOGY (BAYER)	20	153
DOUDNA, JENNIFER, A.	3	140
JINEK, MARTIN	1	137
CHARPENTIER, EMMANUELLE	1	136
UNIVERSITAET WIEN	1	135
CHINESE ACADEMY OF SCIENCES	36	135
MIT	19	124
HARVARD UNIVERSITY	11	120
PAIRWISE PLANTS SERVICES	29	112
YOUNG, JOSHUA K.	17	74
THE BROAD INSTITUTE	15	92
ZHANG FENG	15	71

Titles

AU2014233519A2	METHODS AND COMPOSITIONS FOR INCREASING EFFICIENCY OF TARGETED GENE MODIFICATION USING OLIGONUCLEOTIDE-MEDIATED GENE
AU2014233519B2	METHODS AND COMPOSITIONS FOR INCREASING EFFICIENCY OF TARGETED GENE MODIFICATION USING OLIGONUCLEOTIDE-MEDIATED GENE
AU2014308896A1	Plant genome modification using guide RNA/Cas endonuclease systems and methods of use
AU2014308898A1	Genome modification using guide polynucleotide/Cas endonuclease systems and methods of use
AU2014308898B2	Genome modification using guide polynucleotide/Cas endonuclease systems and methods of use
AU2014308899A1	Methods for producing genetic modifications in a plant genome without incorporating a selectable transgene marker, and compositions thereof
AU2014308899B2	Methods for producing genetic modifications in a plant genome without incorporating a selectable transgene marker, and compositions thereof
AU2014308900A1	A soybean U6 polymerase III promoter and methods of use
AU2015229095A1	Methods and compositions for increasing efficiency of targeted gene modification using oligonucleotide-mediated gene repair
AU2015229095B2	Methods and compositions for increasing efficiency of targeted gene modification using oligonucleotide-mediated gene repair
AU2015288157A1	Compositions and methods for producing plants resistant to glyphosate herbicide
AU2015315651A1	Generation of site-specific-integration sites for complex trait loci in corn and soybean, and methods of use
AU2016228599A1	Method for increasing ability of plant to resist invading DNA virus
AU2016239037A1	Method of applying non-genetic substance to perform site-directed reform of plant genome
AU2016239037B2	Method of applying non-genetic substance to perform site-directed reform of plant genome
AU2016265197A1	Method and hybrids for targeted nucleic acid editing in plants
AU2016269328A1	Cannabis plants having modified expression of THCA synthase

Figure 4 – *Genome editing in plants using CRISPR (CPC C12N2310/20)*

In considering *Figure 4*, the names of individual applicants are also included as they reveal the presence of leading researchers involved in genome editing technology, notably Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) enzymes that can be used as genetic scissors. For instance, Jennifer Doudna and Emmanuelle Charpentier were awarded the 2020 Nobel prize for Chemistry for the development of the CRISPR-Cas9 gene-editing technology. Martin Jinek made a key contribution to the emergence of this technology while working with Jennifer Doudna. The University of California at Berkeley, the Broad Institute of MIT and Harvard, and their affiliates have been involved in ongoing litigation over the scope of patent claims related to CRISPR-Cas9 genome-editing technology.[19] This figure also shows that useful patent indicators are already available that can serve as a baseline for further exploration of this technology as it applies to PGRFA.

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[18] The duplication of titles in *Figure 4* displays the publication of documents at different levels where kind A (first publication level) at the end of the patent publication number normally indicates an application and kind B (second publication level) normally denotes a granted patent.

[19] For an example of more advanced patent analytics applied to CRISPR technology see Navigating Patent Networks in the WIPO Patent Analytics Handbook.

4.4.   Plant Traits

The patent system already includes a useful indicator for activity involving oligonucleotides and plant traits, including genetically (GM) modified traits (CPC code C12Q2600/13). *Figure 5* provides an overview of all activity currently covered by this indicator. *Figure 5* shows data on the applicants, filing trends, and an illustrative selection of titles to aid in interpretation (in this case from Canada). Section 5.1 below explains the relationship between the patent documents obtained by applying this indicator and the gold dataset of patents involving PGRFA and naturally occurring traits.

Applicants	First Filings	Publications
MONSANTO TECHNOLOGY (BAYER)	88	1,146
PIONEER HI-BRED INTERNATIONAL (CORTEVA)	153	987
SYNGENTA PARTICIPATIONS (CHEMCHINA)	99	596
DOW AGROSCIENCES	40	583
RIJK ZWAAN	110	415
DUPONT	42	392
SEMINIS	35	365
NUNHEMS	29	196
CSIRO	20	176
HUAZHONG AGRICULTURAL UNIVERSITY	84	145
CHINESE ACADEMY OF SCIENCES	66	134
BAYER CROPSCIENCE	16	125
SYNGENTA CROP PROTECTION	21	119
AGRIGENETICS	14	115

Titles

CA2187546A1	RPS2 GENE AND USES THEREOF
CA2187546C	RPS2 GENE AND USES THEREOF
CA2187771A1	RPS GENE FAMILY, PRIMERS, PROBES, AND DETECTION METHODS
CA2206673A1	USE OF MOLECULAR MARKERS FOR GENOTYPE DETERMINATION OF THE OGURA RF GENE IN BRASSICA NAPUS
CA2258561A1	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MALE STERILITY
CA2258561C	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MALE STERILITY
CA2280933A1	A METHOD TO IDENTIFY AND BREED CORN WITH INCREASED KERNEL OIL CONCENTRATION
CA2282085A1	MEANS FOR IDENTIFYING NUCLEOTIDE SEQUENCES INVOLVED IN APOMIXIS
CA2288991A1	SOYBEAN HAVING EPISTATIC GENES AFFECTING YIELD
CA2298843A1	GERMPLASM AND MOLECULAR MARKERS FOR DISEASE RESISTANCE IN POTATO
CA2349841A1	CORN EVENT PV-ZMGT32(NK603) AND COMPOSITIONS AND METHODS FOR DETECTION THEREOF
CA2349841C	CORN EVENT PV-ZMGT32(NK603) AND COMPOSITIONS AND METHODS FOR DETECTION THEREOF
CA2358589A1	METHOD FOR PREDICTING FIBER LENGTH USING QTL'S AND MOLECULARMARKERS
CA2379850A1	ENVIRONMENTAL STRESS TOLERANT GENE
CA2398633A1	IDENTIFYING GENES ASSOCIATED WITH A QTL CORN DIGESTIBILITY LOCUS
CA2412852A1	A NUCLEIC ACID-BASED METHOD FOR TREE PHENOTYPE PREDICTION

Figure 5 – Activity involving Oligonucleotides characterised by their use for plant traits (CPC C12Q2600/13)

4.5.   Artificial Intelligence

Figure 6 displays trends for the recently introduced indicator under IPC and CPC subclasses G06N3 for artificial intelligence related activity and PGRFA. For the purpose of illustration of activity in this area we include a selection of titles from family members published in China.[20]

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[20] For a detailed assessment of recent developments in generative AI see: WIPO 2024 Patent Landscape Report: Generative Artificial Intelligence.
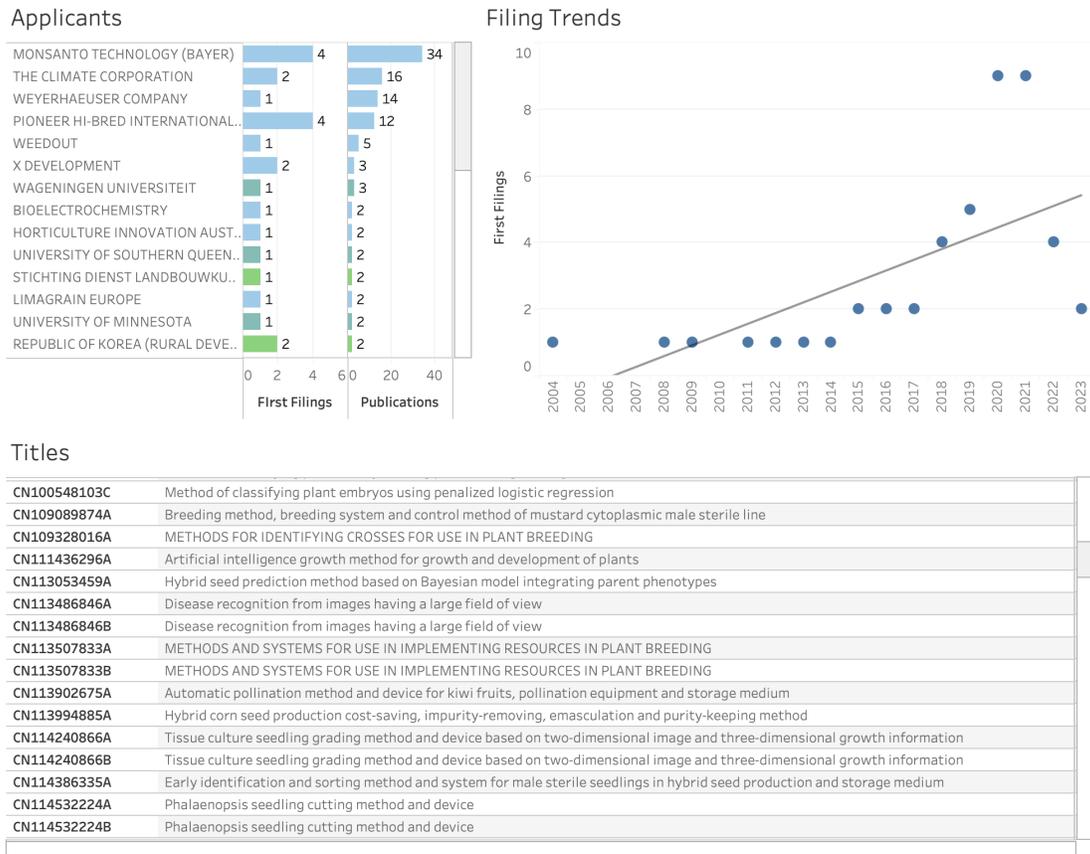
Applicants

Applicant	First Filings	Publications
MONSANTO TECHNOLOGY (BAYER)	4	34
THE CLIMATE CORPORATION	2	16
WEYERHAEUSER COMPANY	1	14
PIONEER HI-BRED INTERNATIONAL..	4	12
WEEDOUT	1	5
X DEVELOPMENT	2	3
WAGENINGEN UNIVERSITEIT	1	3
BIOELECTROCHEMISTRY	1	2
HORTICULTURE INNOVATION AUST..	1	2
UNIVERSITY OF SOUTHERN QUEEN..	1	2
STICHTING DIENST LANDBOUWKU..	1	2
LIMAGRAIN EUROPE	1	2
UNIVERSITY OF MINNESOTA	1	2
REPUBLIC OF KOREA (RURAL DEVE..	2	2

Filing Trends

Titles

CN100548103C	Method of classifying plant embryos using penalized logistic regression
CN109089874A	Breeding method, breeding system and control method of mustard cytoplasmic male sterile line
CN109328016A	METHODS FOR IDENTIFYING CROSSES FOR USE IN PLANT BREEDING
CN111436296A	Artificial intelligence growth method for growth and development of plants
CN113053459A	Hybrid seed prediction method based on Bayesian model integrating parent phenotypes
CN113486846A	Disease recognition from images having a large field of view
CN113486846B	Disease recognition from images having a large field of view
CN113507833A	METHODS AND SYSTEMS FOR USE IN IMPLEMENTING RESOURCES IN PLANT BREEDING
CN113507833B	METHODS AND SYSTEMS FOR USE IN IMPLEMENTING RESOURCES IN PLANT BREEDING
CN113902675A	Automatic pollination method and device for kiwi fruits, pollination equipment and storage medium
CN113994885A	Hybrid corn seed production cost-saving, impurity-removing, emasculation and purity-keeping method
CN114240866A	Tissue culture seedling grading method and device based on two-dimensional image and three-dimensional growth information
CN114240866B	Tissue culture seedling grading method and device based on two-dimensional image and three-dimensional growth information
CN114386335A	Early identification and sorting method and system for male sterile seedlings in hybrid seed production and storage medium
CN114532224A	Phalaenopsis seedling cutting method and device
CN114532224B	Phalaenopsis seedling cutting method and device

Figure 6 *– Artificial Intelligence and PGRFA related patent activity (IPC GO6N3/CPC G06N3)*

Patent activity in artificial intelligence involving PGRFA is clearly emergent. The presence of The Climate Corporation, which describes itself as a digital agriculture company, and X Development (established by Alphabet, the parent company of Google), is suggestive of an interesting potential point of transition in agricultural technology characterized by the emergence of new players who have not traditionally been present in agricultural R&D value chains.

4.6. Time Series Forecast 2020-2030 for First Filings and Publication Trends for Native Traits from the Gold Dataset

Time series forecasting provides a prediction of what is likely to happen based on activity in the past. What is useful about this for the present purposes is that we gain an insight into the likely range of future activity based on past activity.

A forecast for first filings of new patent families for native traits based on the gold dataset for the EPO and PCT filings (where ARIMA(2,1,2) offered the best fit – see above *Box 3* regarding the methodology) predicts that by 2030 first filings of new patent families involving native traits is expected to be steadily growing with a prediction of approximately 30 new filings in 2030 falling

into a predicted range between 19 and 40 filings in the 95% confidence interval.[21] However, a key difficulty in forecasting here is the low overall counts per year and the wide variation in first filings across years.

Another forecast (produced using Auto ARIMA) using the 4,717 family publications from the gold dataset predicts that there are likely to be approximately 389 publications in 2030 with a lower bound in the 95% confidence interval of 319 publications and an upper bound of approximately 457 publications. This suggests that, on the balance of the available data, there is unlikely to be a dramatic surge or radical steepening of patent activity for naturally occurring traits in the period to 2030.

5. Analysis of patent claims with potential to limit subsequent uses of PGRFA for research and breeding

5.1. Presenting a core dataset and an extended dataset of patents involving naturally occurring traits

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. Traits that already exist in PGRFA can be incorporated in new plants through conventional breeding or by applying new genomic techniques (NGTs) to edit the genome of the target plant using as reference the genetic sequence information of a PGRFA that has the desired characteristics. An example of new genomic techniques is the "gene scissors" known as CRISPR/Cas9 introduced in 2012, which allows for precise editing of DNA.

Cultivated plants with introgressed naturally occurring traits, sequences or genes may be patentable in many jurisdictions, as usually these plant-related inventions meet the requirements of novelty and inventiveness, at least insofar as the trait in the original PGRFA or its coding sequence have not yet been described. *Table 2* in Section 5.3, '*What can be patented and where*', provides details about the patentability of naturally occurring traits in plants and other relevant PGRFA-based inventions in different countries.

We used the methods described in Section 3*, 'Summary of Research Methods',* to identify patents involving PGRFA traits. *Figure 7* provides an overview of patent activity in the resulting gold dataset, consisting of 399 core publications (i.e., first filings) in approximately 398 INPADOC patent families, with a total of 4,717 family members (i.e., publications).

The gold patent dataset and its family members are publicly accessible for further exploration through the open access Lens database through the links provided in **Annex I** to this Report.

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[21] Time series forecasting provides a prediction based on past activity and predictions become more uncertain the further into the future they are projected. For that reason, forecasts include confidence intervals at 80% and 95% (e.g., 95 times out of 100 a prediction will be true). We use the 95% confidence interval to illustrate the range of low and high scores predicted by the model for 2030. Forecasts were produced using the fable package in the R statistical programming language. For background, see Hyndman, R. and Athanasopoulos, G. (2021) *Forecasting Principles and Practice*, 3rd edition. OTexts, available at: https://otexts.com/fpp3/.

Figure 7 – *Gold Patent Dataset: International Patent Activity for Naturally Occurring Traits (Data source, The Lens, PATSTAT)*

This figure shows that EPO and PCT filings can be traced back to the early 1990s with a steadily rising pace of activity.[22] While the reported activity is partial as it excludes all national filings that are not prosecuted through the two instruments above, it is also clear that the level of patent activity is, by the standards of the patent system, very low and peaks at just over 30 new first filings in 2020, with more than 200 patent applications globally, and just more than 100 new grants in 2021. Data on applicants in *Figure 7* also reveals that while the overall number of first filings by applicants appears to be low, publication numbers show that top-tier companies are actively pursuing or have secured protection in multiple countries.[23]

Taken across the broader landscape of filings of new patent families at the EPC and PCT involving PGRFA and other commonly used PGR, there were 14,785 family filings associated with the EPC and PCT applications between 1990-2023, of which approximately 398 families involved naturally occurring traits in the gold dataset (for PGRFA only) corresponding to approximately 2.7% of activity across that period. Taking 2020 as the most active filing year, there were 549 EPC/PCT

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[22] The colour code in the bottom right corner of *Figure 7* indicates granted patents in red against the overall number of patent documents belonging the same family in blue. Therefore, as usual, the count of publications includes the granted patents – i.e., is not additional to those.

[23] As anticipated above, filings under these patent instruments lead to multiplier effects where a single filing under an individual instrument may lead to the applications and grants in multiple countries. As such, even low levels of filings may have wider implications across multiple countries. And one patent filing related to one trait could cover hundreds of varieties, which further increases the impact on the market and subsequent users.

families involving PGRFA and other commonly used PGR filed in that year, and 31 for native traits in the 'gold' dataset suggesting that activity rose to 5.6% as a share of activity for that spot year.

In the case of publications, across 1990-2023, there were 259,399 publications under the core worldwide indicators (presented in *Figure 1*), out of which 4,717 publications involved members of the gold dataset (1.8%). At the time of writing, the total number of active patents belonging to the patent families in the 'gold' dataset amounted to approximately just below 1,000 granted patents worldwide in accordance with the status information provided in Lens.org.[24]

In addition, using 2020 as the spot year, there were 11,998 publications in PATSTAT for the core indicators, out of which 250 were members of the gold dataset (2%). Across 1990-2023 reference period, the percentage share of patent activity concerning naturally occurring traits in PGRFA is approximately 2-3% of the total patent activity for PGR related innovation as captured through the most relevant plant indicators. However, the underlying filings display spikes in activity with non-negligible fluctuations from one year to the next.

Furthermore, a total of 129 (32%) of the 399 documents in the gold dataset for native traits and 1,439 (30%) of the 4,717 patent family members for the gold dataset are classified using CPC code C12Q2600/13 - Oligonucleotides and plant traits (which we presented in *Figure 5* above). This provides evidence that in order to more easily differentiate naturally occurring traits related patent activity within the broader group of 'plant traits' related activity (which also includes GM traits) as classified by the CPC, a finer classification system should be adopted.

It is worth emphasising that the majority of the patents in the gold dataset do not indicate the original PGRFA materials that were used to develop the innovations. This is particularly true for innovations which relied on new genomic techniques and where "only" the PGRFA genetic information was used for making genetic changes. In these cases, the original PGRFA is almost impossible to identify unless it is voluntarily disclosed by the patentee.

Box 4 – Deep dive: *Experimenting with Cosine Similarity: identifying a set of 194 additional relevant filings in the USA*

> As explained in Section 3 of this report on the research methods, the gold dataset was constructed by focusing *only* on patent data from the European Patent Convention and the Patent Cooperation Treaty in order to limit noisy records from activity for variety patents and utility patents on plant varieties. This means that every national filing prosecuted exclusively through a national patent office in any country is not captured in the gold dataset (and in *Figure 7* above).
>
> To capture additional patent filings relevant to PGRFA (beyond those prosecuted through the EPC and PCT), we used a standard method in Natural Language Processing called Cosine Similarity in the way we have described in Section 3. This allowed us to identify a total of *676 candidate documents* which we cleaned up manually to remove non-relevant utility patents on varieties and other non-PGRFA related documents (e.g. primarily cotton). The result is a set of **194 additional relevant domestic filings in the USA** (presented in Annex II to the present Report).
>
> Although these US domestic filings do *not* have a multitier effect (i.e., by generating patent family members in other countries) similarly to the patents in the gold set, they represent an important finding and a step towards further refining the AI-driven methodology for the identification of native traits patents based on an expanded 'training set' that comprises both the claims in the gold dataset as well as those previously excluded from the USPTO, accounting for a total of 593 patent filings based on, or involving naturally occurring traits.
>
> Future searches in this area of R&D, should also be complemented by an examination of the additional national filings in languages other than English, notably domestic filings through the China National Intellectual Property Administration (CNIPA), where – based on the available patent indicators – we expect a comparable or higher volume of patent activity than in the USA.

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[24] For more information, see the link to family members in Lens.org which is provided in **Annex I**.

These results and the forecasts presented above in Section 4.6 suggest that in quantitative terms patent activity involving naturally occurring traits is increasing but will continue to be a limited subset of wider patent activity involving PGR related innovation for the foreseeable future. It also confirms the utility of adopting a finer classification system under the IPC and CPC that facilitates the identification of patents involving naturally occurring traits in PGRFA.

5.2. Weighing the potential impact of patent claims on the use of original PGRFA material for further research and breeding

The analysis of the claims in the initial gold dataset of 399 core patent documents allowed us to identify seventeen distinct categories of patent claims related to PGRFA-related inventions, including plants, plant varieties, traits, genes and gene sequences, and other embodiments or innovations based on DSI/GSD derived from the PGRFA.

Table 1 categorizes these seventeen different types of claims (first column), provides an assessment of their potential impact on the subsequent use of PGRFA on which the inventions were based – and on other PGRFA with equivalent elements and characteristics – in accordance with the claims' scope (second column), and includes representative examples of each claim type from the core set (third column).

"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. "Medium impact" claims are those that partially limit the utilization of the PGRFA (e.g., claims over processes to make a plant with a characteristic obtainable by new genomic techniques that do not extend to the obtention of such characteristic by conventional crossing). "Low impact" claims are those that do not limit the utilization of a PGRFA substantially (e.g., claims over a specific marker associated with a characteristic obtainable from the PGRFA). "Usually no impact" claims are those that do not limit the use of the original PGRFA, but only the use of the patented subject matter derived, and substantially different from, the original PGRFA. This could be, for example, the case of utility patents covering specific plant varieties, or patents on artificial variants of a genetic sequence derived from a PGRFA but different from it (and not selected from a group that may comprise the natural variant), as well as patents over genetically modified crop 'events' and related products. These patents usually have a downstream limiting effect on the use of the claimed materials but not an upstream limiting effect on the PGRFA which has been used in their making.

The proposed categorization of the claim types and the related impact assessment is solely made for illustrative purposes to exemplify how different claim typologies may have different implications for the subsequent utilization of the PGRFA materials comprising or underpinning a claimed invention.

Table 1 – *Claim categories in international patent applications related to plant-related inventions based on, or involving naturally occurring traits and/or DSI/GSD derived from PGRFA*

Disclaimers: The referenced patents are presented as examples of patent claims that have (to various degrees) the potential to limit use of the original PGRFA material in the different countries where they are or can be granted. This does not mean that the respective applicants were bound by and/or in breach of an SMTA or other contractual or legal obligations.

The legal status of individual patents or applications in different jurisdictions (pending, granted, rejected, revoked, withdrawn or abandoned) and their licensing status is not specifically considered in the present study. The claim examples presented below are illustrative only, there are derived from international patent applications filed through the PCT or with the EPO, and they do not necessarily reflect the final claim construction resulting from the examination and amendments of individual applications of family members in various countries. Ultimately, granted claims in patents belonging to the same family may be different from one country to another, and from the initial patent application.

The information presented in this Report may be used at the discretion of the user and in no case can it be considered a substitute for specialised legal advice or dedicated freedom to operate (FTO) analysis in regard to the ability to proceed with the research, development and/or commercial production of a new product or process without the risk of infringing the intellectual property rights of any third party.

Claim Type	Impact on the use of the PGRFA on which the invention is based, and/or on homologous traits and genes from other PGRFA, for research and breeding	Examples (Text in red denotes particularly important portions of a claim to illustrate the relevant examples)
Variety patents		
1. New specific variety obtained from breeding with the original material NB: "variety patents" are relevant only in the USA and Canada. Several of the varieties presented in the PINTO Database[25] have corresponding variety patents in the USA.	Usually none	Not included the search that led to the initial core set of 399 patent families.

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[25] PINTO (Patent Information and Transparency On-line) was created by the European Seed Association Euroseeds with the aim of improving transparency regarding plant varieties that might fall under the scope of patents or patent applications. Although there are many publicly accessible patent databases, PINTO is unique since it provides the link between a plant variety and a patent or patent application, information which is currently not available elsewhere. Available at: https://euroseeds.eu/pinto-patent-information-and-transparency-on-line/.

Plants and their parts		
2. "Cultivated" plant with a trait obtainable (or introgressed) from the original material, its parts (including seeds, and fruits) Note: The term "obtainable" does not mean that the trait is actually "obtained" from the original material but only that it is identical to what is in the deposit, so it can come also from a progeny or a sister. NB: While since 2017 breeders can no longer obtain European patents with claims on plants with native traits at the EPO, they can still obtain patents with claims which constrain the use of plants with native traits including claims on treated seeds and resulting plant materials (see below No. 3).	High	Annex I – Line 4 - WO2024255994A1 [Claim 11] Lettuce plant according to any one of the claims 1 to 10, wherein the one or more MRC4 resistance gene(s) is obtainable, derived, or originates from a lettuce plant deposited under number NCIMB 44113, NCIMB 44114, NCIMB 44115 or NCIMB 44116. Annex I – Line 75 - EP4175463A1 [Claim 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 or in Lactuca sativa line 18LEN002364, representative seed of L sativa 18LEN002364 having been deposited with the NCIMB under Accession No. NCIMB 43625, and wherein said introgressed sequence is located on chromosome 2 and comprises one or more of the following SNP markers: a) a G genotype in the heterozygous or homozygous state for SNP marker SL1831 in SEQ ID NO: 1; b) an A genotype in the heterozygous or homozygous state for SNP marker SL1847 in SEQ ID NO: 6; c) a G genotype in the heterozygous or homozygous state for SNP marker SL1887 in SEQ ID NO: 11 ; and/or d) a C genotype in the heterozygous or homozygous state for SNP marker SL1883 in SEQ ID NO: 16; wherein the resistance of the plant to Bremia lactucae is enhanced as compared with a L sativa plant lacking said introgressed sequence. Annex 1 – Line 189 - EP3206478A1 [Claim 1] A cultivated Cucumis sativus var. sativus plant comprising an introgression fragment from a wild cucumber or a wild relative of cucumber on chromosome 2 in homozygous or heterozygous form, wherein said introgression fragment confers an increase in cucumber fruit yield.
3. Seed for growing a cultivated plant comprising a sequence from the original material, wherein the seed are technically treated (e.g., coloured or pelleted) in a generic (i.e., non-inventive) way. Note: In EPC countries, these claims are an emerging strategy to circumvent the exception for plants obtained exclusively by essentially biological processes under Rule 28(2) EPC, which are, in principle, not patentable. NB: in some crops like sugar beet pelleting is mandatory as non-pelleted seed cannot be sawn using mechanical planters. Only pelleted seed is commercialized. In other species (e.g., cucumber, tomato), seed treatment is optional and also non-treated seed are commercialized.	Medium to high (Depending on crop)	Annex 1 – Line 71 - EP3696188A1 [Claim 5] Seed of a Cercospora-resistant plant, characterized in that the plant contains the nucleic acid molecule according to claim 1, wherein the plant which contains the nucleic acid molecule as introgression belongs to the subspecies Beta vulgaris subsp. vulgaris, wherein the seed comprises the nucleic acid molecule according to claim 1 transgenically or as introgression, and, wherein the seed has been technically treated, whereby the technical treatment is selected from the group consisting of: (a) Polishing, (b) Pelleting, (c) Incrustation, (d) Colouring.
4. "Cultivated" plant with a mutation inspired by and identical to the mutation in the original material, developed with new genomic techniques (NGTs) Note: In this example, the patentee identified in a PGRFA a variant of an endogenous gene which confers improved disease resistant. Instead of "just" claiming the new gene, the patentee claimed the specific	High	Annex I – Line 9 - WO2024240681A1 [Claim 8] The plant, or plant part, according to claim 7, wherein the protein comprising at least 96% sequence identity to SEQ ID NO: 8 comprises one or more of the following amino acid changes: Amino acid number 10 to amino acid number 18 are Serines (S) the amino acid at the equivalent position of amino acid 484 of SEQ ID NO: 8 is a Methionine (M) the amino acid at the equivalent position of amino acid 629 of SEQ ID NO: 8 is a Lysine (K) the amino acid at the equivalent position of amino acid 679 of SEQ ID NO: 8 is a Histidine (H) or an Aspartic Acid (D). [Claim 9] The plant, or plant part, according to claim 8, wherein the changes in the gene encoding the protein comprising at least 96% sequence identity to SEQ ID NO: 8 are made using targeted

differences (mutations) between the resistant gene and the susceptible "original", which is a much broader claim.	*(red)*	gene editing of the endogenous gene encoding the protein of SEQ ID NO: 10 or are induced by mutagenesis, such as induced by radiation or chemical mutagens.
5. "Cultivated" plant with a general mutation of a gene inspired by but not specifically claiming (nor disclosing) the specific GR mutation (see also related DNA claims under 12.) Note: This type of claim limits not only the utilization of a PGRFA expressing a native trait, but also similar solutions based on the mode-of-action of the native trait in such PGRFA, since it covers the native trait but also alternative genetic mutations with the same effect. These patents usually only cover the difference between an endogenous gene which does not confer the desired trait and the variant which does. Often these claims only disclose what is changed but not necessarily what the replacement is. For example, a specific amino acid at a specific position is replaced by any other amino acid, or preferable by an amino acid selected from a group of amino acids with similar behaviour. In this example, the specific amino acid found in the natural variant might be part of this group but cannot be easily identified.	High	Annex I – Line 4 - WO2024255994A1 [Claim 1] A downy mildew resistant lettuce plant, wherein said lettuce plant comprises one or more MRC4 resistance gene(s) encoding a MRC4 resistance protein having at least 70% sequence identity with amino acid sequence of SEQ ID No. 6 providing downy mildew resistance, wherein said MRC4 resistance protein comprises a protein motif A represented by SEQ ID No. 9 and a protein motif B represented by SEQ ID No. 10, wherein said lettuce plant is resistant to Bremia lactucae races Bl: 16-37EU.
6. Cultivated plant with a specific mutation of the same gene as mutated in the original material but different from (and not covering) the original material mutation	Usually none	N/A
7. Cultivated plant with new combination of traits from different original materials or with a "generic technical trait" (e.g., herbicide tolerance). Note: A "generic technical trait" means a trait made by technical means (mutagenesis, transformation) which is commonly known and usually already part of the prior art. In this example, the combination of a technical trait with a native trait may be considered to confer a 'technical effect' (for the purpose of assessing the patentability requirements – notably, the inventive step), even if the technical trait does not substantially contribute to the invention as such. In the example, the technical trait is Glyphosate tolerance (i.e., EPSP synthase is the molecular target of the herbicide Glyphosate).	Medium	Annex I – Line 72 - WO2022037967A1 [Claim 11] A plant of the genus Beta or Spinacia comprising a nucleic acid molecule encoding a polypeptide that is able to confer resistance to Cercospora in a plant in which the polypeptide is expressed, characterized in that the nucleic acid molecule comprises a nucleotide sequence which is selected from the group consisting of: (a) a nucleotide sequence that encodes a polypeptide having an amino acid sequence according to SEQ ID No. 3; (b) a nucleotide sequence that comprises the DNA sequence according to SEQ ID No. 2; (c) a nucleotide sequence that comprises a DNA sequence according to SEQ ID No. 1 or SEQ ID No. 53; (d) a nucleotide sequence that hybridizes with a complementary sequence of the nucleotide sequence according to (a), (b), or (c) in 4 x SSC at 65 °C, and subsequent repeated washing in 0.1 x SSC at 65 °C for approximately 1 hour in total; (e) a nucleotide sequence that encodes a polypeptide which has an amino acid sequence that is at least 90% identical to an amino acid sequence according to SEQ ID No. 3; (f) a nucleotide sequence that is at least 90% identical to a DNA sequence according to SEQ ID No. 1 or SEQ ID No. 2; wherein the plant of the genus Beta or Spinacia furthermore comprises an endogenous allele encoding an epsp synthase having at position 179 an amino acid different from proline.

8. Harvested plant material with quality properties harvested from a cultivated plant that has a trait obtainable from the original material (preferably: non-propagating material).	High	Annex I – Line 277 EP2494055A1 [Claim 1] A tomato fruit with significantly increased fruit firmness at the harvesting stage linked to at least one genetic element in the cultivated tomato plant producing said tomato fruit, wherein said firmness is from between 1 .2 to 2.0 times greater than that of fruit from a control tomato plant which does not have the said at least one genetic element.
"Genetic parts"		
9. Isolated, unmodified DNA sequence from the original material. Note: this type of claims is not possible in most countries including in the US; however, they are possible in EPO countries and in China (CN).	High	Annex I – Line 103 - EP3993613A4 [Claim 20] An isolated polynucleotide comprising at least one scaffold having a nucleic acid sequence at least 70% homologous to a nucleic acid sequence set forth in any one of SEQ ID NOs: 1-31 or a part thereof, wherein the polynucleotide, when introduced into a wheat plant, confers or enhances resistance of the wheat plant to leaf rust disease and strip rust disease. Annex I – Line 71 - EP3696188A1 [Claim 1] Nucleic acid molecule which encodes a polypeptide that is able to confer resistance to Cercospora in a plant in which the polypeptide is expressed, characterized in that the nucleic acid molecule comprises a nucleotide sequence which is selected from (a) a nucleotide sequence that encodes a polypeptide having an amino acid sequence according to SEQ ID No. 3 ; (b) a nucleotide sequence that comprises the DNA sequence according to SEQ ID No. 2 ; (c) a nucleotide sequence that comprises a DNA sequence according to SEQ ID No. 1 or SEQ ID No. 53 ; (d) a nucleotide sequence that hybridizes with a complementary sequence of the nucleotide sequence according to (a), (b), or (c), under stringent conditions, wherein stringent hybridization conditions are: hybridization in 4 x SSC at 65 °C, and subsequent repeated washing in 0.1 x SSC at 65 °C for approximately 1 hour in total; (e) a nucleotide sequence that encodes a polypeptide which has an amino acid sequence that is at least 90% identical to an amino acid sequence according to SEQ ID No. 3 over the entire length; (f) a nucleotide sequence that is at least 90% identical to a DNA sequence according to SEQ ID No. 1 or SEQ ID No. 2 over the entire length; wherein the resistance to Cercospora is a resistance to Cercospora beticola, or the plant belongs to the subspecies Beta vulgaris subsp. vulgaris.
10. A recombinant (man-made) construct comprising or encoding for a sequence from the original material without specification of the promoter and other heterologous elements. Note: Such claim would limit any use for transgenic approaches but would still allow for use by conventional breeding. Depending on how complex introgression is, this is usually still a viable alternative. In consequence, the impact is just partially limiting further use of the materials i.e., medium.	Medium	Annex I – Line 19 - WO2024132095A1 [Claim 23] Use of a gene construct plasmid for introducing one or more resistance gene(s) into the genome of a plant or plant cell, wherein the gene construct is comprised of a resistance gene RCB1 and/or a resistance gene RCB2 according to any of the claims 12 to 17 operably linked to expression providing sequences in said plant. Annex I – Line 103 - EP3993613A4 [Claim 30] A nucleic acid construct comprising the isolated polynucleotide of any one of claims 20-29, further comprising at least one regulatory element.
11. Modified, non-natural DNA sequence as part of a recombinant construct	Usually none	N/A
12. DNA sequence of an endogenous gene with mutations inspired by but not specifically	Medium to high	Annex I – Line 400 - WO2018029300A1 [Claim 1] Nucleic acid molecule which encodes a polypeptide which is capable of conferring resistance to a pathogen in a plant in which the

claiming (nor disclosing) the specific GR mutation		polypeptide is expressed, characterized in that the nucleic acid molecule comprises a nucleotide sequence which is selected from (a) a nucleotide sequence which encodes a polypeptide with an amino acid sequence according to SEQ ID NO: 2 or a polypeptide with an amino acid sequence which is at least 70% identical to SEQ ID NO: 2, in which at least one amino acid exchange is present due to one or more mutations of the nucleotide sequence, preferably wherein lysine (K) at position 307 and/or glutamine (Q) at position 437 is exchanged for another amino acid; […]
13. Specific molecular marker	Low to medium	Annex I – Line 2 - EP4338585A1 [Claim 22] A DNA marker for selecting a spinach plant having an RTM-1 gene, wherein the DNA marker is composed of at least one SNP selected from the group consisting of a SNP specified by chr4_8488603 of the spinach plant, a SNP specified by chr4_8494600 of the spinach plant, a SNP specified by chr4_8510715 of the spinach plant, and SNPs strongly linked to these SNPs.

Methods & uses

Note: in many countries the protection of these claims extends to the plant made with the method.

14. Process or method of using the original material, which is available as a public accession, for breeding or as a trait source to develop a new plant characterized by that trait (e.g., "A method of using public accession XYZ to breed a variety with trait A") Note: In many countries the scope of method claims extends to the product made with the patented method (i.e., the plant).	High	Annex I - Line 188 - EP3206479A1 [Claim 29] Use of a recombinant chromosome 6 comprising an introgression fragment from a wild cucumber plant or wild relative of cucumber, said introgression fragment comprising an allele conferring enhanced fruit yield, for breeding cucumber varieties having enhanced fruit yield, wherein said recombinant chromosomes 6 is the recombinant chromosome 6 as found in seeds deposited under accession number NCIMB 42262, or is derived from said recombinant chromosome 6. [Specific accession not disclosed] Annex I – Line 191 - EP3054766A4 [Claim 22] A method for producing an agronomic ally elite spinach plant that comprises in its genome at least one locus conferring broad-spectrum resistance to Peronospora farinosa f. sp. spinaciae (Pfs), the method comprising: (i) crossing a first spinach plant with a second spinach plant, wherein the first plant comprises in its genome at least one locus from Spinacia tetrandra that confers broad-spectrum resistance to Peronospora farinosa f. sp. Spinaciae, and wherein the second plant lacks said locus; and (ii) selecting at least a first progeny spinach plant resulting from said crossing that comprises said locus. [Two S. tetrandra accessions, designated GB 1860 and GB 1861, were found to carry resistance to all races tested.] Annex I – Line 192 - EP3198016A4 [Claim 22] A method for producing a hybrid Solanum lycopersicum plant with elevated Brix levels, comprising crossing a first Solanum lycopersicum parent plant with a second Solanum lycopersicum plant of a different genotype, wherein the first parent plant comprises a Lin5 allele from Solanum pennellii and a Penl allele from Solanum pennellii, wherein the Lin5 and Penl alleles confer elevated Brix levels relative to a plant lacking the Lin5 and Penl alleles [Solanum pennellii LA716].
15. Process of using a deposited cultivated plant comprising the trait derived from the original material for breeding or as trait source (deposited under Budapest Treaty) (i.e., "A method of using Budapest Treaty Accession XYZ to breed a variety with trait A")	High	Annex I – Line 189 - EP3206478A1 [Claim 29] Use of a recombinant chromosome 2 comprising an introgression fragment from a wild cucumber plant or wild relative of cucumber, said introgression fragment comprising an allele conferring enhanced fruit yield, for breeding cucumber varieties having enhanced fruit yield, wherein said recombinant chromosomes 2 is the recombinant chromosome 2 as found in seeds deposited under accession number NCIMB 42262, or is derived from said recombinant chromosome 2.

16. Process or method of making a cultivated plant comprising an identical mutation (or a generalized gene modification covering it) using new genomic techniques (NGTs) Note: This type of claims may include, for instance, a method claim for making a cultivated plant comprising a genetic modification resulting in the mode-of-action conferred by the native trait – covering the native traits but also alternative changes with the same effect – by using a technical process e.g., random or targeted mutagenesis, transformation. Patents that include process related claims, while not including claims over the resulting products or embodiments (as such) are very common in countries that do not allow direct claims on plants. These claims would only block the utilization of the PGRFA through modern breeding techniques but not through conventional crossing.	Medium	Annex I – Line 50 - EP4376596A1 [Claim 5] A method for generating or producing a maize plant or plant part and/or for improving (stover) digestibility, comprising introducing into the genome of a maize plant or plant part the polynucleotide as defined any of claims 1 to 3. [Claim 8] The method according to claim 5 or 6, wherein introducing includes stable or transient integration by means of transformation including Agrobacterium-mediated transformation, transfection, microinjection, biolistic bombardment, insertion using gene editing technology like CRISPR systems (e g. CRISPR/Cas, in particular CRISPR/Cas9 or CRISPR/CasI2), CRISPR/CasX, or CRISPR/CasY), TALENs, zinc finger nucleases or meganucleases, homologous recombination optionally by means of one of the gene editing technology including preferably a repair template, modification of endogenous gene using random or targeted mutagenesis like TILLING or above mentioned gene editing technology or mutagenesis mediated by transposon or transposable element. Annex I – Line 9 - WO2024240681A1 [Claim 13] A method of modifying the endogenous gene on melon chromosome 5, encoding a protein of SEQ ID NO: 10, by targeted gene editing or by induced by mutagenesis, such as induced by radiation or chemical mutagens, whereby the gene is modified so that the encoded protein comprising at least 96% sequence identity to SEQ ID NO: 8 comprises one or more of the following amino acid changes: Amino acid number 10 to amino acid number 18 are Serines (S) the amino acid at the equivalent position of amino acid 484 of SEQ ID NO: 8 is a Methionine (M) the amino acid at the equivalent position of amino acid 629 of SEQ ID NO: 8 is a Lysine (K) the amino acid at the equivalent position of amino acid 679 of SEQ ID NO: 8 is a Histidine (H) or an Aspartic Acid (D).
17. Process of identifying/selecting plants comprising or using a marker derived from the original material, or the process of using of sequence derived from the original material as marker to develop new varieties Note: these are "working processes" and not "production processes" which would extend to the resulting plants.	Low	Annex I – Line 102 - EP3993609A1 [Claim 9] Method for identifying a plant being resistant to Tomato spotted wilt virus, or TSWV, according to any one of the claims 1 to 8, the method comprises the step of establishing the presence of first resistance providing genomic fragment comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 12, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 22, SEQ ID No. 24, and SEQ ID No. 26 in the genome of the plant.

5.3.   The Territoriality of Patent Law: What can (or can't) be patented and where

Not all the types of claims we have described in *Table 1* are allowable or granted in every country. Plant varieties, plants, or naturally occurring DNA sequences are explicitly excluded from patentability in many countries. However, even in such countries, it is still possible to obtain valid claims which cover a plant (without naming a specific variety), its parts and components, and/or their uses. As mentioned before, very few countries allow for utility patents on specific plant varieties. In some countries, the patentability of breeding processes depends on the definition of "essentially biological processes" as non-patentable subject matter, and such definition may also differ from one jurisdiction to another. *Table 2* summarizes where broad categories of claim types can be patented or not.

***Table 2** – What can (or can't) be patented and where: selected examples*

	Subject matter of a plant-related invention	Where it can (or can't) be patented, and related exclusions
1	Variety patents	Australia, Canada, Japan, Korea and the USA allow patents over specific plant varieties. Most other countries do not generally allow claims to individually named varieties but only to plants in general.
2	Plants and their parts (including traits)	Many countries allow patents on plants and their parts, including the harvested products. These countries include countries of category 1 of this Table plus Israel, Mexico, European Patent Organization (EPO) countries, Eurasian Patent Organization countries, Malaysia, Norway, New Zealand, Philippines, Singapore, Taiwan, Uruguay, Vietnam and South Africa, among others. The European Patent Office (EPO) does not allow claims on plants exclusively obtained by essentially biological processes if filed after July 1, 2017. However, even under the European Patent Convention (EPC) it is possible to overcome this limitation by obtaining claims over these plants' parts, such as claims on seed or products that have been technically treated (e.g. silage). After July 1, 2017, the EPO accepts the patentability of genetic mutations that are identical to genetic parts in existing PGRFA as long as they have been obtained by technical means (e.g., by new genomic techniques such as genome editing). In the European patent jargon, these genetic mutations are not considered naturally occurring traits because they have not been obtained by essentially biological processes – even when the genetic sequences and the resulting traits are *de facto* identical to the sequences and traits found in nature. No claims on plants or other propagatable material are allowed in Brazil, China (P.R.), India, Saudi Arabia, Thailand, and most countries in the Global South, but "indirect" protection through claims on DNA, genome, or methods can be obtained. An exception is Argentina, where no claim (including process claims) can extend to plant material.
3	Genetic parts	Several countries allow patents over genetic parts and components, but they may be subject to various limitations: - Patent claims over isolated, unmodified naturally occurring DNA sequences (including molecular markers and genes) are not allowed in many countries, including USA. However, even in these jurisdictions, demonstrating that a DNA sequence is pre-existing in nature can be challenging, unless the source is disclosed by the applicant, which is not usually the case.

		- Patent claims over isolated, unmodified naturally occurring DNA sequences are allowed under the European Patent Convention and in China, as long as the sequence was not published before.
		At the same time, in many countries, molecular markers may be generally used in research and breeding under the experimental use/research exemption.
4	Processes and Methods	These typologies of claims are accepted in almost all countries.
		The European Patent Office may accept patentability of a method involving existing PGRFA only if the patentee provides for a deposit of such PGRFA under the Budapest Treaty. Disclosure of a public accession instead of a Budapest Treaty deposit is not considered sufficient because the availability of such accessions cannot be ensured over the entire terms of the patent (20 years from filing).

It is important to highlight that none of the claim types presented in *Table 1* limit physical access to the original material as such. If the original material is an accession that is available in the Multilateral System, the effect of a patent containing one or several claim categories presented in *Table 1* would only be to limit what a researcher or breeder may do:

a) with the material received under an SMTA when one or more of its characteristics or traits are covered by the claims,
b) with any resulting planting materials (or varieties derived from such materials that retain any patented traits or characteristics), and
c) with other PGRFA that naturally present those same traits or characteristics.

Box 5 – Deep dive: *Hypothetical scenario illustrating the potential impact of product claims covering a "cultivated" plant with a mutation inspired by and identical to the mutation in the original material, developed with new genomic techniques (NGTs), and related process claims*

> Let's imagine a **hypothetical scenario**, in which a researcher obtains samples of PGRFA with the SMTA from a national genebank which maintains these materials under the ITPGRFA's Multilateral System.
>
> The researcher identifies in some of these accessions a variant of a gene which confers improved disease resistance in the species he is working on. Using genome editing, he manages to mutate the relevant gene in his target plants so that the resulting gene is identical to the resistant variant he has identified in the MLS accessions, and the resulting plant expresses the disease resistance he was seeking.
>
> He obtains a patent in five countries including claims on the sequence of the resistant gene variant, the process to obtain such gene variant and the resulting trait using NGTs, and the plant of the target species containing such gene variant and expressing improved disease resistance.
>
> Subsequent researchers can continue having access with the SMTA to the original accessions that are available in the Multilateral System. However, in the five countries where the patents have been granted, researchers will have to ask the patent owner's permission to investigate the patented gene variants that confer the disease resistance naturally present in the MLS accessions, and to introgress these gene variants into new plants.
>
> In principle, nothing in the patent prevents other researchers from using freely the original MLS accessions in research and breeding on other traits. Researchers outside of the five countries where these patents have been granted can also use the original accessions for any research and breeding purposes, including replicating the patented processes, gene variants and traits for the development of new varieties that they can commercialize in any country except in those where the patents have been granted and are in force.

6. Discussion

6.1. Main Findings

Quick recap of the main findings:

Prepared for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025.

- Trends show an increase in patent applications and grants in areas of plant research and development relevant to PGRFA, including for inventions involving naturally occurring traits, sequences and genes, although these types of patents represent a small fraction of the total patent activity concerning PGR innovation. Native traits related patent activity in the 'gold' dataset (i.e., excluding sole national filings, notably in the US and China) constitutes approximately 2 to 3% of the total patent activity resulting from plant-related research and development (i.e., 259,399 publications) as captured through the most relevant PGRFA indicators (see above *Figure 1* – as we have highlighted in Section 4.1, such indicators also capture a variety of other inventions related to PGR that are non-food/feed related and/or in research areas beyond crop genetic improvement).
- The preliminary findings of this Landscape Report show that there are at least 12 distinct typologies of commonly grated patent claims (out of 17) that present a medium or higher impact on restricting the subsequent use of the PGRFA materials on which the claimed inventions are based (i.e., upstream effects). Hence, depending on how the claims are constructed, these patents can limit to various degrees the subsequent use of the PGRFA on which the claimed invention is based as well as homologous features or characteristics naturally present in other PGRFA for research, breeding and training. Their effects, however, are limited to the patents' geographical scope and by the scope of the claims themselves.
- The current features of the data architecture and its availability in international patent databases do not make it possible to assess how many patents have been applied and granted for inventions that incorporate or are based on PGRFA materials from the Multilateral System. Therefore, there is an information deficit regarding whether MLS materials are being used or not by patentees in different countries (our research was limited to only materials provided by CGIAR centers). Incidentally, we are aware of two patents in the 'gold' dataset which were developed from accessions that are also currently available through the Multilateral System from sources other than CGIAR centers.)
- The use of distinctive identifiers for the disclosure of MLS accessions in the texts of patent documents, combined with appropriate guidance to applicants on the required form of disclosure, will be essential to address this information gap and promote transparency and mutual supportiveness between the Plant Treaty and the International Patent System.

6.2. Issues for possible further consideration by the WG-EFMLS

In light of the methodological challenges we encountered in our research so far, and the preliminary findings described above, we include here a list of issues for consideration by the Working Group to take up on its own, or to recommend to the Secretariat, the Governing Body or a reformed *Ad Hoc* Technical Advisory Committee on the MLS and the SMTA.

To address the information gaps that we have encountered in our research and that will represent impediments to future attempts to monitor relevant developments, including payments due by recipients or subscribers under the enhanced MLS, and compliance with respect to the patenting of MLS materials, the following issues could be further considered:

- Include a requirement in the SMTA that recipients disclose, in patent applications, the MLS materials, and any derived DSI/GSD, on which their inventions are based, mentioning DOIs and/or other distinctive standardized identifiers to be elaborated for the disclosure of MLS accessions in patent documents, in accordance with a standardized formula/protocol. NB: The revised draft Resolution for the WG-EFMLS-13 already includes an invitation to

Prepared for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025.

patent applicants to do so (see paragraph 16).[26] However, without including a corresponding obligation in the revised SMTA, this cannot be considered a legal requirement. A contractual disclosure requirement in the SMTA would be consistent and synergetic with the new WIPO Treaty on Intellectual Property, Genetic Resources and Associated Traditional Knowledge (WIPO Treaty), while also making it clear that relevant information needs to be disclosed in a publicly accessible way as part of the patent application process.

- Collaborate with WIPO and the EPO, and other regional and national patent offices, to develop new, tailored patent classifications to enhance transparency and searchability of relevant patents. The international patent system routinely updates its classification systems to address developments in science and technology, and to address the interests of Member States of global and regional patent instruments. On the global level, the main classification system is the International Patent Classification (IPC) administered by WIPO. The Cooperative Patent Classification (CPC) administered by the European Patent Office and the US Patent and Trademark Office offers a much more detailed level of classification and is increasingly used by other major patent offices around the world. The Secretary of the Plant Treaty could liaise and work with those offices to identify or create new classifications, or further elaborate existing subclasses and indicators, to identify, through existing standard methods, patents that involve: i) naturally occurring or 'native' traits in patent documents;[27] ii) DSI/GSD-related inventions derived from PGRFA based on the use of New Genomic Techniques; iii) Artificial Intelligence and PGRFA-related applications.

To promote clarity for Contracting Parties and stakeholders providing and using PGRFA through the Multilateral System, the following issues could also be considered:

- Develop an explanatory note on the relationship between different kinds of patent claims and the provisions in Treaty Article 12.3(d) and SMTA Article 6.2 (this task could be undertaken, for instance, by the proposed reformed Technical Advisory Committee on the MLS and the SMTA, as proposed by the Co-chairs. In addition, the Governing Body might wish to consider modalities for adopting such a note in the form of an agreed interpretation of the above provisions.
- Incorporate the content of paragraph 49 of the revised draft Resolution into the SMTA.[28] (As noted above in the context of a possible disclosure obligation, a limitation on what

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[26] FAO (2025), *Package of Measures to Enhance the Functioning of the Multilateral System: proposal by the Co-Chairs to address the improvements requested by the Working Group*, IT/OWG-EFMLS-13/25/4.1, p. 4, available at: https://openknowledge.fao.org/server/api/core/bitstreams/ea33b34e-593d-40c9-a427-f183279216e2/content.

[27] At present, the relevant indicators do not disaggregate down enough – i.e. the family level would need to disaggregate down to the genus or species levels, which already happens, for instance, with A61K36 for medicinal plants. A61K36 is an example of a more detailed classification for plants that reflects the interest of Member States in more detailed information on traditional medicines. The same approach could be considered for PGRFA relevant to the Plant Treaty. Available at: https://ipcpub.wipo.int/?notion=scheme&version=20250101&symbol=none&menulang=en&lang=en&viewmode=f&fipcpc=no&showdeleted=yes&indexes=no&headings=yes&notes=yes&direction=o2n&initial=A&cwid=none&tree=no&searchmode=smart.

[28] Paragraph 49 of the revised draft Resolution (see above fn. 26) states that the Governing Body:

"*Affirms* that digital sequence information/genetic sequence data on plant genetic resources for food and agriculture in the Multilateral System should not be subject to intellectual property rights or other rights that would limit the facilitated access to the plant genetic resources for food and agriculture from which the digital sequence information/genetic sequence data was derived".

Prepared for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025.

recipients can do with DSI/GSD will not be legally binding on recipients unless included in the SMTA).

6.3. Possible follow-up research

- Expanding scope of searches for MLS materials cited in patent applications beyond those potentially received from CGIAR centers, to include materials from other large providers of PGRFA from national, regional and international genebanks.
- Future patent searches in this area of R&D, could also be complemented by an examination of additional national filings for native traits related patents in languages other than English, notably domestic filings through the China National Intellectual Property Administration (CNIPA), where – based on the available patent indicators – we expect a comparable or higher volume of relevant patent activity than in the USA.
- Furthering the qualitative and quantitative analysis (e.g. by providing a quantification by claim type) of all granted claims in active patents belonging to the patent families in the 'gold' dataset – approximately just below 1000 granted patents worldwide in accordance with the status information provided in Lens.org.

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Acknowledgements & Authors' Contributions

Prepared for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025.

Annex I – Core Patent Dataset comprising 399 patent documents (first filings) in families related to naturally occurring ('native') traits

First filings (399) link to the supplementary Excell file on CGSpace:
https://hdl.handle.net/10568/173779.

First filings (399) available in Lens.org at:
https://www.lens.org/lens/search/patent/list?collectionId=231925.

Family members (4717) for the core set available in Lens.org at:
https://www.lens.org/lens/search/patent/list?collectionId=231964.

Annex II – Cosine Similarity Patent Dataset of US Domestic Filings (excluded from the PCT and EPC searches used to construct the Core Patent Dataset)

First Filings (194) Related to Naturally Occurring ('Native') Traits in the USA, link to the supplementary Excell file on CGSpace: https://hdl.handle.net/10568/173778.

Prepared for consideration by the Members of the WG-EFMLS-13, April 1-4, 2025.