



联合国
粮食及
农业组织



国际条约
粮食和农业
植物遗传资源

暂定议程议题 16.4

管理机构第九届会议

2022 年 9 月 19-24 日，印度新德里

根据《国际条约》第 15 条与管理机构签订协定的 机构报告

内容提要

本文件载有根据《国际条约》第 15 条与管理机构签署协定的国际机构提交的报告。各份报告按秘书处收到的原文载于本文件附录 2-4，供管理机构审议。本文还载有本两年度秘书根据第 15 条的国际种质资源收集品开展的最新活动情况。

征求指导意见

提请管理机构审议本文所载报告及其他信息，并结合附录 1 的决议草案要点，提供进一步指导。

I. 引言

1. 管理机构定期收到根据《国际条约》第 15 条与管理机构签订协定的国际机构的报告。这些报告涉及根据多边体系条款管理和分发种质的情况，还涉及与收集品的有序保管和当前在《国际条约》框架内开展的合作活动有关的问题。
2. 管理机构在第八届会议上，要求第 15 条规定的签署机构继续向管理机构会议提供报告。¹在管理机构第九届会议上，截至本文件发布之日，秘书收到了以下机构的报告：
 - 国际生物盐化农业中心；
 - 国际农业研究磋商组织的各个中心；
 - 热带农业研究与高等教育中心。
3. 本文件附录 2-4 所载报告按收到的原文提供给管理机构。秘书预计在本文件发布后还会收到其他报告，并将在增编中提供这些报告。
4. 本文件包含对现有报告的综述，还介绍了秘书在本两年度开展的支持执行现有第 15 条协定的活动的最新情况，包括根据《国际条约》第 15.1(g)条对据报受到威胁的收集品履行其职责。本文件还向管理机构通报了秘书为推动新协定所做的努力。

II. 收到的报告摘要

5. 管理机构在第八届会议上，对与国际生物盐化农业中心签订的第 15 条协定表示欢迎，并邀请其加强与秘书和相关机构在实施该协定和政策指导方面的合作。国际生物盐化农业中心的报告证实，自 2019 年签署第 15 条协定以来，该组织一直按照《国际条约》的要求管理其种质分发业务。报告通报了该两年度的种子活力测试、再生和特征分析活动，以及样本的国际分发情况。国际生物盐化农业中心还报告了根据《多种作物基础性状描述符表》进行的种质记录，以及正在进行的《国际条约》第 17 条全球信息系统数字对象标识符的分配。
6. 国际农业研究磋商组织的报告提供了截至 2021 年 12 月 31 日由 2006 年签署第 15 条协定的 11 个国际农业研究磋商组织中心维护的种质资源收集品的最新情况，并指出多边体系中共有 722 525 份遗传材料，根据 61 000 份《标准材料转让协定》分发了 600 多万份样本。报告还指出，自 2010 年以来，各中心从 142 个不同国家的提供者那里获得了 8 万份完全不同的材料，这些遗传材料是根据《标准材料转让协定》或其他协议获得的，其中提供者允许各中心分发与《标准材料转让协定》有关的材

¹ 第 12/2019 号决议，第二部分。

料。该报告描述了维护和增加收集品价值的活动，包括信息系统和数字对象标识符、预育种和育种活动。

7. 国际农业研究磋商组织的报告还提到了《国际农业研究磋商组织中心基因库改进遗传材料管理的指导说明》，该说明促进了国际农业研究磋商组织中心在现有适用政策范围内对国际收集品管理的某些方面进行协调统一。正如报告所澄清的那样，该说明本身并没有提出新的政策；相反，它反映并推动了各中心长期以来在根据各种框架管理国际收集品方面形成的最佳做法，首先是它们与粮农组织签署的 1994 年受托协定，后来是与《国际条约》管理机构签署的第 15 条协定。

8. 国际农业研究磋商组织的报告还提供了关于各中心因 2019 冠状病毒病（COVID-19）疫情而在日常管理收集品方面遇到的挑战的最新情况，并总结了国际农业研究磋商组织参与《国际条约》闭会期间政策工作的情况，特别关注关于加强多边体系的非正式磋商、关于数字序列信息的讨论以及农民权利。

9. 热带农业研究与高等教育中心的报告提供了关于咖啡、可可和其他作物的实地收集品以及该机构保存在冷藏室中的收集品的最新情况。报告提供了关于根据《标准材料转让协定》所做的收购和分配的最新情况。报告指出，已对一些面临风险的咖啡收集品进行了繁殖更新，并且在全球作物多样性信托基金（作物信托基金）“生物多样性促进机会、生计和发展”项目最近的支持下，也将对冷藏室的收集品进行繁殖更新。报告提到了在美国农业部的支持下，对可可和咖啡遗传材料的分子特性进行了鉴定。

III. 秘书处的活动

磋商

10. 根据管理机构第八届会议的要求，秘书继续与第 15 条机构就管理机构提供的协定和政策指导的实施情况进行定期磋商。特别是，秘书与国际生物盐化农业中心和太平洋共同体就《标准材料转让协定》的运作、种质信息系统和数字对象标识符进行了磋商；与特立尼达和多巴哥的西印度大学就可可采集重新建立了联系；出席了与国际农业研究磋商组织基因库和“同一个国际农业研究磋商组织”改革进程有关的正式会议和非正式磋商。

11. 关于“同一个国际农业研究磋商组织”，国际农业研究磋商组织向第九届会议提交的报告指出，根据“同一个国际农业研究磋商组织”对治理和业务结构的调整和整合，国际农业研究磋商组织各中心将保持其本身作为独立法律实体的法律地位，其在第 15 条协定下的义务不会受到任何实质性影响。预计“同一个国际农业研究磋商组织”将促进向管理机构提交更快、更定期、更协调的报告，并通过加强与《国际条约》的单一联络点，使整个国际农业研究磋商组织的参与更加积极有效。

12. 如报告所述，尽管国际林业研究中心—世界混农林业中心和国际热带半干旱地区作物研究所目前选择不加入“同一个国际农业研究磋商组织”的统一管理安排，但它们仍然是国际农业研究磋商组织各中心，其第 15 条协定不受影响。国际热带半干旱地区作物研究所和国际林业研究中心--世界混农林业中心将继续确保其基因库的运作和维护符合国际标准。国际热带半干旱地区作物研究所和国际林业研究中心—世界混农林业中心将继续为国际社会保存材料，并履行其对国际农业、粮食体系和景观管理的使命。

13. 秘书加入了专家组编写了《国际农业研究磋商组织—作物信托基金基因库成本和运作的系统级审查报告》，该报告于 2020 年 10 月发布。²该专家组审查了国际农业研究磋商组织基因库的运作和成本，并提出了未来资源分配的优先事项。为了解决基因库在全球快速变化和不断发展的技术背景下的作用，该专家组与科学领袖、基因库管理人员、政策制定者和国际农业研究磋商组织高级管理人员进行了一系列磋商。该专家组还与查塔姆研究所合作，组织了“查塔姆研究所对话：挑战时刻中作物的多样性——可持续发展中基因库的作用”。³

受到威胁的收集品

14. 关于其有序维护面临风险或威胁的国际收集品，管理机构第八届会议注意到正在进行的努力，包括哥斯达黎加、科特迪瓦和巴布亚新几内亚政府的努力，并要求秘书继续履行其职责并提供支持。在本两年度，秘书继续就科特迪瓦和巴布亚新几内亚的椰子收集品状况交流信息。关于科特迪瓦的非正式交流传达了信息，保证不会再出现以前报告的在收集地区进行房地产开发的类似威胁。关于巴布亚新几内亚的椰子收集品的交流，包括在利益共享基金的一个积极的分区域项目背景下进行的交流，报告了在将收集品迁移到不同地区以及在该地区其他收集品中重复独特的遗传材料方面取得的进展。

15. 关于热带农业研究与高等教育中心在哥斯达黎加的收集品，秘书能够在两个不同的场合与作物信托基金共同获得并提供即时的资金支持，首先是紧急维修冷藏室，随后是部分搬迁咖啡收集品。

16. 热带农业研究与高等教育中心的报告总结了国际条约秘书处和作物信托基金为保护咖啡收集品而继续推动的机构间合作。秘书与世界咖啡研究组织和作物信托基金就长期支持咖啡收集品进行了讨论。最近，秘书了解到，在对咖啡遗传材料进行分子特性鉴定后，热带农业研究与高等教育中心可能会从独特基因型的备份中受益，并逐步由美国农业部复制很大一部分的收集品。秘书将继续与热带农业研究与

² www.genebanks.org/wp-content/uploads/2020/11/GCO-Report_261020.pdf.

³ www.genebanks.org/news-activities/news/chatham-house-dialogue/.

高等教育中心和相关合作伙伴积极接触，以确保有序地维护和提供收集品，并履行第 15 条协议的义务。

国际椰子共同体和国际椰子遗传资源网络

17. 关于国际椰子遗传资源网络，管理机构在第八届会议上欢迎国际椰子共同体成为国际椰子遗传资源网络的新东道主和协调者，并邀请国际椰子共同体加强与秘书的协作。在本两年度，秘书通过提请粮农组织注意的国际生物多样性组织和国际商会之间的一项协议，以及随后与科特迪瓦和巴布亚新几内亚签订的两项第 15 条协定的修正函，促进了国际椰子遗传资源网络责任的正式移交。

18. 管理机构还邀请尚未签署《国际条约》第 15 条协定的国际椰子遗传资源网络收集品的东道国政府签署协定。在国际椰子共同体协调下开展的各种国际椰子遗传资源网络合作活动中，秘书继续与印度尼西亚和巴西的代表联络，这两个国家在《国际条约》之前已经与粮农组织签署了协议，并与国际椰子遗传资源网络其他成员国的代表进行了磋商。虽然到目前为止，与上述东道国政府签订新的第 15 条协定的前景是暂时的，但国际椰子遗传资源网络的可能重组可能会导致一些国家收集品在网络中获得更多的相关性，并作为具有全球相关性的参考收集品参与该网络。

新协定

19. 秘书在与国际橄榄理事会就该理事会管理的更广泛的国际收集品网络中的三个橄榄种质参考收集品的讨论中取得了重大进展。预计对第 15 条协定的审议将在 2022 年秋季的理事会会议上正式提出。

20. 在本两年度，由于旅行限制和其他限制，确保与新的相关国际机构达成协定的其他潜在方法受到限制，因此，没有提出新的前景。在不久的将来，随着互动条件的不断改善，将重新作出努力。

超低温保存

21. 关于超低温保存，可以回顾的是，管理机构在第八届会议上欢迎比利时政府提出的建议，即在鲁汶天主教大学——生物多样性国际基因库建立一个安全备份超低温保存设施，以保护各组织希望长期安全备份的植物材料，作为长期保护克隆作物和顽固种子的总体战略的一部分。

22. 国际农业研究磋商组织向第九届会议提交的报告指出，2020 年和 2021 年，国际生物多样性组织、国际热带农业中心、国际马铃薯中心和国际热带农业研究所（即国际农业研究磋商组织中保持克隆作物收集并正在实施超低温保存的中心）和作物信托基金发起了全球植物超低温保存倡议（GPCI）的发展。在 2021 年 6 月秘书与作物信托基金共同举办的网络研讨会上，介绍了全球植物超低温保存倡议。全球

植物超低温保存倡议将设立区域性的“卓越超低温保存中心”枢纽，首先在欧洲（比利时）、拉丁美洲（秘鲁）和非洲（尼日利亚）设立。据报道，全球植物超低温保存倡议被纳入国际农业研究磋商组织基因库倡议的工作计划中，该计划将寻求建立这些中心，以提供安全支持，创建区域和全球做法共同体，扩大超低温保存的作物范围，并提供能力建设和培训。

23. 国际农业研究磋商组织的报告进一步指出，全球植物超低温保存倡议下的三个中心将与世界各地的伙伴合作，根据《国际条约》对种质收集品进行超低温保存。

IV. 征求指导意见

24. 请管理机构审议本文件中提供的报告和信息，并结合本文件附录 1 中的可能通过的决议的内容草案提供指导。

附录 1

决议要点草案

(将纳入关于与其他国际组织合作的第**/2022号决议草案)

管理机构:

回顾《国际条约》第 15.1 条和第 15.5 条的规定，以及管理机构以前关于根据《国际条约》第 15 条签订协定的机构的决议；

1. **注意到**已根据《国际条约》第 15 条签订协定的机构在报告中提供的信息，**赞扬**那些提交报告的机构的宝贵内容，并**敦促**它们继续向管理机构今后的会议提供类似信息；
2. **请**尚未提交任何报告的机构在管理机构第十届会议上提交报告，并**请**秘书向这些机构发出这一邀请；
3. **还请**秘书在财政资源允许的情况下，继续与根据《国际条约》第 15 条签订协定的机构就实施相关协定和政策指导，包括就《标准材料转让协定》收集品遗传材料得转让，举行定期或周期性磋商，并在每届会议上向管理机构报告；
4. **注意到**正在进行努力安置那些有序保管存在风险或受到威胁的国际收集品，并**请**秘书继续行使其职责，根据《国际条约》第 15 条提供支持，酌情与所在国政府密切协作，并与其他有能力为这些工作提供资金、技术和其他必要支持的有关政府和相关机构合作；
5. **敦促**各缔约方、捐助方和其他利益相关方提供必要的物资支持，推动相关工作；
6. **再次邀请**国际椰子遗传资源网络中尚未签署协定的国际收集品的东道国政府根据《国际条约》第 15 条签署协定，以便将网络中的所有国际收集品纳入《国际条约》的管辖范围；
7. **请**秘书继续努力确保与其他相关国际机构达成符合《国际条约》第 15 条要求的协定；
8. **注意到**在“同一个国际农业研究磋商组织”的改革中，国际农业研究磋商组织各中心保持其本身作为独立法律实体的法律地位，与国际农业研究磋商组织各中心，包括那些选择不加入“同一个国际农业研究磋商组织”统一治理安排的中心的第 15 条协定仍然有效；

9. **进一步注意到**《国际农业研究磋商组织—作物信托基金基因库成本和运作的系统级审查报告》，并请国际农业研究磋商组织系统在执行管理机构制定的政策和标准以及提供培训、能力建设和支持数据管理等益处方面发挥促进作用；
10. **赞赏地注意到**国际农业研究磋商组织与《国际条约》秘书处在《国际农业研究磋商组织中心基因库改进遗传材料管理的指导说明》方面的合作，并**请**国际农业研究磋商组织中心继续将管理机构的政策指导纳入粮食和农业植物遗传资源的国际收藏品管理；
11. **欢迎**全球植物超低温保存倡议为克隆作物提供安全保障，**请**维持该倡议的国际农业研究磋商组织中心和全球作物多样性信托基金为超低温保存的有效运作提供能力建设和培训，并**请**秘书与促进该倡议的国际农业研究磋商组织各中心、国际农业研究磋商组织基因库倡议、全球作物多样性信托基金和其他相关利益相关方进行联络，以支持《国际条约》框架内的超低温保存治理和政策安排。

Biennial report (2020-21) by ICBA on the implementation of the agreement under Article 15 of the International Treaty on the Plant Genetic Resources for Food and Agriculture (ITPGRFA)

ICBA joined ITPGRFA as signatory

On 10th March 2019, ICBA signed an agreement during an awards ceremony of the [Khalifa International Award for Date Palm and Agricultural Innovation](#) in Abu Dhabi in the presence of H.H. Sheikh Nahayan Mubarak Al Nahayan, Minister of Tolerance of the UAE, within the framework of Article 15 of the FAO [International Treaty on Plant Genetic Resources for Food and Agriculture](#). After the agreement to the article 15, the crop germplasm collection stored in ICBA's gene bank formally became a part of the [Multilateral System](#) (MLS) of Access and Benefit-sharing (ABS), adding to the world's largest global gene pool of plant genetic material, available to farmers, plant breeders and scientists for the sustainable production of food from plants. This accord between the two institutions helped the researchers and other stakeholders to access the data on seeds of different crops/plants conserved in the ICBA genebank.

After signing the accord, the ICBA genebank complies with all the rules and regulations set by the treaty.

Seed Acquisition

ICBA has been collecting and conserving seeds of proven or potentially salt-tolerant plant species for research purposes at ICBA and other institutes with similar research interests. All seed samples added to the genebank collection have been acquired legally with relevant technical documentation. Most of the seeds ICBA has in its genebank have been obtained from international organizations, like ICARDA, ICRISAT, CIMMYT, USDA, ILRI, which follow the prevailing international rules of seed dissemination. During 2020-21, ICBA collected seeds of more than 790 accessions belonging to 11 crops (Table-1). After receiving, the germplasm was properly documented and conserved in the genebank.

Table-1. Crop accessions obtained during 2020-21

S.N.	Crop	Species	# of accessions	Source
1	Amaranth	<i>Amaranthus sp.</i>	70	AVRDC
2	Finger millet	<i>Eleusine coracana</i>	80	ICRISAT
3	Flax	<i>Linum usitatissimum</i>	142	USDA
4	Fonio	<i>Digitaria sp.</i>	50	NACGRAB
5	Foxtail millet	<i>Setaria italica</i>	33	ICRISAT
6	Moth bean	<i>Vigna aconitifolia</i>	50	USDA
7	Pearl millet	<i>Pennisetum glaucum</i>	238	ICRISAT
8	Proso millet	<i>Panicum miliaceum</i>	26	ICRISAT

9	Quinoa	<i>Chenopodium quinoa</i>	87	USDA
10	Rice	<i>Oryza sativa</i>	14	BIRRI
11	Suaeda	<i>Suaeda salsa</i>	1	SDNU
12	Wheat	<i>Triticum sp.</i>	1	UAE

Seed Viability Tests

The viability of the seed accession is a measure of how many seeds are alive and could develop into plants that will reproduce themselves, given the appropriate conditions. It is essential to know that the seeds that are stored in a genebank will grow to produce plants. Therefore, they must have high viability (>85%) at the start and during storage. ICBA genebank uses standard germination tests for various crops to find seed viability and rejuvenate those seed stocks whose germinability is dropped below the threshold of 85%. For this purpose, hundreds of accessions of different crops are tested for their viability every year. During 2020-21, seeds of about 1,880 cultivars that represent 19 crops tested for their viability (Table-2)

Table-2 Seed germination tests during 2020-21 at ICBA

S.N.	Crop	Species	# of accessions
1	Atriplex	<i>Atriplex sp.</i>	35
2	Barley	<i>Hordeum vulgare</i>	100
3	Barnyard millet	<i>Echinochloa sp.</i>	149
4	Beet	<i>Beta Vulgaris</i>	100
5	Birdwood grass	<i>Cenchrus setigerus</i>	1
6	Blue panicgrass	<i>Panicum antidotale</i>	4
7	Bristle grass	<i>Pennisetum divisum</i>	1
8	Colocynthis	<i>Citrullus colocynthis</i>	29
9	Deqana	<i>Coelachyrum piercei</i>	2
10	Mangrove grass	<i>Aeluropus lagopoides</i>	1
11	Mung bean	<i>Vigna radiata</i>	392
12	Oatgrass	<i>Centropodia forskalii</i>	1
13	Quinoa	<i>Chenoodium quinoa</i>	108
14	Safflower	<i>Carthamus tinctorius</i>	595
15	Salt grass	<i>Sporobolus spicatus</i>	4
16	Slender buffelgrass	<i>Cenchrus pennisetiformis</i>	3
17	Sorghum	<i>Sorghum bicolor</i>	302
18	Triticale	\times <i>Triticosecale</i>	20
19	Wheat	<i>Triticum aestivum</i>	36

Seed Regeneration

The most critical part of material conservation is that the seeds maintained in the genebank should be true to the type and show the accession's representative characteristics. Therefore, rejuvenation of the accession is necessary and must be carried out in the correct way to maintain the characteristics of the original population. Regeneration is also essential when the seeds' amounts go below a critical level. ICBA genebank works on regenerating crop accessions with lower viability or a lower number of seeds. The seeds of more than 2,300 accessions of 15 different crops multiplied during 2020-21 at ICBA field research facilities (Table-3).

Table -3. Seed multiplication of various crops at ICBA

S.N.	Crop	Species	# of accessions
1	Amaranth	<i>Amaranthus sp.</i>	279
2	Barley	<i>Hordeum vulgare</i>	6
3	Barnyard grasses	<i>Echinochloa sp.</i>	137
4	Buckwheat	<i>Fagopyrum esculentum</i>	1
5	Cowpea	<i>Vigna unguiculata</i>	4
6	Mung bean	<i>Vigna radiata</i>	403
7	Mustard	<i>Brassica juncea</i>	1
8	Pearl millet	<i>Pennisetum glaucum</i>	1
9	Quinoa	<i>Chenopodium quinoa</i>	392
10	Safflower	<i>Carthamus tinctorius</i>	220
11	Sorghum	<i>Sorghum bicolor</i>	3
12	Sunflower	<i>Helianthus annuus</i>	1
13	Teff	<i>Eragrostis tef</i>	354
14	Triticale	\times <i>Triticosecale</i>	503
15	White lupin	<i>Lupinus albus</i>	38

Characterization of Crops

Characterization of germplasm by its agronomic and morphological traits indicates the expression/variation of the botanical features. It is extremely important for the gene bank to enable the global research community to hunt and narrow down the search for genotypes/donors with the desired traits. It is also helpful for its taxonomical classification, which ultimately helps select the suitable cultivar for different purposes. Nevertheless, it is essential to accurately describe its characteristics, relationship with the environment, and usage. ICBA characterized about 1,500 accessions of five important crops during 2020-21 (Table-4).

Table-4. Characterization of crops at ICBA

S.N.	Crop	Species	# of accessions
1	Amaranth	<i>Amaranthus sp.</i>	287
2	Barnyard grass	<i>Echinochloa sp.</i>	145
3	Mung bean	<i>Vigna radiata</i>	404
4	Teff	<i>Eragrostis tef</i>	367
5	Triticale	× <i>Triticosecale</i>	289

Seed Distribution

The ICBA is a non-profit institute; hence its genebank is not a commercial distributor of the seed it possesses. However, based on the U.N. list of Country Development Index (CDI), ICBA may charge the production cost of the seed to the requesters from the developed countries. The seeds of different accessions are accessible free of cost to any government/public sector, international research organizations and/or non-profit organizations from under-developed/developing countries user around the world for research and education purposes. ICBA followed the standard rules (national and international) to distribute crop/plant seeds to stakeholders in the UAE and other countries of the world. ICBA genebank supplied more than 650 seed samples of 18 different crops (Table-5) to eleven countries (Bahrain, Botswana, Gambia, India, Liberia, Morocco, Mozambique, Oman, Togo, UAE, Uzbekistan) around the world.

Table-5. Seed distribution by ICBA genebank during 2020-21

S.N.	crop	Species	seed samples
1	Amaranth	<i>Amaranthus sp.</i>	131
2	Barley	<i>Hordeum vulgare</i>	30
3	Blue panic	<i>Panicum antidotale</i>	1
4	Buffel grass	<i>Cenchrus ciliaris</i>	5
5	Colocynth	<i>Citrullus colocynthis</i>	2
6	Cowpea	<i>Vigna unguiculata</i>	9
7	Foxtail millet	<i>Setaria italica</i>	33
8	Lablab	<i>Lablab purpureus</i>	1
9	Pearl millet	<i>Pennisetum glaucum</i>	266
10	Quinoa	<i>Chenopodium quinoa</i>	104
11	Rice	<i>Oryza sativa</i>	21
12	Safflower	<i>Carthamus tinctorius</i>	1
13	Salicornia	<i>Salicornia europaea</i>	2
14	Sea wattle	<i>Acacia ampliceps</i>	2
15	Sesbania	<i>Sesbania sp.</i>	6
16	Sorghum	<i>Sorghum bicolor</i>	29

17	Triticale	<i>×Triticosecale</i>	5
18	Wheat	<i>Triticum aestivum</i>	5

Documentation of ICBA Genebank Accessions

Data on ICBA genebank accessions have been prepared according to the Multi-Crop Passport Descriptors [MCPD] standard. ICBA updates its data on genebank accessions every December and sends them to the FAO (PGRFA). The last update on the accessions preserved in the ICBA genebank was done in December 2021 and sent to the PGRFA ([Document link](#)).

Assignment of DOI

The adoption of Digital Object Identifiers (DOI) in the Global Information System (GLIS) of the International Treaty offers a powerful tool for accurately and permanently identifying Plant Genetic Resources for Food and Agriculture (PGRFA). DOIs are the key to standardizing germplasm identification, facilitating information sharing, and ensuring more effective genebanks. Keeping in view its importance, we assigned DOI's to 95% of the accessions in our genebank in 2021 ([Document link](#)). The rest of the work will be done within 2022.

CGIAR Report Concerning Centers' Implementation of their Article 15 agreements: or the 9th Session of the Governing Body of the International Treaty on Plant Genetic Resources for Food and Agriculture



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Executive summary

This report provides an update on the status, as of December 31, 2021, of the plant genetic resources for food and agriculture (PGRFA) collections maintained by the eleven CGIAR Centers that signed Article 15 agreements with the Governing Body of the International Treaty on Plant Genetic Resources for Food and Agriculture (Plant Treaty) in 2006. As of December 31, 2021, these Centers held over 722,525 accessions of crop, forage and tree germplasm which they maintain in their genebanks and make available under the standard material transfer agreement (SMTA).

During the 15 years of their operation under the Plant Treaty framework, from January 2007 to December 2021 inclusive, CGIAR Centers' genebanks and breeding programs distributed over 6 million PGRFA samples under 61,000 SMTAs. Twenty nine percent of those samples were sent to recipients in Asia, 19% to recipients in Africa, 19% to recipients in Europe, 14% to Latin America and the Caribbean, 11% to the Near East, and 7% and 1% to North America and Southwest Pacific respectively.

Since 2010, the Centers have acquired 80,000 distinct PGRFA from providers in 142 different countries, under the SMTA or under other agreements whereby the providers gave the Centers permission to subsequently distribute the material concerned with the SMTA. Approximately 18% of these materials came from new collecting expeditions. In the period 2019-2021, Centers organized new collecting expeditions in more than 10 countries. The most recent expeditions, in late 2021, led to the collecting of more than 4,000 samples that are currently being processed for incorporation into national and international genebanks.

Centers engage in a range of activities to maintain, and add value to, the PGRFA collections which they hold, on behalf of the international community, under the Plant Treaty framework. This report highlights a range of such activities including Centers' efforts to: maintain collections free of pests and diseases; develop tools and methods to identify gaps in the international collections and improve information management systems.

The COVID pandemic created some challenges for CGIAR Centers in their day-to-day management of their Article 15 collections. Given many host countries' restrictions on travel and the number of people who could enter workplaces, Centers had to keep operations going with reduced overall staff, or staff working in shifts. Some accession regeneration work had to be suspended. In a few Centers, Germplasm Health Units were not able to function fully, so those Centers were unable to distribute material temporarily. The pandemic highlighted the vulnerability of PGRFA collections of vegetatively propagated crops in particular, given the need for relatively constant 'hands on' attention by genebank staff.

The report includes examples of plant pre-breeding and breeding that CGIAR scientists carried out in CGIAR Research Programs (CRPs). Between 2017 and 2020, using improved germplasm from CGIAR breeding programs, national partners and seed companies across Africa, Latin America and Asia released 290 new maize varieties, 224 new wheat varieties, 130 new varieties of lentil, groundnut, chickpea, sorghum, pearl millet, pigeonpea, soybean, and finger millet, and 87 varieties of sweet potato, potato, cassava and yam. Results of a number of impact studies, undertaken from 2019-2020, focusing on the diffusion and use of varieties derived from CGIAR improved germplasm are presented.

Since the Eighth session of the Governing Body in 2019, CGIAR has been actively engaged in a range of additional intersessional policy making processes under the Plant Treaty

framework. For example, they engaged in a number of informal consultations with contracting parties and other stakeholders concerning the possibility of resuming a process to enhance the functioning of the multilateral system of access and benefit sharing, and, as part of that effort, finding a solution for addressing the governance of digital sequence information. CGIAR also participated in meetings of the Ad Hoc Technical Expert Group on Farmers' Rights, and made written submissions to those meetings drawing on the experiences of CGIAR research programs.

Introduction

CGIAR regularly makes reports to the biennial meetings of the Governing Body of the International Treaty on Plant Genetic Resources for Food and Agriculture (Plant Treaty), concerning the CGIAR Centers' operations under the framework of their 2006 Article 15 agreements with the Governing Body, and their contributions to the implementation of the Plant Treaty more generally¹.

These reports always include core information about holdings and distributions of PGRFA by the Centers under the Plant Treaty framework, and CGIAR contributions to Treaty-related activities and outcomes over the previous biennia.

In addition, CGIAR takes advantage of these biennial reports to periodically highlight additional aspects of our management and use of PGRFA both by genebanks and the breeding programs. For example, our report to the Seventh Session of the Governing Body in 2017 featured additional, unprecedented focus on CGIAR Centers' characterization and plant breeding activities. The CGIAR report to the Eight Session of the Governing Body featured additional information about the Centers' efforts to develop genebank Quality Management Systems, and to use genomic information to analyze genetic diversity within accessions. In this report, we once again include information about Centers' crop and forage pre-breeding and breeding activities in recent years, highlighting new activities since our 2017 report. We also include a section on collective efforts across the genebanks to analyze gaps in PGRFA collections.

CGIAR is submitting an additional, separate report to this session of the Governing Body concerning the status of implementation of the CGIAR Intellectual Assets Principles, as requested by the Governing Body through Resolution 2/2019.

We want to remind delegates to the Governing Body meeting that since 2012, first, the CGIAR Research Program on Genebanks, and later, the CGIAR Genebank Platform, have published annual reports concerning the Centers' management of the Article 15 collections. These reports are available online². We encourage Governing Body delegates to familiarize themselves with these reports.

Finally, we would like to mourn the passing of Dr. Barbara H. Wells, CGIAR Global Director of Genetic Innovation, and Director General of the International Potato Center (CIP). Dr. Wells died on February 16, 2022. We would like to express our gratitude for her dedication to the conservation and sustainable use of plant genetic resources for the benefit of developing countries and smallholder farmers.

¹ CGIAR reports to the Second, Third, Fourth, Sixth, Seventh and Eight Sessions of the Governing Body are available at <http://www.fao.org/3/a-be157e.pdf>, <http://www.fao.org/3/a-be109e.pdf>, <http://www.fao.org/3/a-be118e.pdf>, <http://www.fao.org/3/a-mo439e.pdf>, <http://www.fao.org/3/a-mu437e.pdf>; and <https://www.fao.org/3/nb776en/nb776en.pdf> respectively

² <https://www.genebanks.org/resources/annual-reports/>

Holdings, distributions and acquisitions under the Plant Treaty framework

Holdings by CGIAR Centers' Genebanks

The eleven CGIAR Centers that signed Article 15 agreements with the Governing Body of the Plant Treaty in 2006 currently conserve and make available, using the standard material transfer agreement (SMTA), a total of 722,525 accessions of crop, tree and forage germplasm. In addition, Centers maintain approximately 17,000 accessions that are not available under the Plant Treaty's multilateral system since they are maintained under black-box or other legal conditions that don't allow their distribution with the SMTA. Details concerning the Centers, crop collections and numbers of accessions available for distribution under the SMTA are included in Table 1.

Table 1: PGRFA conserved and made available by CGIAR Centers' genebanks pursuant to their Article 15 agreements with the Governing Body

Center	Crop	Accessions available with SMTA
AfricaRice	Rice	19,696
Bioversity	Banana	1,682
CIAT	Beans	37,934
	Cassava	5,965
	Forages	22,662
CIMMYT	Maize	28,694
	Wheat	135,021
CIP	Andean roots and tubers	1,178
	Potato	7,367
	sweet potato	6,143
ICARDA	Barley	31,843
	Chickpea	15,230
	faba bean	9,594
	Forages	25,358
	Grasspea	4,301
	Lentil	14,295
	Pea	4,593
	Wheat	41,967
ICRAF	fruit trees	8,246

	multipurpose trees	6,744
ICRISAT	Chickpea	20,258
	Groundnut	15,237
	pearl millet	24,355
	pigeon pea	13,534
	small millets	11,683
	Sorghum	42,750
	IITA	Banana
Cassava		3,184
Cowpea		17,051
Maize		1,561
misc legumes		6,747
Yam		5,929
ILRI	Forages	3,918
IRRI	Rice	127,413
	Total	722,525

Source: Global Crop Diversity Trust/CGIAR On-line Reporting Tool, covering period up to December 31, 2021.

Distribution of PGRFA by CGIAR Centers

Internal and external distributions

There is considerable fluctuation, from year to year, in the ratio of materials the CGIAR Centers' genebanks send to recipients within the CGIAR (mainly breeders) and to recipients outside the CGIAR, as can be seen in Figure 1. Since 2017, the Centers' genebanks have been distributing proportionately more materials to recipients outside the CGIAR. Some Centers do not have crop breeding programs (e.g., Bioversity, ILRI), so they have very few, or no, internal transfers. Most of the Centers do not fill out new SMTA for internal transfers, since doing so would mean entail a legal entity making a legal agreement with itself. Nonetheless, all such transfers are considered pursuant to the terms of the SMTA and all recipients of materials within Centers are bound by its terms and conditions.

All data on distributions by CGIAR Centers using the SMTA in following subsections present distributions to recipients outside the Centers concerned.

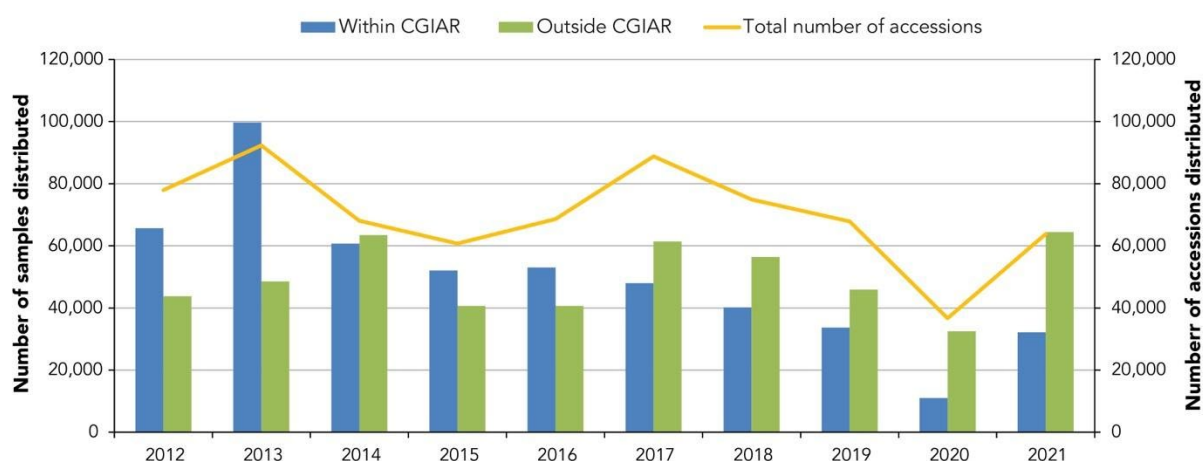


Figure 1: Samples and accessions distributed annually by CGIAR genebanks from 2012 to 2021. Source: CGIAR Genebank Platform, Annual Report 2021.

The CGIAR Centers have distributed over six million PGRFA samples under SMTAs during the 15 years they have been operating under the Plant Treaty framework. The majority of the PGRFA distributed were improved materials from the Centers' breeding programs. While it varies from year to year, twenty to twenty-five percent of the materials distributed are from the genebanks. Table 2 provides details of materials distributed (from both genebanks and breeding programs³) by each CGIAR Center.

Table 2: CGIAR Centers' transfers of PGRFA with SMTAs, 2007 to 2021/22. PUD stands for PGRFA under Development.

Center	SMTAs	Samples	PUD	From	To
AfricaRice	598	53,351	30,714	2007-03-05	2022-01-29
Bioversity	554	8,595	831	2007-01-24	2021-11-18
CIAT	3,077	298,291	36,646	2007-01-05	2022-02-24
CIMMYT	26,644	3,211,789	0	2007-03-16	2021-12-21
CIP	788	22,503	12,221	2007-01-19	2022-05-05
ICARDA	11,531	992,246	873,178	2007-02-13	2021-12-21
ICRAF	358	1,719	0	2011-09-03	2022-03-03
ICRISAT	6,048	297,367	100,532	2006-12-07	2021-11-26
IITA	1,172	48,891	0	2007-03-07	2022-02-09
ILRI	944	13,712	0	2007-02-22	2022-02-14
IRRI	9,317	764,594	441,382	2007-01-04	2022-02-09

Source: Plant Treaty Secretariat⁴.

³ Not all Article 15 Centers have breeding programs, e.g., Bioversity, ICRAF, ILRI.

⁴ Data obtained from Easy-SMTA, except for ICRISAT transfers of PUD. This figure was obtained from ICRISAT.

Eighty percent of the materials referred to in Table 2 were sent to recipients in developing countries. Twenty percent was sent to recipients in developed countries. More details concerning regional distributions of PGRFA by CGIAR Centers are provided in Figure 2.

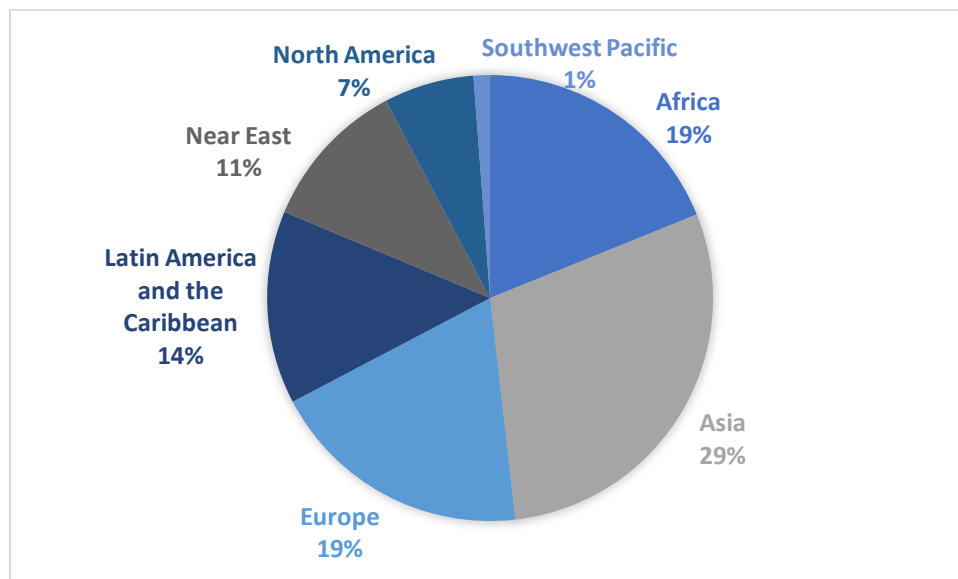
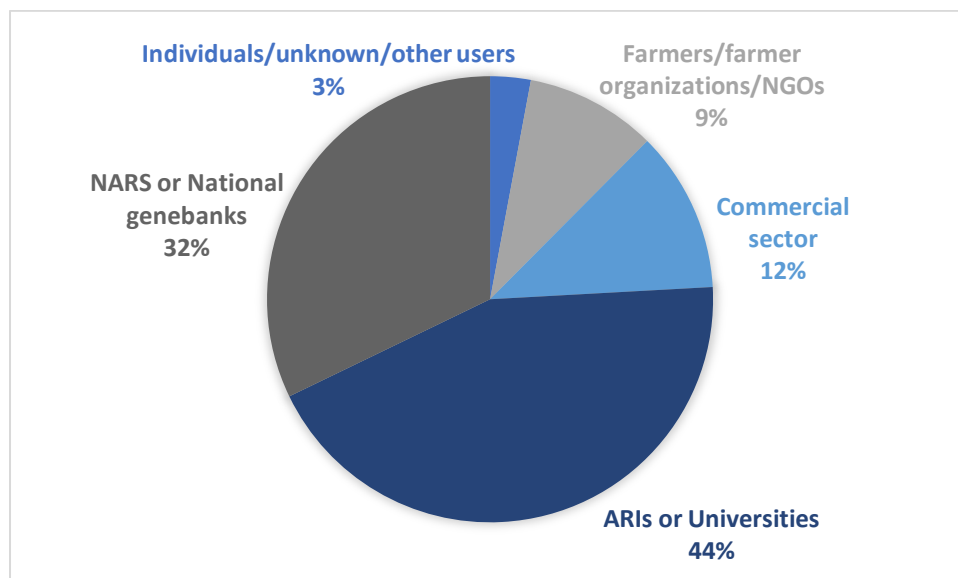


Figure 2: Regions of recipients of germplasm samples from CGIAR Centers' genebanks and breeding programs 2007-2021 inclusive.

Figure 3 provides percentages for each type of recipients of samples from the CGIAR Centers' genebanks for years 2019-2021⁵, with the largest groups being advanced research institutes and universities, and NARS and national genebanks. Transfers to commercial sector represented 13%, 15% and 7% of CGIAR Centers' genebanks' transfers in 2019, 2020 and 2021 respectively.



⁵ Reports of SMTA transfers by providers to the Secretariat/Governing Body, following GB Resolution 5/2009, do not identify general classes of recipients (e.g., public research organizations, seed company, farmer, genebank, etc). CGIAR/GCDT collect such information independently for the genebanks. There is no centralized system for recording this information from the CGIAR breeding programs. To address this gap, CGIAR and Treaty Secretariat have undertaken to develop mechanisms through which Centers can voluntarily report types of recipients when they report their SMTA transfers in the future.

Figure 3: Types of recipients of germplasm samples distributed by CGIAR Centers' genebanks 2019-2021 inclusive.

Distribution of non-Annex 1 materials

Only 1% of the PGRFA samples distributed by the Centers belongs to non-Annex 1 crops. In the last 10 years (2012-2021), CGIAR Centers have distributed an average of 5,500 samples per year of approximately 140 species of non-Annex 1 crops, forages and trees; with annual figures fluctuating from 3,300 in 2012 to 8,100 in 2019. Groundnut, soybean, Bambara groundnut, foxtail millet and various forages have the highest numbers of distribution.

Following the decision of the Second Session of the Governing Body in 2009, the CGIAR Centers have been using the SMTA to distribute non-Annex 1 materials from their in-trust germplasm collections and other materials acquired with permission from the providers for the Center to make it available using the SMTA. Since that time, the CGIAR Centers have communicated repeatedly to the Governing Body that they would like to continue this practice. While the amount of non-annex 1 materials distributed by the Centers is small, transaction costs associated with maintaining a system for distributing non-Annex 1 materials differently from Annex 1 materials would be significantly greater. The Centers appreciate the administrative efficacy of being allowed to use the same transfer instrument for both Annex 1 and non-Annex 1 materials.

Transfer of PGRFA under Development

CGIAR provided details in reports to the Sixth and Seventh sessions of the Governing Body concerning Centers' management of PGRFA under Development. In this report, therefore we only provide a few highlights.

Some Centers identify all their improved materials derived from multilateral system germplasm as PGRFA under development. Other Centers choose not to do so when they are not adding terms and conditions to those in the SMTA when distributing PGRFA under Development. Centers may (and frequently do) introduce Center-improved materials into the genebanks, where they receive accession numbers, and are distributed along with other materials in the genebanks.

When transferring PGRFA under Development, Centers may impose a range of additional terms and conditions, including one or more of the following, requiring recipients to:

- share characterization, evaluation, research data;
- acknowledge the sources of materials if/when research findings and data are published;
- obtain approval before passing the material to subsequent recipients;
- either notify, or obtain approval before seeking to register or commercialize new varieties incorporating the PGRFA under Development;
- provide a sample of any released varieties to the genebank;
- acknowledge the provider when derived material is commercialized;
- not commercialize the material in the form received; and
- acknowledge that the PGRFA under Development is the intellectual property of the Provider.

In addition to needing to comply with the Plant Treaty and the SMTA, the Centers' management (including distribution) of PGRFA under Development also must be compliant

with the CGIAR Principles on the Management of Intellectual Assets (IA Principles)⁶. The IA Principles underscore that Centers must provide facilitated access to PGRFA in accordance with their Article 15 agreements; they also provide guidance on how the CGIAR Centers can exercise the discretion they have as Providers of PGRFA under Development under the Plant Treaty. The IA Principles address (and limit) the kinds of restrictions that Centers can place on Center-improved materials and establish threshold criteria for justifications that Centers must satisfy for creating such restrictions. More information about the IA Principles is provided in *'The status of implementation of the CGIAR Principles on the Management of Intellectual Assets: a submission from CGIAR to the Ninth Session of the Plant Treaty's Governing Body'*⁷.

Acquisitions of PGRFA by CGIAR Centers' Genebanks

Over the course of twelve years, from 2010 to 2021 inclusive, the CGIAR Centers' genebanks acquired over 123,000 samples⁸ of distinct PGRFA to include in their Article 15 collections. Approximately 65% of those materials (i.e., 80,000 distinct PGRFA) came from providers in 142 different countries. The remaining 35% came from the Centers' own breeding programs. Eighty four percent of the materials received from countries came from developing countries or countries with economies in transition. Approximately 18% of these materials came from new collecting expeditions; the other 82% was material that was already in ex situ conditions prior to being sent to the Centers (Figure 4).

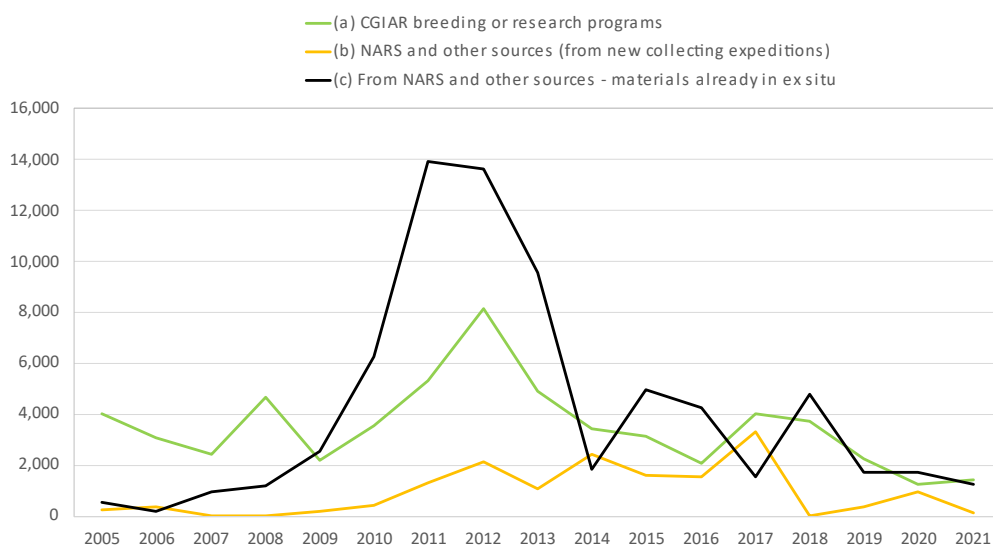


Figure 4: Numbers of distinct PGRFA acquired by CGIAR Centers' genebanks 2005-2021 from CGIAR research programs (black), from ex situ collections maintained by national agricultural research organizations (yellow) and from new collecting expeditions conducted

⁶ The full text of the Intellectual Asset Principles is available at <https://hdl.handle.net/10947/4486>

⁷ [insert URL if it is posted before this report is posted]

⁸ This figure does not include the approx. 4,000 samples collected by CGIAR Centers and partners in late 2021, as explained at the end of this section. These samples are being processed for introduction in national and international genebanks. Not all of them will be kept in CGIAR genebanks (e.g. samples of non-CGIAR mandate crops).

by national agricultural research organizations (green). Source: Adapted from Halewood, Jamora, López et al. 2020.

The materials provided by countries were of 25 crops approximately: Rice, banana, beans, cassava, wheat, barley, grasspea, pea, lentils, chickpea, faba bean, maize, potato, sweet potato, Andean tubers, finger millet, pearl millet, small millets, sorghum, pigeon pea, yam, cocoyam, cowpea, and Bambara groundnut; and also of various species of forages and trees.

All of the materials from providers in countries were either received under the standard material transfer agreement (SMTA) or under other agreements whereby the providers gave the Centers permission to subsequently distribute the material concerned with the SMTA. In this context, it is interesting to note that 31 of the countries from which the materials were made available were not contracting parties to the Plant Treaty, yet they were still willing to provide the materials, and have them subsequently redistributed by the CGIAR Centers, under the conditions established by the Plant Treaty. We did not analyze whether some other countries which are now Plant Treaty members made materials available before becoming members.

Approximately one third of the PGRFA acquired by the genebanks from providers in countries between 2010 and 2019 were associated with a project coordinated by the Global Crop Diversity Trust from 2007 to 2012 called “Securing the Biological Basis of Agriculture”, funded by the Bill and Melinda Gates Foundation and the Grains Research and Development Corporation. That project provided financial and technical support for organizations around the world to regenerate unique *ex situ* PGRFA that were at risk of being lost, to send a copy of the regenerated materials to an internationally recognized genebank, to send a copy for safety back-up in the Svalbard Global Seed Vault, and to make the materials available through the multilateral system of access and benefit sharing. Activities with 84 national partners in 54 countries resulted in the regeneration of approximately 73,000 threatened accessions, of which more than half were duplicated in CGIAR Centers’ genebanks with permission to make them available through the multilateral system.

As of 2019, another 2256 samples of 1508 unique accessions collected from 25 countries were sent to CGIAR Centers’ genebanks (ICARDA, ICRISAT, IRRI, IITA, CIP) by the Millennium Seed Bank (MSB), associated with the project called “Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives” coordinated by the Global Crop Diversity Trust from 2011 to 2021. This project, with funding from the Norwegian government, provided financial and technical support for project partners to target and collect wild species related to crops, to create a safety back-up, and make collected material available through the multilateral system.

At the end of 2021, the CGIAR Genebank Platform coordinated new collecting missions in Chad, Mauritania, Niger, Sudan, South Sudan, Togo, and Papua New Guinea. The expeditions were undertaken by NARS partners in collaboration with Bioversity, ICRISAT, IITA and ICARDA and resulted in the collecting of approx. 4, 000 distinct samples of more than 30 species from over 200 sites from which the Centers and national partners has never previously collected samples. Some of the materials collected were of crop species (such as breadfruit and traditional vegetables) that are not mandate species for CGIAR. All collected materials are being introduced as new accessions into national genebanks and CGIAR Centers’ genebanks (or also other relevant international genebanks for crops not maintained by the CGIAR Centers’ genebanks). In all cases, they will be made available by the organizations hosting the collections using the Plant Treaty’s SMTA. As part of the collecting

projects, NARS scientist extension workers and farmers were trained in collecting, documenting and conserving plant genetic resources. At the same time, nearly 500 accessions were repatriated from CGIAR Centers' genebanks to Chad, Niger and Sudan. In addition, the Genebank Platform and the CGIAR Centers supplied essential equipment to national genebanks.

Prevention of transboundary spread of pests and phytosanitary safety of germplasm

The transboundary spread of pathogens, pests, and noxious weeds (collectively referred to as pests) is one of the biggest threats to global food security and biodiversity. Germplasm (seed) has an inherent ability to serve as a carrier of pests acquired from the mother plants or as a passive carrier of surface contaminants or admixtures. Thus, the international movement of germplasm has been recognized as a pathway for pest dissemination into new geographies and potential risk for the transboundary spread of pests. The introduction of exotic pests can have devastating consequences, as observed in several parts of the world, especially in the low- and middle-income countries, which lack sufficient capacity to monitor seeds for pests to prevent the introduction or respond rapidly to control the introduced pests. The outbreaks of fall armyworm in Africa and Asia, wheat blast in Bangladesh and Zambia, maize lethal necrosis caused due to the introduction of maize chlorotic mottle virus in East Africa and the banana bunchy top virus and the *Fusarium oxysporum* Tropical Race 4 of banana are some of the major transboundary pests that gained notoriety in the last one decade. Member states which are signatory to the FAO-International Plant Protection Convention (IPPC) or Plant Health Treaty adopted quarantine measures to control the introduction and spread of pests through the exchange of plant and plant productions, including germplasm.

The CGIAR Centers recognize pests as a serious threat to germplasm collections, conservation, regeneration, and global distribution. The Centers also recognize the importance of ensuring the provision of germplasm free of pests to the requestors from various countries. The Centers' Germplasm Health Units (GHUs), supported through the CGIAR Genebank Platform, in conjunction with the national plant protection organizations (NPPOs), ensure compliance with the Plant Health Treaty. These measures include the production of pest-free germplasm, germplasm health certification using a range of standard methods to ascertain germplasm freedom from quarantine pathogens, and procurement of permits from NPPOs to fulfil the phytosanitary obligations of the recipient countries. Centers only distribute germplasm free of regulated quarantine pests and meet the phytosanitary conditions set by the importing countries.

In 2019-2021, GHUs of the 11 CGIAR Centers have tested 712,471 samples corresponding to over 30 crop species (Table 3). Most of the tested samples (around 68.2%) were for conservation actions in genebanks, with the rest being for import or export of germplasm. On average, 8.1% of the samples analyzed were infected, and replaced with clean germplasm or subjected to phytosanitary treatments to generate clean pest-free germplasm. Most of the pests detected are native to specific species. Viral pathogens are most frequently intercepted in the germplasm of legumes and clonal crops. On occasion, considerable resources are required in staff time, testing facilities, and multiple tests (at an average cost of \$10 per sample) to ensure that materials are healthy before being distributed. In these three years, GHUs facilitated 3,941 events of germplasm exchanges, reaching about 120 to 130 countries per year. The Covid19 pandemic had a minor impact on the germplasm exchanges facilitated by the CGIAR centers, thanks to various safety protocols for the safety of the working staff to comply with the requests for germplasm from multiple stakeholders.

For instance, CGIAR GHUs facilitated 1445 exchange events in 2019, which reduced to 1149 in 2020 but increased in 2021 to 1347.

Table 3: Germplasm samples subjected to health certification in 2019, 2020 and 2021

	2019	2020	2021
AfricaRice	6,852	106,430	10,888
Bioversity	376	420	250
CIAT	17,830	6,436	9,297
CIMMYT	5,364	6,169	5,014
CIP	4,645	4,442	2,464
ICARDA	57,201	46,778	48,404
ICRAF	102	274	570
ICRISAT	19,219	11,757	14,630
IITA	84,863	105,671	95,826
ILRI	7,103	7,375	10,515
IRRI	-	-	15,306

Source: Global Crop Diversity Trust/CGIAR Centers' Genebanks On-line Reporting Tool

In the three years, the CGIAR GHUs has improved operational efficiency by creating new tools and procedures for phytosanitary cleaning of germplasm and seed health indexing and enhancing staff skills and infrastructure. It includes developing and adopting high-throughput sequencing (HTS)-based virus indexing methods, especially for the clonally propagated crops such as banana, cassava, potato, sweetpotato, and yam. The HTS-based techniques offer a unique advantage of detecting both characterized and new viruses and help fast-track virus indexing and health certification. Efforts are also being made to establish protocols for the non-invasive detection of pathogens in seeds using multi-spectral imaging methods coupled with machine learning approaches. The GHUs have tested and adopted new seed treatment chemicals in preparedness for some of the existing reagents being phased out, considering the low effectiveness or environmental safety. The GHUs have installed fully functional GHU facilities in AfricaRice, ICRAF, and ILRI. In the case of other GHUs, laboratories and screenhouses were refurbished and replaced worn-out equipment with new modern equipment to increase the testing capacity and throughput. GHUs have developed standard operating procedures (SOPs) for all the key activities and operations of GHUs and institutionalized Quality Management Systems (QMS), including ISO accreditation to Alliance CIAT, CIMMYT, and CIP.

In addition, GHUs have been working towards developing a quality accredited system termed the 'GreenPass' protocol. The GreenPass would enable rapid distribution of phytosanitary-clean germplasm from CGIAR Centers to partners. Continued consultations with key stakeholders, including FAO International Plant Protection Convention (FAO-IPPC), FAO, and NPPOs, to identify needs and develop a roadmap for exploring/developing a GreenPass protocol. If adopted, the GreenPass protocol would avoid delays in germplasm distribution due to redundant phytosanitary procedures.

During 2019-21, GHUs organized at least one workshop in each of the eleven Article 15 Centers to train internal staff and national partners in applying phytosanitary procedures and seed health indexing using a range of conventional and molecular methods. At least 100 national partners benefited from the GHU capacity development efforts through various training workshops organized in the 11 Centers.

As part of the GHU Community of Practice (CoP), GHUs have organized phytosanitary awareness activities each year on the topic "GHUs in combating invasive pests and

diseases and safe distribution of germplasm". All GHUs organized activities to raise awareness about the importance of phytosanitary health, emerging transboundary pests and pathogens, new risks to germplasm health and GHUs preparedness to tackle challenges. As part of the CoP, all GHUs organized or participated in events to mark the UN's International Year of Plant Health in 2020, extended to mid-2021, to enable planned activities curtailed in 2020 due to the Covid19 pandemic. In November 2020 and February 2021, a global webinar series took place to promote the role of GHUs in preventing the transboundary movement of pests and diseases. Several webinars and meetings were conducted to discuss future scenarios, needs for germplasm health and bio-risk mitigation, global efforts to contain the spread of invasive transboundary pests, best practices in GHUs, and their engagement and collaboration with national and international plant health organizations.

GHUs have continued to update and maintain the optimum capacity to meet changing pest dynamics and phytosanitary regulations crucial for sustaining CGIAR's mission of distributing germplasm to its own and partners' programs involved in R4D for food and nutritional food security and conservation of biodiversity.

Information systems and the use of Digital Object Identifiers under the Global Information System

Information systems

Genesys continues to evolve to serve the genetic resources community and users for accession-specific information from both the CGIAR's and national programs' genebanks globally. Under the framework of the CGIAR Genebank Platform and in cooperation with the Global Crop Diversity Trust, Centers have continued to contribute to Genesys' development. Information about all CGIAR genebank accessions that are available under the SMTA can be found on Genesys. Over the last five years, the Centers have significantly increased the amount of passport data that is available for those accessions⁹. Similar amounts of accession level information are also available on the World Information and Early Warning System on PGRFA (WIEWS) and the Plant Treaty's Global Information System (GLIS).

In 2019, CGIAR Centers' genebanks decided to adopt a common genebank information management solution. Since 2019, the CGIAR Genebank Platform has supported the development of a 'next generation' version of the GRIN-Global database called GRIN Global Community Edition (GG-CE). The Community Edition aims to bring the community of users together to improve the data base's usability and functionality. GG-CE was installed on cloud infrastructure, populated and made available for evaluation to all CGIAR Centers' genebanks in 2021-22.

Use of Digital Object Identifiers under the Global Information System

As of end of 2021, GLIS Digital Object Identifiers (DOIs) have been assigned to 99% of accessions conserved by CGIAR Centers' genebanks. All Centers include GLIS DOIs of germplasm in Annex 1 of the SMTA when transferring PGRFA samples from the genebanks to requestors. In addition, some centers include DOIs on seed packages, envelopes or tubes containing germplasm for distribution. In 2019, ICRISAT adopted guidelines that make the

⁹ Genesys applies a passport data completeness index (PDCI) that uses the presence or absence of data points in the documentation of a genebank accession, taking into account the presence or value of other data points. For example, a wild accession should have a well-defined collection site but no variety name. Any type of accession, wild, landrace, breeding material or modern variety, can attain a maximal score of ten for this index. Theo van Hintum, Frank Menting and Elisabeth van Strien (2011). Quality indicators for passport data in ex situ genebanks. *Plant Genetic Resources*, 9, pp 478-485. doi:[10.1017/S1479262111000682](https://doi.org/10.1017/S1479262111000682)

use of DOIs compulsory for all materials that are distributed by the Center with a SMTA or a different MTA, including early generation and fixed breeding lines. As of the end of 2021, 20,919 DOIs had been assigned to ICRISAT germplasm with status “Breeding” and 8 DOIs with status “Synthetic population”. Minting DOIs to ICRISAT improved germplasm has allowed the GLIS to generate quite extensive ancestry graphs like the one presented in Figure 5.

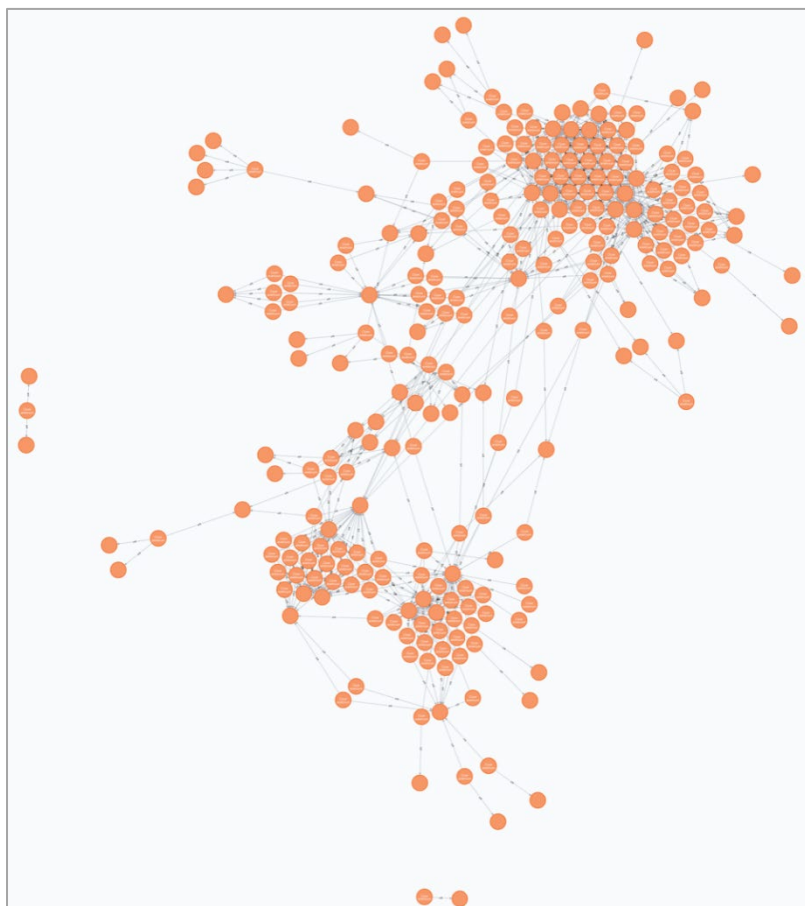


Figure 5: Ancestry graph generated by the GLIS through the use of DOIs assigned to ICRISAT germplasm.

Other CGIAR Centers are not currently minting GLIS DOIs for breeding materials in a systematic manner, but discussions are ongoing on how to best integrate DOIs into breeders’ work streams, including by linking genebanks’ databases with the breeders’ databases.

GLIS DOIs are displayed on the websites of all eleven Centers and Genesys (<https://www.genesys-pgr.org/welcome>) when users search for and order germplasm conserved in the CGIAR Centers’ genebanks. In addition, GLIS DOIs of *Musa* accessions maintained by Bioversity International are included in the databases of the *Musa* Germplasm Information System (MGIS, <https://www.crop-diversity.org/mgis/>). MGIS provides phenotypic and genotypic data in addition to passport data. The CIP genebank also maintains a search and order system that includes DOIs linking accession and trait information (<https://genebank.cipotato.org/gringlobal/search.aspx>).

Some Centers include GLIS DOIs in online platforms that focus primarily on genomic sequence information, like the Banana Genome Hub (<https://banana-genome-hub.southgreen.fr/>) and the rice-specific platform SNP-Seek (<http://snp-seek.irri.org/>).

Scientists from CGIAR Centers and partners have published peer reviewed journal articles that include GLIS DOIs of the germplasm involved in the work described in the articles, for example: Sansaloni et al. 2020 Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. *Nature Communications*, 11; Kyriakidou, M., Anglin, N.L., Ellis, D. *et al.* 2020. Genome assembly of six polyploid potato genomes. *Sci Data* 7; Anglin NL, Robles R, Rossel G, Alagon R, Panta A, Jarret RL, Manrique N and Ellis D. 2021. Genetic Identity, Diversity, and Population Structure of CIP's Sweetpotato (*I. batatas*) Germplasm Collection. *Front. Plant Sci* 12; Varshney, R.K., Roorkiwal, M., Sun, S. *et al.* 2021. A chickpea genetic variation map based on the sequencing of 3,366 genomes. *Nature* 599.

Centers, and likely all other DOI users, are encountering challenges referencing GLIS DOIs in journal articles. A major attraction of the DOI system is the potential to associate GLIS DOIs for PGRFA with DOIs for associated information, such as DOIs for publications and online datasets, thus bringing associated information within the scope of GLIS and ensuring that it does in fact remain associated with the PGRFA it describes. However, the technology to do so automatically does not allow to retrieve DOIs that are embedded in the main body of a publication, including text, tables, figures and supplementary information. Currently, to enable GLIS to automatically discover the GLIS DOIs referred to in a publication, all those GLIS DOIs must be listed in the reference section. However, listing PGRFA in the reference section is not standard practice, so journal editors need to develop and implement appropriate new standards. The Plant Treaty Secretariat and CGIAR scientists are working closely with journal editors to implement appropriate standards for listing GLIS DOIs in references; and in the longer term to seek an improved solution. The advances have been slow. In the meantime, on an informal basis, some scientists in some CGIAR Centers (e.g., CIP), have adopted the practice of informing the Plant Treaty Secretariat about new journal articles where DOIs have been cited, for upload onto GLIS. CGIAR is open to explore options for GLIS users to be able to upload the citations onto GLIS themselves, while it continues to collaborate with the Plant Treaty Secretariat for the automation of this function.

Highlights of efforts to add value to CGIAR collections, manage them more efficiently, and increase their use

Tool for identifying promising subsets of accessions from CGIAR collections

Curators and users often have very specific requests for genetic material within a given collection. But *ex situ* collections are vast, making it difficult for users to peruse passport data on an accession-by-accession basis. Furthermore, passport data is often not well integrated with data climate and soil conditions from the collection sites, which further complicates addressing certain germplasm requests.

Scientists working under the CGIAR Genebank Platform, in consultation with experts from CGIAR genebanks and other national and international genebanks, have developed and released a generic subsetting tool that helps CGIAR and NARS curators, and external users mine passport, climate, and soil data to identify groups (sets) of accessions that best suit their needs. The tool combines the formerly existing Genesys capabilities for filtering passport data, with novel data mining approaches that allow users to rapidly narrow down any collection into a small subset that satisfies their needs. In the example provided below (Figure 6), a user with interest in soil fertility and drought has selected the relevant indicators, mined all existing banana landrace collections and identified four potential subsets. Subsets 3 (in yellow, located in Tanzania –not shown on the map) and 4 (in green – in Vietnam), contain landrace accessions that were collected from relatively dry sites.

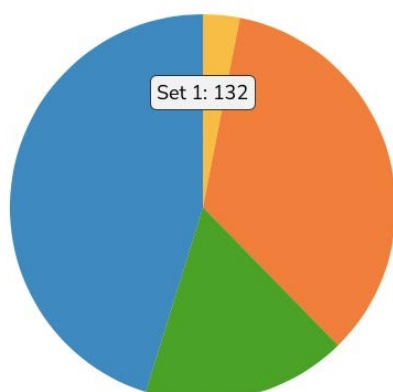
330 accessions

Crop: banana

Excluding Historical

Biological status: Traditi..

Results of the analysis



Summary

Potential Set	No. of unique location	No. of accessions	Total precipitation	Number of water stress days	pH	Average VPD
Set 1	41	132	238.78	7.65	4.17	0.68
Set 2	46	101	131.04	7.63	4.26	0.60
Set 3	7	9	6.91	19.90	4.29	1.28
Set 4	32	50	77.87	13.19	4.38	1.28

Subset 1: The set contains 132 accessions. **Subset 2:** The set contains 101 accessions. **Subset 3:** The set contains 9 accessions.

Subset 4: The set contains 50 accessions.

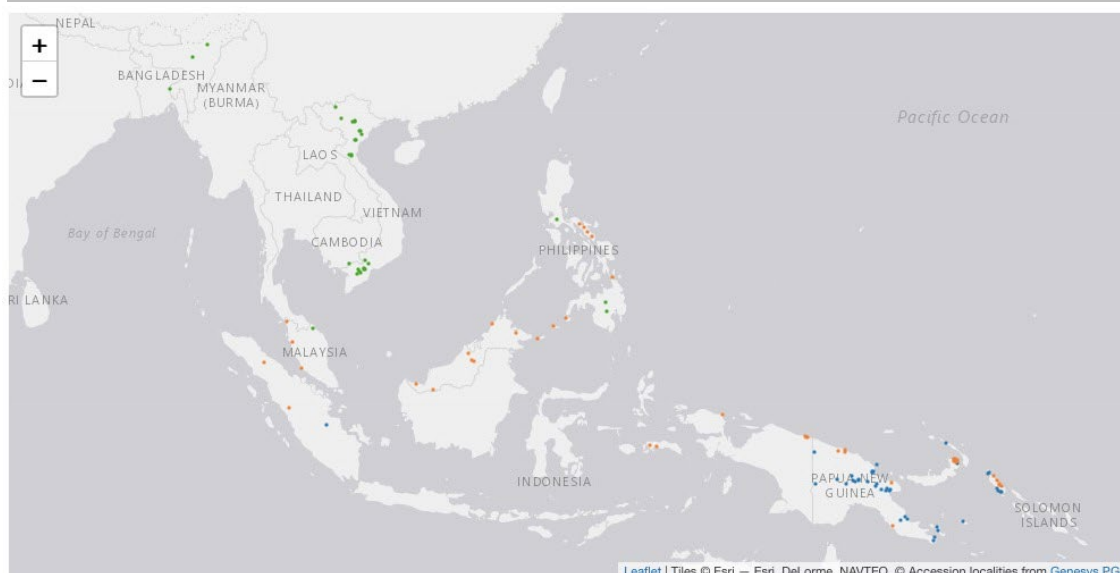


Figure 6: Subsets of banana landraces included in Genesys that were collected in places with selected climatic characteristics (total precipitation; number of water stress days, average vapor-pressure deficit-VPD) and soil characteristics (pH).

The tool is currently a beta release in the Genesys testing environment (Genesys Sandbox), and will be operationally available in the official Genesys website on the second quarter of 2022.

Identifying and filling gaps in the collections

CGIAR Centers have undertaken a series of activities, coordinated by the Global Crop Diversity Trust under the Conservation Module of the CGIAR Genebank Platform, to measure the representation of crop genetic diversity conserved ex situ, identify gaps in collections and guide and prioritize collecting expeditions. Three complementary approaches were used and combined to identify the gaps.

First, Diversity Trees have been constructed for 22 crops' genepools¹⁰. The cowpea diversity tree is reproduced in Figure 7. The trees are developed using published literature and expert knowledge to quantify the distribution of diversity in each crop genepool, leading to quantitative estimates of gaps by comparison with the actual composition of collections.

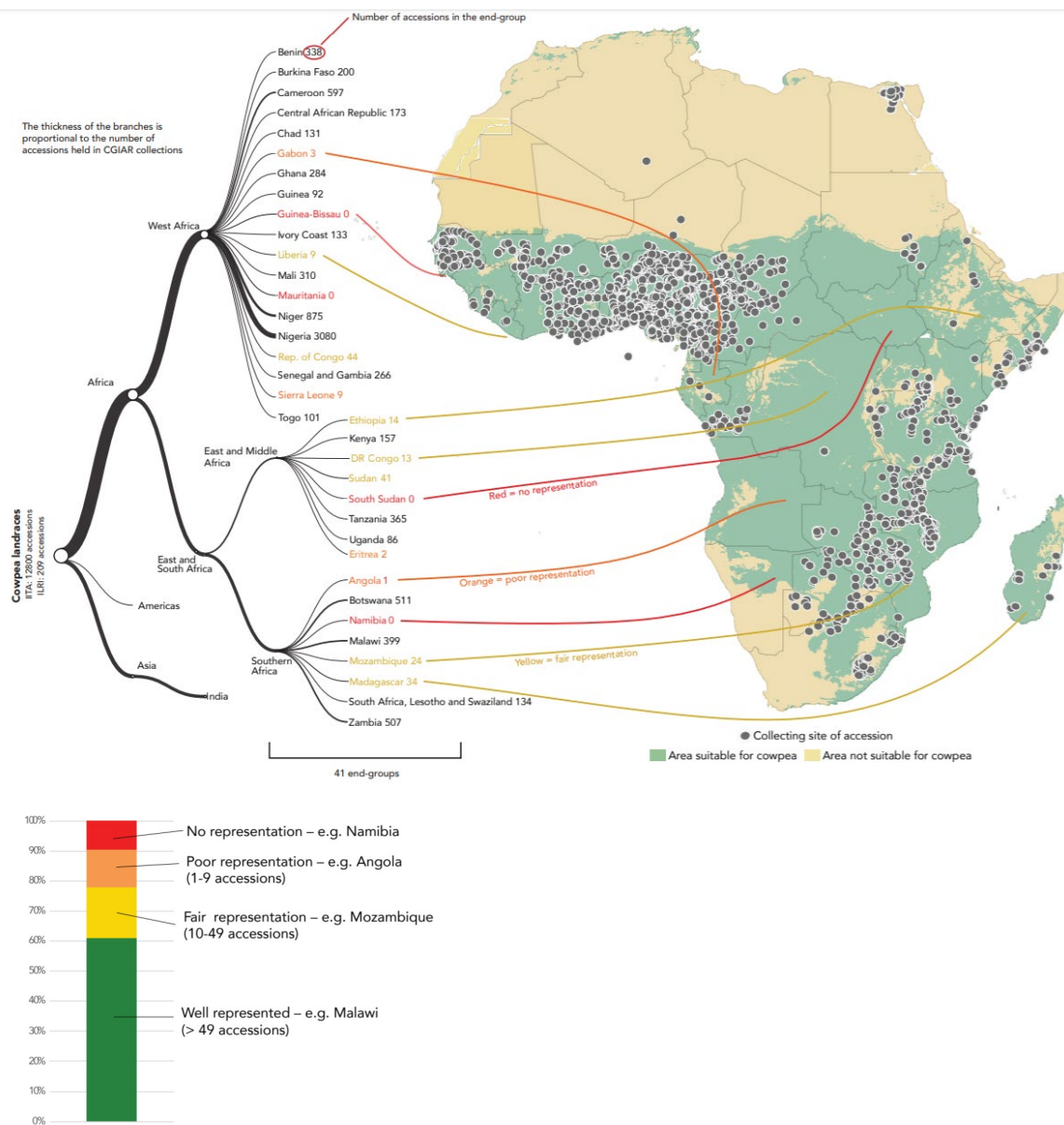


Figure 7: Cowpea Diversity Tree. Source: Giovannini, 2019¹¹.

Second, spatial analyses have been undertaken using a method developed by CIAT to assess the eco-geographic gaps and coverage of current CGIAR crop collections. The method, which works best for collections with a high percentage of available information on the latitude-longitude of origin of accessions, builds models that help predict the geographic distribution of landraces (using spatial, climate, soil, and socio-economic data) and then compares these distributions with the locations where landraces have been collected. This

¹⁰ Each genepool may include several crops, for example the wheat tree includes durum wheat and bread wheat. Diversity trees are available on Genesys at <https://genesys-pgr.p.gitlab.croprust.org/diversity-tree-editor/#>

¹¹ Giovannini, P. 2019. *Cowpea landrace diversity in the CGIAR collections: Finding and filling the gaps*. Poster presented at the side event entitled Tools and Metrics for Global Priority Setting: Diversity Trees, during the 8th meeting of the Governing Body of the Plant Treaty.

method has been described in detail in Ramírez-Villegas et al. 2020¹² and the results are available in the Landrace Gap Analysis dashboard¹³. All spatial analyses will be published in a multi-crop peer-reviewed study in the journal *Nature Plants*¹⁴. Figure 8 shows maps of total predicted diversity for crop wild relatives and landraces globally (top map) and total diversity in need of further collecting (i.e., gaps, bottom map).

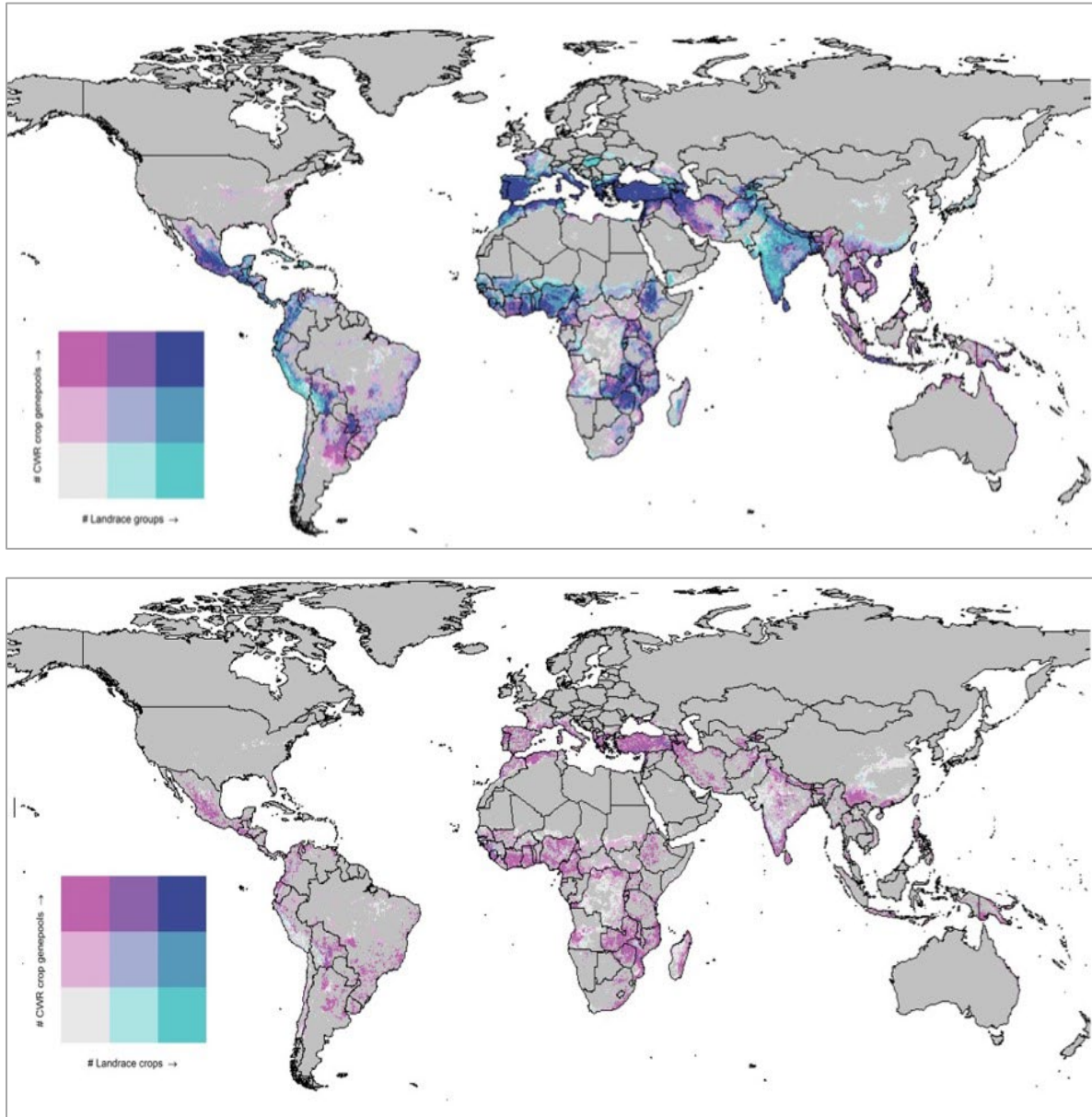


Figure 8: Total predicted diversity for crop wild relatives and landraces globally (top map) and total diversity in need of further collecting (i.e., gaps, bottom map).

Third, a method for trait-based gap analyses has been developed by ICARDA. This approach focuses on analysis of distribution of adaptive priority traits in relation to the

¹² Ramírez-Villegas, J., Khoury, C.K., Achicanoy, H.A., Mendez, A.C., Diaz, M.V., Sosa, C.C., Debouck, D.G., Kehel, Z., Guarino, L. 2020. A gap analysis modelling framework to prioritize collecting for ex situ conservation of crop landraces. *Biodiversity Research*. DOI: 10.1111/ddi.13046

¹³ https://surveylandraces.shinyapps.io/LGA_dashboard/

¹⁴ Ramírez-Villegas et al. 2022. State of ex situ conservation of landrace groups of 25 major crops. *Nature Plants*. DOI: 10.1038/s41477-022-01144-8

environment using machine learning algorithms to make predictions. It works best where landraces have been associated with an environment where they have evolved for long enough for their traits to become adaptive. This method presupposes well-characterized collections.

Table 4 summarizes the current status of gap analyses by crop.

Table 4: Status of gap analyses by crop

Crop	Diversity Tree	Spatial analysis	Trait analysis
Banana / Plantain	Tree for all the genepool with accessions mapped	Banana, done using no landrace groups	
Rice	Tree for all the genepool with accessions mapped	African rice, based on genetic clusters. Asian rice, based on groups (indica, temperate japonica, tropical japonica, aus, aromatic)	Rice yellow mottle virus (African rice), apiculus color at post-harvest, awn color, auricle color, basal leaf sheath color, culm diameter, collar color, culm angle, endosperm (common/non-waxy, glutinous/waxy or indeterminate), flag leaf angle, rice blast resistance, sheath blight resistance, tungro Virus resistance
Barley	Tree for all the genepool with accessions mapped	Done based on winter/spring and domestication (2-row vs. 6-row)	Frost tolerance, grain cover, growth class, kernel number, net blotch resistance, spot blotch resistance, powdery mildew resistance
Grasspea	Tree for all the genepool with accessions mapped	Completed, analyses performed at crop level	
Wheat	Tree for all the genepool with accessions mapped	Durum wheat and bread wheat, based on genetic and environmental clusters	Scab resistance, Septoria resistance, cold tolerance, common bunt resistance, filling period, stem rust resistance, yellow rust resistance
Maize	Tree for all the genepool with accessions mapped	Americas (based on genetic clusters) and Africa (based on environmental clusters)	Maize chlorotic mottle virus resistance, tar spot resistance
Beans	Tree for all the genepool with	Common bean (Americas), analysed using genepools	

	accessions mapped	(Andean, Mesoamerican)	
Groundnut	Tree for all the genepool with accessions mapped	Completed using major types (fastigiata, hypogaea)	
Pea	Tree for all the genepool with accessions mapped	Completed using major types (arvense, sativum)	
Sweet Potato	Tree for all the genepool with accessions mapped	Completed using environmental types / lineages (northern, southern)	
Sorghum	Tree for all the genepool with accessions mapped	Based on basic races	Shoot fly resistance, grain mould resistance
Bambara Groundnut	Tree for all the genepool with accessions mapped	Not performed yet, planned for 2022.	
Cowpea	Tree for all the genepool with accessions mapped	Completed using clusters based on characterization data	
Potato	Tree for all the genepool with accessions mapped	Done based on the taxonomy of Spooner, and also of Hawkes	Late blight, cyst nematode pa2 resistance, cyst nematode pa3 resistance, root knot nematode resistance
Chickpea	Tree for all the genepool with accessions mapped	Completed using major types (desi, kabuli)	Leaf miner resistance, <i>Callosobruchus chinensis</i> resistance, susceptibility to cold, cyst nematode resistance, frost damage
Faba bean	Tree for all the genepool with accessions mapped	Completed with analyses performed at crop level	Growth habit, pod distribution

Alfalfa	Tree for all the genepool with accessions mapped	Not performed.	
Lentil	Tree for all the genepool with accessions mapped	Completed using environmental groups	Susceptibility to Orobanchae, susceptibility to cold, pod shedding (one week after maturity), pod dehiscence (one week after maturity), stem pigmentation (at seedling)
Cassava	Tree for all the genepool with accessions mapped	Completed using environmental groups	Resistance to <i>Cercospora Vicosae</i> , bacterial blight, <i>Phoma sp.</i> and Antracnosis
Finger Millet	Tree for all the genepool with accessions mapped	Completed using major types (compacta, elongata, plana, vulgaris)	
Pearl Millet	Tree for all the genepool with accessions mapped	Completed using environmental groups	
Taro	Tree for all the genepool with accessions mapped	Asia and the Pacific, done at crop level with CePaCT.	
Breadfruit	N/A	Completed with analyses performed at crop level	
Yam	N/A	Completed using major groups (enantiophyllum, lasiophyton, opsophyton, macrogynodium)	
Pigeonpea	N/A	Completed with analyses performed at crop level	

The results of these analyses have been incorporated in the updated conservation strategies for several crops as part of a project funded by the German Federal Ministry of Food and

Agriculture (BMEL)¹⁵. Also, Centers have organized collecting expeditions informed by these analyses' results, combined with additional information such as availability of relevant materials in other collections around the world, the feasibility of collecting missions, etc. Many of the approx. 4,000 unique PGRFA collected by the Centers and NARS in late 2021 with support from the Genebank Initiative, described in the section about acquisitions above, were targeted as a result of these gap analyses.

Guidance Note for CGIAR Centers' Genebanks for Improving Accession Management

In 2020, the CGIAR Genebank Platform, working with the genebank managers, in close collaboration with the Secretariats of the Plant Treaty and the FAO Commission on Genetic Resources for Food and Agriculture developed a 'Guidance note for CGIAR Genebanks on improving accession management'. The note was reviewed by the Director Generals of the 'Article 15 Centers' in January 2020 and approved by the CGIAR Executive Management Team in April 2022.

The Guidance Note promotes harmonization across the Centers with respect to certain aspects of their management of international collections of PGRFA, including the vocabulary, form and scheduling of their joint communications concerning their management of those collections, within the context of existing applicable policies. The note does not present a new policy *per se*; rather, it reflects and promotes best practices that Centers have developed over time in managing the international collections under the frameworks of, first, their 1994 In Trust Agreements with FAO and, later, their Article 15 Agreements with the Governing Body of the Plant Treaty.

The note describes four classes of PGRFA curation, which all Centers will use to describe their collections, including when they share information with the Governing Body of the Plant Treaty, the UNFAO CGRFA and other stakeholders. The four curation classes are: Fully curated, Partially curated, Archived, and Historical. Each class represents a different level of activity provided by the Centers in the curation of the materials concerned. More detailed technical guidelines to assist managers in optimizing processes, making decisions to designate accessions to a particular curation class and de-archiving will be developed in the near future.

Effects of the COVID pandemic on the operations of CGIAR Centers' genebanks

The COVID-19 pandemic required a major reassignment of genebank and GHU staff to working remotely or working in shifts. As a result, the genebanks had to work hard, and be creative, to ensure there were sustaining sufficient staff in the laboratories, screen-houses and fields to carry out critical operations to be able to avoid the loss of accessions. These activities included monitoring cold rooms, subculturing in vitro accessions and processing seed from harvest to cold room.

Some of the genebanks' regeneration and multiplication activities were affected. In a small number of cases, harvests were lost. For example, in 2020 CIP had to cancel the field season for sweetpotato, and IRRI had to abandon a small part of the rice harvest. Sometimes the harvest took place late (e.g., Andean roots and tubers at CIP) or the processing or newly harvested material was delayed (e.g., rice at IRRI). These delays affected the quality and longevity of the harvested material.

¹⁵ <https://www.croprtrust.org/science-blog/breathing-new-life-into-the-global-crop-conservation-strategies/>

Seed viability testing was also interrupted in most genebanks during the height of the pandemic-related restrictions in most countries; those activities have since been resumed in all the Centers concerned.

GHUs continued to provide phytosanitation services for transfers, but regular testing of collections had to be interrupted in some cases. For example, CIAT had to almost completely suspend its work to eliminate quarantinable pathogens (viruses, phytoplasma) from in-vitro accessions of cassava.

Most of the genebanks were able to continue responding to requests for germplasm. In 2020, both germplasm requests and distributions declined by around 50% compared to other years around this time. Ultimately, the Centers were able to provide germplasm in response to 90% of requests received during that time.

Large tissue culture collections (>5000 accessions) were the most vulnerable to staff reductions as a result of lockdown measures, since they require continuous monitoring and subculturing by trained staff working in relatively small spaces. Procedures were modified to ensure all accessions were given necessary attention, which included reducing numbers of samples per accession, deploying staff from other teams to help and running shifts over the weekend. Some samples were lost, but the Center were able to replace them with safety duplicates.

The Crop Trust coordinated with the CGIAR System Organization and Centers' risk specialists to undertake a genebank risk assessment in June 2020 with the aim of ensuring that measures were in place to facilitate remote working, including strengthening automated alarm and temperature control systems in cold rooms and drying rooms, and installing remote cameras, irrigation systems and extra laminar flow cabinets. Insights gained from those assessments have been incorporated into revised versions of the genebanks' risk management strategies. Several Centers invested in automated irrigation equipment in 2021 to ensure that harvests were not jeopardized by restrictions on workers going into the fields.

Reports were made periodically during the year 2020 to the Plant Treaty Secretariat and the Plant Treaty Bureau on the status of operations in the CGIAR genebanks during the pandemic. In September 2020, the Plant Treaty Secretariat, the Crop Trust and FAO hosted a virtual meeting on the "Impact of the COVID-19 pandemic on the conservation, use and exchange of plant genetic diversity".

Highlights of CGIAR crop and forage pre-breeding and breeding work

In this subsection, we provide some examples of plant pre-breeding and breeding carried out by CGIAR Research Programs (CRPs). NB: we are not attempting to provide an exhaustive overview; time and space would not allow. Instead, we limit ourselves to providing one or two examples of work for each crop across the relevant CRP over the course of 2019-2021.

The results shared here are available on the public CGIAR Results Dashboard. We encourage delegates to the Governing Body meeting who would like to know more about Centers' crop improvement efforts to visit the CGIAR Results Dashboard: <https://www.cgiar.org/food-security-impact/results-dashboard/>. Much of the content of this sub-section on plant pre-breeding and breeding is derived from the CRP reports on the Results Dashboard.

Between 2019-2021, some of the breeding programs' focus has been dictated by the emergence and spread of new pests and diseases. Heat and drought have continued to gain

importance in CGIAR breeding programs for sub-Saharan Africa and South Asia. Most breeding programs have now integrated nutritional aspects in their work, and some of them have increased their focus on traits that facilitate crop production at a market scale.

CGIAR scientists working on different crops (including maize, wheat, rice and some legumes) have successfully worked with marker-assisted recurrent selection in the last decade. Advancing further, through the Genomic Selection method, CGIAR scientists used genetic information of new, improved lines to predict their performance for key attributes, using information from their relatives, without needing to physically evaluate the lines themselves. By improving logistics, and lowering the cost of obtaining genetic information and making it more accessible, CGIAR scientists adapted these methodologies – traditionally the reserve of well-funded private sector R&D programs – to resource constrained breeding programs focusing on small holder farmers in Africa, Asia and Latin America. The CGIAR breeders have demonstrated successful breeding program-scale use of Genomic Selection in these regions, considerably reducing the operational cost of first year field evaluation testing phase, enabling evaluation of a larger number of new lines.

The following paragraphs provide examples of CGIAR research programs' work at various stages of the breeding process.

Pre-breeding

Phenotypic characterization

Since 2012, the CGIAR Wheat Program, with the co-funding of National Agricultural Research Institutes, has maintained the Global Network of Precision Wheat Phenotyping Platforms (PWPP). The aim is to create multi-location phenotypic data on selected traits, applying defined good practices, promoting the germplasm exchange and increasing coordination in wheat phenotyping. These phenotyping hubs include locations affected by strong selection pressures for specific traits due to the presence of diseases or abiotic stresses. To date, more than ten platforms are fully operational. They cover a wide range of geographies and target traits, from wheat blast in Bolivia and Bangladesh to rust pathogens in Turkey and head blight in China. For example, the phenotyping platform in Njoro, Kenya, supports breeders to identify and develop new lines which are resistant to stem rust race Ug99. Over the last decade, up to 50,000 wheat lines per year from up to 25 countries were assessed and over 100 wheat cultivars Ug99 resistant were released to the benefit of smallholder wheat farmers worldwide.

As part of the project AGENT, funded by the European Union program Horizon 2020, ICARDA is screening 500 wheat and 500 barley genebank accessions for response to major fungal diseases: yellow rust and spot blotch. The project AGENT aims to unlock the full potential of wheat and barley collections stored in genebanks around the globe by using FAIR international data standards and an open digital infrastructure.

IRRI evaluated a set of 220 Aus rice genotypes for root architecture in field trials and in greenhouses. Through this evaluation, IRRI identified that nodal root diameter has an important role in deep root growth¹⁶.

Genotypic characterization

As part of CIMMYT work to mainstream biofortification in wheat breeding, CIMMYT scientists carried out a genome-wide association study (GWAS) to characterize grain Zn

¹⁶ Liao, Q., Chebotarov, D. Islam, M.S. et al. Aus rice root architecture variation contributing to grain yield under drought suggests a key role of nodal root diameter class. *Plant, Cell and Environment*. 2022 March; 45 (3)

concentrations in a set of 330 breeding bread wheat lines that had been grown in the field over 3 years across a range of environments in India and Mexico as part of a HarvestPlus breeding program. GWAS analysis revealed 39 marker-trait associations for grain Zn. Two larger effect QTL regions were found on chromosomes 2 and 7. Candidate genes (among them zinc finger motif of transcription-factors and metal-ion binding genes) were associated with the QTL. The linked markers and associated candidate genes identified are being validated in new biparental mapping populations for marker-assisted breeding.

IRRI and partners developed a platinum standard pan-genome resource that represents the population structure of Asian rice¹⁷. In 2021, IRRI developed a novel SNP chip to distinguish different subtypes of rice, and 12,000 genebank accessions were genotyped and their correct groupings were identified. Using GWAS approach, rice researchers at IRRI identified novel set of genetic factors that were associated with pre-harvest sprouting in japonica rice.

In 2017-2021, ICRISAT, IITA and CIAT made advances in genomic sequencing and development of markers for selected traits in legume species. At ICRISAT, 195 accessions of wild Cicer, seven 14 of wild Cajanus and 38 of wild Arachis were sequenced and used for genetic/genome diversity and to identify haplotypes, candidate genes. Diagnostic molecular markers were developed for a number of priority traits in pearl millet, sorghum, chickpea, pigeonpea, finger millet, soybean and cowpea. For example, in chickpea, 10 SNP panel was developed for drought tolerance, fusarium wilt and Ascochyta blight resistance for use in early generation selection. For pearl millet and sorghum, scientists identified QTLs for traits that are particularly important in West and Central Africa, including drought tolerance/root growth, resistance to Striga and downy mildew disease. In chickpea, a global genetic variation map based on the sequencing of 3,366 genomes was reported and a pan-genome of 592 Mb was assembled to describe genomic diversity across cultivated and wild progenitors¹⁸. In groundnut, SNP markers alleles were used to identify alleles conferring high oleic content. For common bean, improved markers were developed by CIAT in collaboration with USDA for bean golden yellow mosaic virus.

In finger millet, a 10 SNP panel for blast resistance was developed for routine use in ICRISAT breeding program. Quality Control panels of germplasm identity and purity were developed for all ICRISAT mandate crops for parental identification.

AfricaRice and its partners evaluated amylose content of 1,020 *Oryza glaberrima* accessions conserved at the AfricaRice genebank. Amylose content is one of the quality traits that influence texture and taste of cooked rice, but the genetic control of amylose content in *O. glaberrima* still remains poorly understood. The study reported high variation in amylose content and showed an overall mean which is higher than the value reported in *O. sativa*. Researchers conducted genome-wide association studies (GWAS) to map the genomic regions associated with amylose content in a panel of 386 *O. glaberrima* accessions and identified 3 genomic regions that individually explained up to 12% of the phenotypic variation of amylose content in *O. glaberrima*. One of the GWAS findings was the very narrow genetic variation among the *O. glaberrima* accessions included in the panel. To identify the most genetically diverse set of *O. glaberrima* collection for future use in breeding and gene discovery (including AC), the entire *O. glaberrima* collection conserved at the AfricaRice genebank was genotyped and a core collection of 350 accessions that captured 97% of the

¹⁷ Zhou, Y., Chebotarov, D., Kudrna, D. et al. A platinum standard pan-genome resource that represents the population structure of Asian rice. *Sci Data* 7, 113 (2020). <https://doi.org/10.1038/s41597-020-0438-2>

¹⁸ Varshney RK, Roorkiwal M, Sun Set al. A chickpea genetic variation map based on the sequencing of 3,366 genomes. *Nature*. 2021 Nov; 599 (7886). doi: 10.1038/s41586-021-04066-1.

molecular variation was developed. Currently, the entire collection is being evaluated for quality and nutritional traits and the core collection for diverse agronomic and biotic traits.

Genetic base broadening

ICARDA performed interspecific crosses of barley with *H. spontaneum* which have allowed to develop populations and elite lines with resistance to major foliar diseases, with higher beta-glucans, Iron and Zinc contents and with some having good performance in grain and straw.

Scientists from ICRISAT, IITA, and CIRAD/CERAAS (Center d'étude régional pour l'amélioration de l'adaptation à la sécheresse) used crop wild relatives in the following crops: chickpea (for Botrytis grey mould (BGM) resistance); groundnut (for resistance to rust and late leaf spot); pearl millet (for heat tolerance at flowering stage, and tolerance to blast); pigeonpea (for resistance to pod borer); finger millet (for tolerance to blast disease) and cowpea (for drought tolerance at seedling stage, and heat tolerance). ICRISAT and IITA used (and will continue to use) promising wild genetic materials to harbor novel genes as donors for introgression and development of pre-breeding populations. Introgressed lines were evaluated and screened for their reaction to a range of biotic and abiotic pressures, including heat, drought and blast in the case of pearl millet, and pod borer infestation in the case of pigeonpea. In pearl millet, pre-breeding populations were developed using wild *Pennisetum violaceum* for heat tolerance.

As part of the initiative "Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives", in 2016-2021, ICARDA made advances in the development of grass pea resistance to parasitic Broomrape weeds (*Orobanche* spp.) using wild *Lathyrus* species. Despite its immense value in human food, animal feed, and ecosystem services, grass pea (*Lathyrus sativus*) cultivation in the Mediterranean region has almost been abandoned because of high incidence of *Orobanche* and high susceptibility of existing grass pea varieties. In 2016-2018, ICARDA screened 285 accessions representing 13 *Lathyrus* species for their resistance to *Orobanche crenata* and *O. foetida*, with the objective to identify species with high or complete resistance, for their introgression in *Lathyrus sativus*. Based on the results of the study, ICARDA scientists investigated crossability of *Lathyrus sativus* with six wild species which had showed high resistance. In 2019-2021, F1, F2 and F3 fertile plants were obtained from crosses between *Lathyrus sativus* and *L. articulatus*, *L. cicera*, *L. heirosolymitanus*, *L. inconspicuus*, *L. marmoratus* and *L. ochrus*. They represent a valuable source of *Orobanche* resistance for grass pea breeding programmes.

CIP scientists have worked with partners with United States Department of Agriculture (USDA) and Agriculture and Agri-Food Canada (AAFC), to build genomic resources for the development of climate smart potato varieties. The partnership is starting its second phase in 2022. Its focus is on sequencing accessions of wild relatives of potato and breeding lines. Data will be made public through the Potato Genome Diversity Portal (<https://potatogenomeportal.org/website>).

Genetic improvement

By leveraging tropical insect-resistant maize germplasm developed in Mexico, coupled with elite stress-resilient maize germplasm developed in sub-Saharan Africa, CIMMYT has worked since 2017 to identify and validate sources of genetic resistance to fall armyworm in Africa. This included screening over 3,500 hybrids in 2018 and 2019. In 2020, a promising set of eight hybrids were tested against four widely used commercial hybrids as checks. These tests took place in screenhouses, on station, and on farm, in Kenya and Tanzania.

These trials led to three tolerant hybrids that will be nominated for varietal release in target countries in sub-Saharan Africa, especially in eastern and southern Africa.

Great strides were made in developing maize germplasm with resistance to maize lethal necrosis disease (MLN) in 2017-2020, using both innovative technologies and novel maize genetic materials from around the world. MAIZE scientists worked with Corteva Agriscience to identify one of the genes that confers strong resistance against MLN. With fine-mapping, a strategy that combines laboratory molecular tools with field phenotyping, scientists narrowed their search to fewer than eight genes (from a total of ~40,000 in the maize genome). A promising candidate among these eight genes are being validated via gene editing in MLN-susceptible parental lines to determine whether it confers resistance to MLN. Gene editing, compared to other breeding methods, allows scientists to shave off one third of the time it would take to develop new MLN resistant lines, expediting development and release of improved varieties to farmers.

Early maturing is one of the traits sought by the pigeonpea and cowpea breeding programs of ICRISAT and IITA, to adapt production to water deficiencies in South Asia and sub-Saharan Africa. In 2018-2020, scientists tested and selected early maturing pigeonpea and cowpea cultivars. In pigeonpea, high-yielding introgression lines with resistance for fusarium wilt, sterility mosaic and phytophthora blight were identified and are in advanced stages of evaluation in national programs.

ICRISAT's sorghum breeders used genotypes with high transpiration efficiency under high vapor pressure deficit for developing drought-tolerant sorghum hybrids with high biomass yields. These new hybrid lines are currently being tested.

Rice researchers at IRRI made major progress towards understanding and improving both grain quality and grain yield simultaneously in rice breeding lines. OSPTTR gene was found to be important to get good yield without a penalty on quality.

Release, adoption and impact of improved varieties derived from CGIAR breeding

From 2017 to 2020, using improved germplasm from CGIAR breeding programs, national partners and seed companies across Africa, Latin America and Asia released 290 new maize varieties, 224 new wheat varieties, 130 new varieties of lentil, groundnut, chickpea, sorghum, pearl millet, soybean and finger millet, and 87 varieties of sweet potato, potato, cassava and yam. During 2020-21, about 73 rice varieties developed by IRRI were released in 16 countries.

Impact studies conducted in 2019-2021 presented the impacts of varieties derived from CGIAR improved germplasm in previous years. We summarize some of the most salient impacts from those studies in the following paragraphs:

According to the DNA-fingerprinted adoption data, about 66% of cassava producers in Nigeria have adopted improved varieties that are derived from IITA improved germplasm, contributing to 82% productive gain for 3.1 million households, and facilitating approximately 2 million individuals to escape poverty¹⁹. Improved cassava varieties derived in part from CIAT-related materials were adopted and grown in 2.7 million hectares across Vietnam, Thailand, Cambodia, Laos, Myanmar, The Philippines, Indonesia, China and India,

¹⁹ Assfaw Wossen, T., Girma Tessema, G., Abdoulaye, T., Rabbi, I. Y., Olanrewaju, A., Bentley, J., ... & Manyong, V. (2017). The cassava monitoring survey in Nigeria: final report (p.66). Ibadan: IITA.; ISPC. (2018). *What is the True Impact of Improved Cassava Varieties in Nigeria?*, Brief N. 64. Rome: Independent Science and Partnership Council.

representing 68% of the total hectares of cassava production in the nine countries. However, the level of adoption of varieties varies from country to country²⁰.

In 2012, the Heat Tolerant Maize for Asia (HTMA) project started to address heat stress in a context of an increasing demand for maize production. The first heat-tolerant maize hybrids were ready for release in India, Bangladesh, and Nepal within three years of the program's inception. Between 2015 and 2020, more than 50 heat stress tolerant, CIMMYT-derived maize hybrids were licensed to public and private sector partners for varietal release and deployment in the region. Out of the total licensed hybrids, 16 have been officially released/registered for commercialization and made available to farmers in stress-vulnerable ecologies. Others are currently part of national performance trials for official release. As of 2020, 6 stress-resilient maize hybrids are being deployed on over 20,000 ha in vulnerable ecologies of South Asia, by around 47,000 farmer household members. The project made a major impact in Nepal, which is making strides towards hybrid seed self-sufficiency after previously relying almost 100% on imported seed²¹.

The Tropical Legumes project, funded by the Bill & Melinda Gates Foundation and implemented by ICRISAT, CIAT and IITA together with 15 national agricultural research system partners in sub-Saharan Africa and South Asia during 2007-2019, facilitated the development of 266 improved legume varieties and the production of about 497,901 tons of certified seeds of the target legume crops in Burkina Faso, Ghana, Mali, Niger, Nigeria, Senegal, Ethiopia, Kenya, Malawi, Mozambique, Tanzania, Uganda and Zimbabwe, and India and Bangladesh. The certified seeds have been planted on about 5.0 million ha by more than 25 million smallholder farmers in the 15 countries and beyond, producing about 6.1 million tons of grain worth US\$ 3.2 billion. Furthermore, the project also trained 52 next generation scientists, by supporting 34 Master degree and 18 Ph D degree students²². For this project, in 2021, ICRISAT was awarded the Africa Food Prize, in recognition for helping 25 million farmers in 13 countries to improve income and food production.

Global Plant Cryopreservation Initiative

In 2017, Bioversity International commissioned the Global Crop Diversity Trust to lead a feasibility study for a safety back-up cryopreservation facility²³. This study assessed the need for safety duplicates of genetic resources collections that cannot be conserved as seed long-term in the Svalbard Global Seed Vault including vegetatively propagated crops and crops with recalcitrant or short-lived seed.

The study concluded that:

- Cryopreservation is the best long-term conservation option for these collections;

²⁰ Labarta, R., Wossen and Le, D.P. 2018. *The Adoption of Improved Cassava Varieties in South and Southeast Asia*. Paper prepared for the 9th ASAE International Conference: Transformation in agricultural and food economy in Asia 11-13 January 2017 Bangkok, Thailand.

²¹ Zaidi, P.H. et al. 2020. Stress-resilient maize for climate-vulnerable ecologies in the Asian tropics. *AJCS* 14(08); Prasanna, B.M. et al. 2021. Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments. *Theoretical and Applied Genetics* 134;

²² Varshney, R.K., Ojiewo, C., Monyo, E. 2019. A decade of Tropical Legumes projects: Development and adoption of improved varieties, creation of market-demand to benefit smallholder farmers and empowerment of national programs in sub-Saharan Africa and South Asia. *Plant Breeding*

²³ Acker, J.P., Adkins, S., Alves, A., Horna, D. and Toll, J. (2017) Feasibility study for a safety back-up cryopreservation facility. Independent expert report: July 2017. Rome (Italy): Bioversity International. 100p. Available at https://cgspace.cgiar.org/bitstream/handle/10568/91009/Feasibility_Acker_2017pdf.pdf?sequence=1

- Cryopreservation has huge benefits for long-term safety back-up of these collections;
- There is a critical need to accelerate the cryopreservation of clonal and recalcitrant seed collections;
- The CGIAR is ideally situated to develop a proposal and seek donor sponsorship to meet these needs.

At the Eighth meeting of the Governing Body, a proposal was made by the Government of Belgium to host a safety backup cryopreservation facility in the Catholic University of Leuven (KUL) Bioversity International Genebank to safeguard plant materials that organizations want safely backed-up for the long term, as part of an overarching strategy for long-term conservation of clonal crops and recalcitrant seeds (Resolution 12/2019, regarding cooperation with other international bodies and organizations).

In 2020 and 2021, Bioversity International, CIAT, CIP and IITA (CGIAR Centers that maintain collections of clonal crops and are currently implementing cryopreservation) and the Global Crop Diversity Trust initiated the development of the Global Plant Cryopreservation Initiative (GPCI) to respond to the feasibility study.

The GPCI was presented at the meeting *Cryopreservation: A long-term strategy for hard-to- conserve PGRFA collections in a post-COVID world*, co-organized by the Secretariat of the Plant Treaty and the Global Crop Diversity Trust, with the sponsorship of the Government of Belgium, on 25 June 2021.

Building on the success of cryopreservation in potato and banana, where more than 80% of the global in-trust collections have been safeguarded in cryobanks under strict quality guidelines, the GPCI will establish regional “Center of Cryopreservation Excellence” hubs, starting in Europe (Belgium), Latin America (Peru) and Africa (Nigeria). This work has been integrated in the program of work of the CGIAR Genebank Initiative, which will seek to set up these hubs with the objectives to:

- Provide safety back up
- Create regional and global communities of practice around cryopreservation
- Expand cryopreservation to other crops, beyond potato and banana
- Become centres of excellence for capacity building and training

The hubs will work with partners worldwide to cryopreserve germplasm collections in line with the Plant Treaty.

CGIAR involvement in Plant Treaty intersessional processes (since the Eighth session of the Governing Body)

CGIAR has actively participated in several processes and activities during the intersessional period, including those highlighted in the following subsections. Much of CGIAR's engagement in these processes was coordinated by the Policy Module of the CGIAR Genebank Platform, in consultation with relevant research groups and leadership bodies within CGIAR.

Informal consultations with respect to enhancing the functioning of the Multilateral System of Access and Benefit Sharing

The Eighth session of the Governing Body suspended the negotiations of the Ad Hoc Open-ended Working Group to Enhance the Functioning of the Multilateral System of Access and Benefit-sharing (WG-EFMLS). At the same time, it invited contracting parties and

stakeholders to engage in informal consultations, during the intersessional period, concerning options for further work to enhance the multilateral system. Over its six years of negotiations, the WG-EFMLS was quite effective in distilling down a range of options to include in a final package of measures to enhance the multilateral system, including potentially expanding the scope of coverage of Annex 1 beyond the current list of 64 crops and forages, and creating a subscription system to facilitate predictable, time-limited payments from users with minimal transaction costs in the form of tracking and tracing. Over the last three years, CGIAR representatives have maintained contacts with a range of contracting parties and stakeholders to assess whether it will be possible to relaunch some new process to take advantage of, and carry forward, some of the excellent work of the WG-EFMLS, and ultimately adopt a new set of measure to improve the functioning of the multilateral system. CGIAR representatives also participated in the meeting organized by the Government of Switzerland and the Plant Treaty Secretariat entitled “Preparation for GB-9 discussion on possible steps forward on the Enhancement of the Multilateral System (MLS) of the International Treaty”, on December 14, 2021.

As part of its intersessional efforts, CGIAR has also actively monitored and participated in discussions during the last biennium concerning digital sequence information (DSI)²⁴ under the framework of the Convention on Biological Diversity. This is important, given that whatever package of measures to enhance the Plant Treaty’s multilateral system will need to be consistent with, and informed by, progress on DSI under the Convention on Biological Diversity (CBD).

CGIAR appreciates why many contracting parties are concerned about the gap in technological capacity of many developing countries to generate and use DSI. CGIAR recognizes the importance of monetary benefit sharing. At the same time, the ongoing, and potential future, gains through non-monetary benefit sharing (that is tech transfer, information sharing, capacity strengthening) are much larger. A long-term solution for ABS for DSI must involve capacity strengthening and tech transfer to close technology gaps. Research and development organization like CGIAR already do play an important role with respect to generating and sharing non-monetary benefits and ‘addressing the technology divide’; we feel the research community can and should play a still more active role in pursuit of this objective.

CGIAR is concerned about the potential impact of newly created norms on open science. If new norms requiring benefit-sharing from use of DSI are developed, they must not interrupt availability and exchange of data for use in agricultural research and development. CGIAR has reported to the Governing Body and to the CBD Conference of the Parties in the past on how our own activities to conserve genetic diversity, and to improve crops and breeds for food security and sustainable rural development depends on access to, and use of, DSI. CGIAR has undertaken to develop another such report for CBD by the end of 2022, drawing on our work on conservation and improvement of crop, forage, agroforestry, livestock and fish genetic resources.

For the same reasons that CGIAR appreciates the Plant Treaty’s multilateral system of access and benefit sharing for PGRFA, CGIAR is concerned that bilaterally oriented approaches to regulating access to DSI, tracking and tracing uses of sequence data in development of particular research products could be extremely difficult, high in transaction

²⁴ Here we use DSI as a placeholder term, according to international negotiations under the Plant Treaty and the Convention on Biological Diversity.

costs, and create incentives for system avoidance. By contrast, CGIAR has stated that if new norms are going to be created, they should embrace multilateral approaches.

The simplest multilateral approach, at least from the perspective of research and development organizations, would be for national governments to agree to assume responsibility for making payments to a centralized benefit-sharing mechanism on behalf of their constituent commercializers, based on a to-be-agreed formula, for example, annual seed sales in the country. The national government could decide to collect from constituent companies, or not. With such an approach, DSI generation, sharing, and access could not be affected at all.

Alternative multilateral approaches which involve payments by actual DIS users involve the introduction of mechanisms for triggering payments. In this context, CGIAR has highlighted the advantages of the lightest weight options, which would generate predictable new funds to be shared, but also involve the least possible disruption for data accessibility and use. In the negotiations to enhance the Plant Treaty's multilateral system of access and benefit sharing, CGIAR highlighted the potential advantages of building on the subscription system option, with the adoption of incrementally higher subscription fees to reflect value of access to DSI (in addition to the material genetic resource).

Under the CBD, building on our experiences operating under the Plant Treaty's multilateral system, we have advocated consideration of similar multilateral approaches, preserving open access architecture with obligations for payment that are delinked from need to track and trace use of DSI in new products (e.g., membership fees), including, potentially, payments from commercial organizations who provide fee-for-sequencing services, on the sale of reagents.

CGIAR has also repeatedly raised concerns about the possibly inadvertent, but not impossible, outcome of ending up with two different regulatory regimes: one for material genetic resources, and another for DSI derived from those resources, for example, material PGRFA being regulated under the Plant Treaty and DSI derived from those PGRFA being regulated under a new regime under the CBD. Whatever emerges from the next period of negotiations across the different international fora must be harmonized and in synch, keeping administrative burdens to a minimum for actors conserving, using, and sharing genetic resources and DSI.

Farmers' Rights

Article 3 of the CGIAR IA Principles state that

3.1. CGIAR recognizes the indispensable role of farmers, indigenous communities, agricultural professionals and scientists in conserving and improving genetic resources.

3.2. CGIAR seeks to be respectful of national and international efforts to protect and promote farmers' rights as envisaged by the Treaty and support the development of appropriate policies and procedures for their recognition and promotion.

Each year, Centers report to the CGIAR System Organization concerning their implementation of the IA Principles, including Article 3. The annual CGIAR reports on Intellectual Asset management include summaries of what the Centers do, including some illustrative examples. For more information about Centers efforts to promote Farmers Rights,

delegates to the Governing Body meeting are encouraged to review those reports; they are all available on the URL entitled 'Intellectual Assets Reports'²⁵ on the CGIAR website.

CGIAR representatives participated in the following (virtual) meetings as part of the process to develop decision making tools for the implementation of farmers rights under Article 9 of the Plant Treaty:

- Second meeting of the Ad Hoc Technical Expert Group on Farmers' Rights (AHTEG-FR-2) 20-23 May 2019. The CGIAR Genebank Platform coordinated development of "CGIAR Centers' submission on best practices/measures of implementing Article 9 of the ITPGRFA" for that meeting.²⁶
- Third meeting of the Ad Hoc Technical Expert Group on Farmers' Rights (AHTEG-FR-3) 25-28 September 2020
- Farmers' Rights Webinar organized by the Secretariat of the Plant Treaty in preparation for the Fourth meeting of the Ad Hoc Technical Expert Group on Farmers' Rights (AHTEG)
- Fourth meeting of the Ad Hoc Technical Expert Group on Farmers' Rights, 4-7 May 2021

Here are short summaries of examples included in CGIAR Intellectual Assets Management reports for 2020 and 2021 concerning CGIAR research programs and Centers promotion of farmers rights in the context of their research and development work in 2019-2020 (NB: the CGIAR Intellectual Asset Management Report for 2021 is not yet finalized as of the date of submission of this report):

Despite the restrictions derived from the pandemics, in 2019, 2020 and 2021 CIP repatriated, on request, 1,837, 438 and 299 potato accessions respectively to a total of 21 farmer communities and associations located predominantly in Peru's Puno and Apurimac regions. CIP's repatriation program, in place since 1997, returns traditional potato cultivars to the farming communities from which they originate and whose ancestors developed and conserved potato landraces for millennium. In 2021, 88 accessions of native potato landraces were donated by farmers to CIP genebank through the SMTA, making these accessions available for distribution under the multilateral system. When the CGIAR Research Program Roots, Tubers and Bananas came to an end in 2021, CIP organized a meeting with farmers' communities where the results of the program were presented. The event included a presentation about the Plant Treaty, where farmers' rights were highlighted²⁷.

CIAT initiated a project for the documentation and *in situ* conservation of cassava landraces in the region of Pasco, Peru in 2017 as part of a consortium involving also the Instituto Nacional de Innovación Agraria (INIA), National University Daniel Alcides Carrión (UNDAC), the civil society organization Instituto del Bien Común (IBC) and an organization representing the indigenous Yaneshas peoples, the Federación de Comunidades Nativas Yaneshas (FECONAYA). The project extended until 2020, and its core components included the systematic documentation of existing landrace diversity in cassava producing Yaneshas communities by conducting household surveys, participatory GIS cartography and field sampling, phenological and morphological documentation, plant photography and ethnobotanical inquiries, combined with genetic fingerprinting studies. These data provide a

²⁵ See Intellectual Assets Reports at <https://www.cgiar.org/food-security-impact/intellectual-assets-reports/>

²⁶ CGIAR Centers' submission on best practices/measures of implementing Article 9 of the Plant Treaty, available at <https://www.fao.org/3/ca4123en/ca4123en.pdf>

²⁷ For more information: <https://cipotato.org/es/eventos/monitoreo-diversidad-in-situ/>

robust analysis of cassava diversity and conservation trends, both spatially and temporally. In addition, locally appropriate catalogues and communication materials gave local people insight into their varietal diversity, risk of loss, and management options.

In 2020, ILRI formalized its 'Policy procedure on obtaining prior informed consent in research activities'. This procedure is intended to support farmer participation and engagement as encouraged by ILRI in its research projects, including preparatory meetings to inform proposal design, meetings with farmers and community members at various stages of research implementation to strengthen engagement, and inclusive decision-making and capacity building.

Cooperation with the Plant Treaty Secretariat

CGIAR/Plant Treaty communications are frequent and ongoing. Here we list just a few examples of areas of cooperation in 2020 and 2021, wherein the Plant Treaty Secretariat,

- Participated as special guests/resource people in several of the live sessions that are part of the new, 40-hour, 7 module, on-line course developed in 2021 by the CGIAR Genebank Platform entitled 'Genetic Resources Policies for CGIAR Scientists'. As of May 2022, almost 100 CGIAR breeders, genebank managers, intellectual property experts and legal officers have taken this course. The course will continue in 2022 and beyond.
- Made presentations as part of the Genetic Resources Policy Sessions of the Annual Genebank Meetings co-convened by CGIAR and Crop Trust in 2020 and 2021.
- Attended and presented at 3 Farmers' Rights webinars that The Alliance of Bioversity and CIAT organized.
- Worked with CGIAR staff to develop submissions to the Working Group on the Post 2020 Global Biodiversity Framework, with a particular focus on ensuring the new global framework recognizes, measures and promotes conservation, sustainable use and access and benefit sharing under the Plant Treaty.
- Reviewed successive drafts of the (now approved) Guidance Note for CGIAR Centers' Genebanks for Improving Accession Management, and the (still draft) Guidelines for CGIAR operations under the Plant Treaty Framework'.
- Consulted with Centers and the CGIAR System Organization with respect to the CGIAR reform process, with a particular focus on Centers' Article 15 agreements with the Governing Body.
- Reviewed draft journal articles developed by CGIAR scientists which included analysis of PGRFA conservation, sustainable use and access and benefit sharing under the Plant Treaty framework.
- Responded to occasional requests for advice/feedback from the CGIAR Scientists who convene the CGIAR Genetic Resources Policy Helpdesk.
- Visited and reviewed projects that are supported by the Plant Treaty Benefit-sharing Fund that are coordinated by CGIAR Centers or in which CGIAR scientists are involved.
- Provided opportunities for CGIAR scientists to contribute to the training module, published in 2021, by FAO, on the functioning of the Multilateral System of Access and Benefit-sharing.
- Provided technical support to CGIAR Centers reporting SMTA transfers to the Secretariat and the Governing Body through the on-line reporting system.

- Provided technical support to CGIAR Centers' genebanks, and more recently, a pilot project with ICRISAT breeders, to mint Digital Object Identifiers in the Global Information System.

Introducing One CGIAR

CGIAR is currently in a system-wide reform designed to increase efficiency and effectiveness in response to evolving global challenges. The *CGIAR 2030 Research and Innovation Strategy: Transforming food, land, and water systems in a climate crisis*²⁸ provides an outline of the research and development priorities of CGIAR. As of January 1, 2022, CGIAR research is organized under three action areas: System Transformation, Resilient Agrifood Systems, and Genetic Innovation. Work within those action areas is carried out through the Research Initiatives in Figure 9. More details about the Initiatives can be found on the CGIAR website²⁹.

²⁸ Available at <https://cgspace.cgiar.org/bitstream/handle/10568/110918/OneCGIAR-Strategy.pdf>

²⁹ <https://www.cgiar.org/news-events/news/cgiar-announces-new-portfolio-to-transform-food-land-and-water-systems-in-a-climate-crisis/>

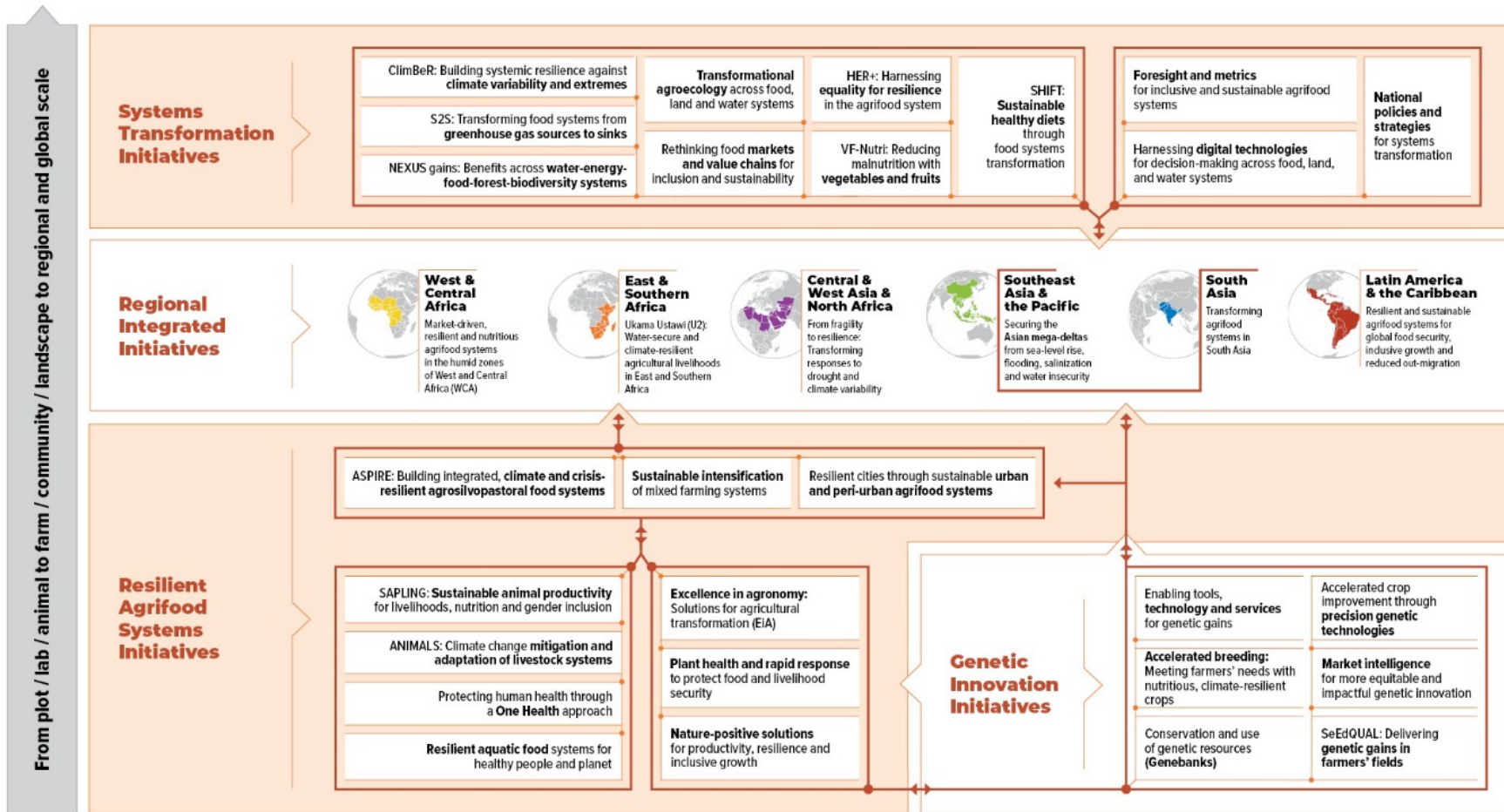


Figure 9: One CGIAR Research Initiatives

Most research and development activities working directly with genetic resources for food and agriculture take place under 'Genetic Innovation', which includes the CGIAR genebanks, plant breeding, and seed systems. Of course, there is also genetic resources-related work taking place in other initiatives, for example, Nature Positive Solutions (which includes work on conservation and sustainable use of agricultural biological diversity), Transformational Agroecology, and Sustainable Healthy Diets, but the bulk of that work will take place under Genetic Innovation.

The One CGIAR reform process has involved considerable realignment and integration of the governance and operational structure of the CGIAR System overall. However, it is important to note that the CGIAR Centers will maintain their legal status as independent legal entities in their own right, and that their Article 15 agreements with the Governing Body of the Plant Treaty will remain in place. CGIAR considers the 'in trust' plant genetic resources maintained by the CGIAR genebanks to be of inestimable value for the international community. CGIAR remains committed to supporting the continued management of collections hosted by International Agricultural Research Centers (IARCs), included within One CGIAR under the framework of the Plant Treaty. One of the advantages of the One CGIAR reform process is that it will facilitate faster, more regular, harmonized reporting to the Governing Body of the Plant Treaty, and, by strengthening a single point of engagement with the Plant Treaty, as preferred by the Governing Body, will enable more proactive efficient CGIAR-wide engagement in activities under the Plant Treaty framework.

Although CIFOR-ICRAF and ICRISAT have not adopted One CGIAR unified governance arrangements at this time, they remain CGIAR Centers that hold Article 15 agreements with the Plant Treaty's Governing Body. ICRISAT and ICRAF will continue to ensure their genebanks are operated and maintained as per international standards. ICRISAT and ICRAF will continue to conserve materials for the international community, under the auspices of the UN FAO and the Plant Treaty, as per the agreements signed in 1994 and 2006, and will continue to deliver their missions to international agriculture, food systems and landscape stewardship.



Informe bienal de CATIE sobre la Implementación del Acuerdo en virtud del Artículo 15 del Tratado Internacional sobre los Recursos Fitogenéticos para la Alimentación y la Agricultura (TIRFAA)

1) Antecedentes

El Centro Agronómico Tropical Investigación y Enseñanza (CATIE) estableció desde finales de la década del 40, colecciones de germoplasma como una estrategia para enfrentar la creciente pérdida de diversidad de algunos de los cultivos de mayor importancia en la región mesoamericana. Las principales labores de nuestro banco de germoplasma es adquirir, conservar, caracterizar y distribuir el germoplasma que por sus atributos, son consideradas de interés prioritario para fortalecer y asegurar la seguridad alimentaria de la región, además de aportar conocimiento científico orientado a la optimización de la conservación de especies de importancia para la alimentación y la agricultura. En mayo de 2004 la gran mayoría del germoplasma fue puesto por CATIE bajo los auspicios de la FAO y desde el 16 de octubre de 2006 en virtud del Acuerdo bajo el Artículo 15, el acceso al germoplasma, (tanto para cultivos del Anexo 1 como para aquellos que no pertenecen al Anexo 1 del TIRFAA) se rige por el Tratado Internacional de Recursos Fitogenéticos para Alimentación y Agricultura (TIRFAA) y su distribución se realiza bajo los términos descritos en el Acuerdo Normalizado de Transferencia de Material (ANTM) en virtud del Artículo 15. Previo a cada reunión del Órgano Rector del TIRFAA las instituciones firmantes de este acuerdo deben someter un informe reportando las actividades de relevancia para la implementación dicho acuerdo para el período correspondiente.

2) Período del informe

Este informe proporciona una actualización de la implementación del acuerdo, así como de las actividades e iniciativas de CATIE para el período comprendido entre agosto 2019 a junio 2022.

3) Conservación

3.1) Conservación en campo

Según los últimos inventarios, realizados en café (2019), cacao (2022) y otras colecciones de campo (2014), CATIE conserva un total de 4.509 accesiones.

A continuación, se detalla las cantidades de accesiones por taxón:

Colección	Cantidad de accesiones conservadas
Café (<i>Coffea spp.</i>)	1.928
Cacao (<i>Theobroma spp.</i>)	1.263
Pejibaye (<i>Bactris gasipaes</i>)	592
Achiote (<i>Bixa orellana</i>)	105

Sapotaceae	123
Sapindaceae	12
Myrtaceae	106
Cítricos (<i>Citrus spp.</i>)	65
Macadamia (<i>Macadamia integrifolia</i>)	17
Arecaceae	83
Varios Taxones	101
Jardín Botánico	114
Total	4.509

A excepción de café y cacao, es necesario para CATIE tener un inventario actualizado para conocer el estado real de conservación especialmente para *Bactris gasipaes*, *Bixa orellana* y las familias Sapotaceae y Myrtaceae, ya que por falta de recursos no ha sido posible hacerlo en los últimos 8 años. El estado sanitario de muchas accesiones de estos cultivos está en estado crítico y con alto riesgo de pérdida debido a la limitación de recursos.

3.2) Conservación de semillas ortodoxas en cámara fría (-18°C)

En cámara fría se conservan un total de 6.202 accesiones de varios taxones, según el inventario recientemente.

El detalle se presenta en el siguiente cuadro:

Especie	Nombre común	Cantidad de accesiones
Amaranthaceae		271
<i>Amaranthus spp.</i>	Amaranto	265
<i>Chenopodium berlandieri</i>	Quinoa	2
<i>Chenopodium quinoa</i>	Quinoa	4
Cucurbitaceae		2.332
<i>Cucurbita argyrosperma</i>	Pipián	111
<i>Cucurbita ficifolia</i>	Chiverre	173
<i>Cucurbita foetidissima</i>		1
<i>Cucurbita lundelliana</i>		4
<i>Cucurbita maxima</i>	Calabaza	9
<i>Cucurbita moschata</i>	Ayote	1.613
<i>Cucurbita pepo</i>	Zucchini	169
<i>Cucurbita sp.</i>		39

<i>Cucumis sativus</i>	Pepino	8
<i>Cucumis melo</i>	Melón	13
<i>Cucumis spp.</i>		4
<i>Lagenaria siceraria</i>	Jícara, Calabaza	147
<i>Otras Cucurbitaceae</i>		41
Fabaceae		1.688
<i>Phaseolus acutifolius</i>	Frijol Tepari	6
<i>Phaseolus coccineus</i>	Cubá, Ayacote	83
<i>Phaseolus dumosus</i>	Cubá, Frijol gordo	41
<i>Phaseolus lunatus</i>	Frijol lima	41
<i>Phaseolus vulgaris</i>	Frijol	680
<i>Phaseolus sp.</i>	Frijol	318
<i>Crotalaria spp.</i>	Crotalaria	32
<i>Lablab purpureus</i>	Lablab	34
<i>Pachyrhizus spp.</i>	Jícama	185
<i>Psophocarpus tetragonolobus</i>	Frijol alado	16
<i>Vigna spp.</i>	Vigna, Frijol mungo	184
<i>Otras Fabaceae</i>		68
Poaceae		412
<i>Zea mays</i>	Maíz	400
<i>Otras Poaceae</i>		12
Solanaceae		1.482
<i>Solanum lycopersicum</i>	Tomate	340
<i>Solanum pimpinellifolium</i>	Tomate silvestre	81
<i>Solanum quitoense</i>	Naranjilla	13
<i>Solanum spp</i>		86
<i>Capsicum annum</i>	Chile	368
<i>Capsicum baccatum</i>	Chile	25
<i>Capsicum chinense</i>	Chile	51
<i>Capsicum frutescens</i>	Chile	274
<i>Capsicum pubescens</i>	Chile	11
<i>Physalis spp.</i>	Uchuva	76
<i>Otras Solanaceae</i>		158
Varias Familias		16
TOTAL		6.202

Durante el período 2019-2022 se adquirieron y dejaron de conservar las siguientes cantidades de accesiones:

Colección	Adquiridas durante el período 2019-2022	Dejadas de conservar durante 2019-2022
Semillas ortodoxas	0	0
Café	0	0
Cacao	30	2
Yuca	0	157
Camote	0	29
Ñame	0	61
TOTAL	30	249

4) Adquisiciones

Durante el período de este informe ingresaron 30 nuevas accesiones de Cacao (AM-1/57; COCA-3348/44; CRU-104; CRU-12; CRU-89; D1; EEG-8; EHH2; EHH29; EHH5; EHH9; F27; F29; F6; F9; ICS-42; IMC-33; IMC-58; IMC-85; LP-3/15; LP-4/8; PA-126; PNG-139; PNG-218; PNG-296; PNG-336; SCA-10; SHRS-02; SHRS-08; SPEC-194/15).

5) Regeneración

Durante el período del informe se regeneraron 202 accesiones de café que estaban en riesgo de pérdida según el inventario hecho en 2019.

Un total de 1.126 accesiones de cultivos de semillas ortodoxas conservados en la cámara fría, necesitan ser regeneradas para aumentar la cantidad de germoplasma disponible para distribución.

El detalle se presenta en el siguiente cuadro:

Taxón	Cantidad de accesiones con prioridad de regeneración
Cucurbita	642
Lycopersicum	292
Capsicum	192
Total	1.126

Recientemente se nos confirmó que recibiremos financiamiento mediante la iniciativa Biodiversity for Opportunities, Livelihoods and Development (BOLD) del Crop Trust para la regeneración de éstas 1.126 accesiones pendientes de regenerar.

En el caso de los materiales conservados en campo, es urgente una regeneración del 100% de las accesiones de frutales en general. La conservación de la colección de Sapotaceae es de suma importancia para la región, pero su renovación ha sido difícil debido al bajo éxito en la injertación. Algunas de ellas están en peligro de extinción como por ejemplo el Pan de vida (*Pouteria hypoglauca*), situación similar ocurre para la colección de Pejibaye, una de las más importantes del mundo, ya que muchas accesiones tienen sólo un árbol.

6) Caracterización

Se caracterizaron molecularmente 1.215 accesiones de cacao y 1.928 accesiones de café gracias al apoyo del Departamento de Agricultura de Estados Unidos (USDA, por sus siglas en inglés).

7) Duplicación

Durante el período 2019-2022 no hubo duplicaciones de germoplasma.

7) Distribución

Usando el Acuerdo Normalizado de Transferencia de Material (ANTM), se distribuyeron 1.413 accesiones a 13 países, incluyendo 912 accesiones de semillas ortodoxas conservados en cámara fría y 446 accesiones de café y 55 accesiones de cacao.

A continuación, se detalla las cantidades y destinos del germoplasma:

Colección	Accesiones distribuidas	Países receptores
Café	446	Costa Rica, Honduras, Taiwán, Guatemala, México, Nicaragua, Panamá, Perú
Cacao	55	Costa Rica, Estados Unidos, Suiza
Semillas ortodoxas	912	Costa Rica, España, Honduras, Taiwán, Guatemala, Sudáfrica, Tanzania,

Los receptores de este germoplasma incluyen agricultores, empresa privada e instituciones de investigación. El detalle de las especies, cantidades, países y otros detalles del material genético distribuido se presenta en el siguiente cuadro:

Tipo de colección	Tipo de Receptor	Cultivo	País	N° Accesiones
Semillas ortodoxas	Agricultores	<i>Amaranthus caudatus</i>	Costa Rica	1
	Agricultores	<i>Amaranthus cruentus</i>	Costa Rica	1
	Agricultores	<i>Cajanus cajan</i>	Costa Rica	2

Agricultores	<i>Cannavalia ensiformis</i>	Costa Rica	2
Agricultores	<i>Capsicum frutescens</i>	Costa Rica	1
Agricultores	<i>Coix lacryma-jobi</i>	Costa Rica	1
Agricultores	<i>Crotalaria longirostrata</i>	Costa Rica	1
Agricultores	<i>Crotalaria sp.</i>	Costa Rica	1
Agricultores	<i>Cucumis sativus</i>	Costa Rica	2
Agricultores	<i>Cucurbita moschata</i>	Costa Rica	2
Agricultores	<i>Cucurbita moschata</i>	Guatemala	45
Agricultores	<i>Cucurbita moschata</i>	Honduras	130
Agricultores	<i>Cyclanthera pedata</i>	Costa Rica	1
Agricultores	<i>Lablab sp.</i>	Costa Rica	1
Agricultores	<i>Lagenaria siceraria</i>	Costa Rica	1
Agricultores	<i>Luffa aegyptiaca</i>	Costa Rica	1
Agricultores	<i>Mucuna deeringiana</i>	Costa Rica	1
Agricultores	<i>Mucuna priurens</i>	Costa Rica	2
Agricultores	<i>Oryza sativa</i>	Costa Rica	1
Agricultores	<i>Pachyrhizus erosus</i>	Costa Rica	4
Agricultores	<i>Pahseolus vulgaris</i>	Costa Rica	5
Agricultores	<i>Phaseolus acutifolius</i>	Guatemala	6
Agricultores	<i>Sicana odorifera</i>	Costa Rica	2
Agricultores	<i>Vigna unguiculata</i>	Costa Rica	2
Agricultores	<i>Vigna radiata</i>	Costa Rica	1
Agricultores	<i>Vigna sp.</i>	Costa Rica	1
Agricultores	<i>Vigna unguiculata</i>	Costa Rica	1
Agricultores	<i>Zea mays</i>	Costa Rica	4
Agricultores	<i>Zea mays</i>	Guatemala	13
Agricultores	<i>Zea mays</i>	Honduras	40
Centro de investigación	<i>Amaranthus spp</i>	Tanzania	265
Centro de investigación	<i>Capsicum annum</i>	Costa Rica	2
Centro de investigación	<i>Cucumis anguria</i>	España	2
Centro de investigación	<i>Cucumis metuliferus</i>	España	1
Centro de investigación	<i>Cucumis sativus</i>	Costa Rica	2
Centro de investigación	<i>Cucurbita argyrosperma</i>	España	1
Centro de investigación	<i>Cucurbita argyrosperma</i>	Taiwan	19
Centro de investigación	<i>Cucurbita ficifolia</i>	Costa Rica	1
Centro de investigación	<i>Cucurbita ficifolia</i>	Taiwan	1

	Centro de investigación	<i>Cucurbita maxima</i>	Taiwan	1
	Centro de investigación	<i>Cucurbita moschata</i>	Costa Rica	17
	Centro de investigación	<i>Cucurbita moschata</i>	España	15
	Centro de investigación	<i>Cucurbita moschata</i>	Sur África	19
	Centro de investigación	<i>Cucurbita moschata</i>	Taiwan	229
	Centro de investigación	<i>Cucurbita pepo</i>	Costa Rica	1
	Centro de investigación	<i>Cucurbita pepo</i>	España	1
	Centro de investigación	<i>Phaseolus coccineus</i>	Costa Rica	2
	Centro de investigación	<i>Phaseolus vulgaris</i>	Costa Rica	17
	Centro de investigación	<i>Phosopocarpus tetragonobulus</i>	Costa Rica	1
	Centro de investigación	<i>Plukenetia volubilis</i>	Costa Rica	1
	Centro de investigación	<i>Solanum lycopersicum</i>	Costa Rica	3
	Centro de investigación	<i>Solanum pimpinellifolium</i>	Costa Rica	2
	Centro de investigación	<i>Solanum quitoense</i>	Costa Rica	1
	Centro de investigación	<i>Vigna unguiculata</i>	Costa Rica	2
	Centro de investigación	<i>Zea mays</i>	Costa Rica	23
	Empresa privada	<i>Capsicum annum</i>	Costa Rica	2
	Empresa privada	<i>Capsicum sp</i>	Costa Rica	3
	Empresa privada	<i>Cucumis sativus</i>	Costa Rica	2
Total				912
Tipo de colección	Tipo de Receptor	Cultivo	País	N° Accesiones
Café	Agricultores	<i>Coffea arabica</i>	Costa Rica	128
	Agricultores	<i>Coffea arabica</i>	Honduras	66
	Agricultores	<i>Coffea arabica</i>	Taiwan	59
	Agricultores	<i>Coffea arabica</i>	Guatemala	21
	Agricultores	<i>Coffea arabica</i>	México	4
	Agricultores	<i>Coffea arabica</i>	Nicaragua	3
	Centro de Investigación	<i>Coffea arabica</i>	Panamá	51
	Centro de Investigación	<i>Coffea arabica</i>	Perú	46
	Centro de Investigación	<i>Coffea arabica</i>	Nicaragua	30
	Centro de Investigación	<i>Coffea arabica</i>	Costa Rica	13
	Centro de Investigación	<i>Coffea canephora</i>	Panamá	13
	Centro de Investigación	<i>Coffea liberica</i>	Nicaragua	12
	Total			
Tipo de colección	Tipo de Receptor	Cultivo	País	N° Accesiones
Cacao	Agricultor	<i>Theobroma cacao</i>	Costa Rica	7

	Agricultor	Theobroma cacao	Costa Rica	22
	Agricultor	Theobroma cacao Theobroma simiarum, T. bicolor, T. grandiflorum, Herrania nyctorodendrum, H. nítida, H. umbrática, H. albiflora	Estados Unidos	15
	Empresa privada	Theobroma cacao	Suiza	11
Total				55

Los cultivos más distribuidos fueron café (*Coffea arabica*) con 442 accesiones, ayote (*Cucurbita moschata*) con 482 accesiones y amaranto (*Amaranthus spp*) con 265 accesiones.

Además, CATIE distribuyó a 10 diferentes usuarios mediante un Acuerdo de Transferencia de Material las 6 variedades mejoradas institucionalmente.

El detalle de esta distribución se presenta a continuación:

Tipo de Receptor	Variedades	País	Cantidad de variedades mejoradas
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Universidad	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Agricultor	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Costa Rica	6
Instituto de investigación	CATIE-R1, CATIE-R4, CATIE-R6, CC-137, ICS-95, PMCT-58	Nicaragua	6

8) Financiamiento para la conservación y uso de los recursos genéticos

La mayoría de los fondos para el manejo agronómico de las colecciones ha sido aportado por CATIE. Además, algunas instituciones y empresas privadas han colaborado para el mantenimiento de las colecciones de café y cacao y regeneración de los cultivos de semillas ortodoxas, dentro de las cuales se puede mencionar las siguientes:

Cultivo	Instituciones y empresas privadas colaboradoras
Cacao	<ul style="list-style-type: none"> • Proyecto MOCCA (Maximizando Oportunidades en Café y Cacao en las Américas) • Embajada de Francia en Costa Rica • Cocoa Research Association Ltd., (UK) • Felchlin Chocolate, (Switzerland)
Café	<ul style="list-style-type: none"> • Embajada de Francia en Costa Rica • San Francisco Bay Coffee (USA) • Felco (Switzerland) • Crop Trust • TIRFAA
Semillas ortodoxas	<ul style="list-style-type: none"> • Crop Trust

Para el caso de “Otras colecciones de campo” en los últimos dos años, el financiamiento no ha sido suficiente para dar un buen mantenimiento y algunas presentan un estado de salud crítico.

9) Colaboraciones interinstitucionales

A inicios del 2021 se conformó un grupo de trabajo interinstitucional entre CATIE (Rolando Cerda, Carlos Araya, Dominique Dessauw y William Solano), Crop Trust (Luigi Guarino, Hannes Dempewolf y Luis Salazar) y la Secretaría del Tratado (Alvaro Toledo y Daniele Manzella) cuyo objetivo es la recaudación conjunta de fondos para salvaguardar a largo plazo la colección internacional de café del CATIE en seguimiento a la acciones definidas en la Estrategia Global de Conservación de Recursos Genéticos de Café.

Los principales resultados obtenidos a la fecha son los siguientes:

- 1) Una propuesta de Planificación para la modernización de la colección de café del CATIE con 4 puntos de acción y el respectivo presupuesto definidos:
 - a) El rescate y reubicación de las accesiones en peligro de pérdida
 - b) Reubicación en CATIE de la Colección Internacional.
 - c) Duplicación de seguridad en un sitio en altura y crioconservada.
 - d) Hacer disponible globalmente la información de la colección



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- 2) Una estrategia definida para crear un fideicomiso de US\$6.2M a 8 años plazo para asegurar la conservación de la colección de café a perpetuidad.
- 3) Un proyecto aprobado para el rescate y reubicación de las accesiones en peligro de pérdida (Punto 1-a)
- 4) Donación de paneles solares para colocar en la cámara fría de semillas.

