THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.1.1: Ex-situ and in-situ conservation methodologies optimised: cross-cutting products				
Next users:	Genebank curators, institutions involved in the conservation of RTB genetic resources; molecular biologists, collaborating NARS programs and CRPs 1, 4, 5, and 7			
End users:	Agronomists, farmers, extension agents who receive RTB genetic resources for evaluation or direct use.			
Expected impact:	Increased income through market diversity; More productive agrobiodiverse farming systems with resilience to climate shocks; Improved nutrition through consumption of more micronutrients-dense RTB			
Products	**Milestones**	**Outcomes**	**Target region & key countries**	**Key partners**
1.1.1.1 Improved and validated medium-term storage procedures (slow-growth in-vitro protocols)	M1.1.1.1.1 (2011) Validation exercise between the four centres finalized for medium-term conservation of cassava, banana, potato, sweetpotato and yams M1.1.1.1.2 (2012) Publication of a training manual on cassava, banana, potato, sweetpotato and yam medium-term conservation procedures	Research outcome: Robust protocols leading to reduced costs of medium-term conservation of germplasm in genebanks more widely used by partners Development outcome: Medium-term conservation procedures adopted by genebank curators and possibility for farmers to grow more diverse RTB crops	Global	Bioversity, CIP, CIAT, IITA
1.1.1.2 Methodology for germplasm integrity assessment during in-vitro storage developed	M1.1.1.2.1 (2011) Plants derived from in-vitro medium-term storage assessed for their trueness-to-type during field verification M1.1.1.2.2 (2015) Plants derived from cryopreserved plant material assessed for their trueness-to-type during field verification	Research outcome: Off-types eliminated from genebanks Development outcome: Users benefit from more reliable germplasm	Global	Bioversity, CIP, CIAT, IITA
1.1.1.3 Improved and validated long-term storage procedures (cryopreservation)	M1.1.1.3.1 (2011) Validation exercise between the four centres finalized for cryopreservation of cassava, banana, potato, sweetpotato and yams M1.1.1.3.2 (2013) Cryopreserved material "black boxed" at another location (preferably another CG centre) M1.1.1.3.3 (2014) Development/optimization of medium- and long-term storage techniques for other RT (e.g. edible aroids)	Research outcome: RTB germplasm of international, regional and national research centres safely duplicated under cryopreserved conditions Development outcome: More efficient germplasm maintenance allows to consolidate unique germplasm accessions and avoid extension of plant material; Farmers accessing more diversity as landraces and incorporating into cropping systems	Global	Bioversity, CIP, CIAT, IITA

1.1.1.4 Conservation techniques for lyophilised leaves, DNA and genomic resources (e.g. BAC libraries...etc.) developed	M1.1.1.4.1 (2012) Storage methodologies developed for lyophilised tissues, DNA and genomic resources M1.1.1.4.2 (2014) Banking initiated for the different material types	Research outcome: Facilitated access to DNA of accessions stored in genebanks to the scientific community Development outcome: More studies on the molecular constitutions of RTB accessions enabled with the distribution of DNA material	Global	Bioversity, CIP, CIAT, IITA
R&D PRODUCT LINE 1.1.2: Increased coverage of gene pools in global genebanks: cross-cutting products				
Next users:	Breeders, curators of genebanks keeping collections of RTB genetic resources.			
End users:	Researchers (molecular biologists, taxonomists, conservationists), farmers and producers who can benefit from more diverse varieties of RTB.			
Expected impact:	Farmers and breeders have access to new material with different traits because gaps in collections are covered and material under risk of extinction is collected.			
Products	**Milestones**	**Outcomes**	**Target region & key countries**	**Key partners**
1.1.2.1 Priorities identified for areas to be explored and material to be collected	M1.1.2.1 (2012) Georeferenced data obtained from herbarium collections and past collecting missions; GIS coordinates consolidated in databases M1.1.2.2 (2014) Potential areas of RTB distribution identified for collecting M1.1.2.3 (2015) Priorities for explorations defined, based on the goal of the mission	Research outcome: Better targeted areas for germplasm collection thanks to the development of detection tools Development outcome: Better representation of germplasm in ex-situ collections for the users	Global	Bioversity, CIP, CIAT, IITA, and key partners involved in RTB conservation
1.1.2.2 Collections integrated in global conservation strategies	M1.1.2.2.1 (2012) Indicators for the integration developed, and major players to relate with identified M1.1.2.2.2 (2012) Negotiation and application for collecting permit at CG Consortium level M1.1.2.2.3 (2014) Half of the identified indicators have their target met M1.1.2.2.4 (2016) The CG collections are known in view of integration in a global conservation strategy	Research outcome: Management of NARS collections improved Development outcome: Improved exchanges between collections	Global	Bioversity, CIP, CIAT, IITA, and key partners involved in RTB conservation

1.1.2.3 Red list of genotypes which are under risk of extinction developed	M1.1.2.3.1 (2012) The format of the "red list" of genotypes has been defined (also in line with IUCN criteria) M1.1.2.3.2 (2013) Geographical areas containing wild species and that are most in danger of habitat lost identified M1.1.2.3.3 (2014) Half of the genotypes have been listed M1.1.2.3.4 (2016) All the target genotypes have been listed	Research outcome: Collecting missions will be able to target the genotypes that are under risks of extinction or the genotypes that are in areas of habitat loss. Development outcome: Genotypes at risk conserved and available to users.Conservation policies and decision makers focused on the areas at risks.	Global	Bioversity, CIP, CIAT, IITA, and key partners involved in RTB conservation
R&D PRODUCT LINE 1.1.3: Collections of RTB evaluated, genotyped, and phenotyped for important traits: cross-cutting products				
Next users:	RTB breeders and agronomists having access to genetic resources with documented traits, and thus fast progressing breeding.			
End users:	Breeding communities, intermediaries collections, farmers			
Expected impact:	Genetic resources in genebanks documented and characterized for added value for their utilization by the breeding communities or to provide directly to RTB dependent population.			
Products	**Milestones**	**Outcomes**	**Target region & key countries**	**Key partners**
1.1.3.1 Core collections of RTB extracted based on molecular and phenotypic evaluation	M1.1.3.1.1 (2013) Target core collections genotyped and phenotyped M1.1.3.1.2 (2015) Core collection established for target collections and target traits for each RTB crops	Research outcome: Breeders use more germplasm stored in the collections Development outcome: Wider access to the international collection material by end users	Global	Bioversity, CIP, CIAT, IITA
1.1.3.2 Comprehensive collections with duplicates and off-types eliminated and unique accessions consolidated	M1.1.3.2.2 (2014) Duplicates in genebanks identified M1.1.3.2.3 (2016) Risk assessments performed: number of duplicates of core collections determined	Research outcome: Genebanks conserve less germplasm whilst keeping the same diversity Development outcome: Accessions can be more adequately identified and more widely shared	Global	Bioversity, CIAT, CIP, IITA and RTB GR collection networks
1.1.3.3 *In silico* comparative genomics including clonal crops genomes for gene candidate prediction carried out	M1.1.3.3.1 (2012) Clustering of full genomes of banana, cassava and potato M1.1.3.3.2 (2014) Ortholog gene prediction by phylogenomics	Research outcome: Researchers and breeders use the available comparative genomics resources to develop new cultivars faster Development outcome: End users accessing more germplasm with improved agronomic and quality traits	Global	Bioversity, CIRAD, LIRMM
R&D PRODUCT LINE 1.1.4: Collections of RTB documented and information freely accessible to users: cross-cutting products				
Next users:	RTB breeders and agronomists having access to information of different genetic resources, genebanks curators			

End users:	Genebanks curators, extensionists, general public, farmers			
Expected impact:	Data about accessions stored in genebanks shared within the RTB communities for research and breeding. More users of the general public are reached and be looking for a specialized knowledge about RTB genetic resources.			
Products	**Milestones**	**Outcomes**	**Target region & key countries**	**Key partners**
1.1.4.1 Core common software for genebank management system including high quality standards applied across RTB international genebanks	M1.1.4.1.1 (2011) Comparative study of Genebank management systems already in use in RTB centres, ICIS and GRIN-Global M1.1.4.1.2 (2012) Definition and integration of a standard for fields, state, management, ontology. Publication of data dictionary. M1.1.4.1.3 (2013) Definition and development of standard modules OR adoption of GRIN-Global	Research Outcome: Genebank management systems share standards and are interoperable/compatible Development outcome: Users of the management systems can share / compare data easily	RTB relevant countries	CIP, Bioversity, CIAT, IITA IRRI, CIMMYT, USDA
1.1.4.2 Common RTB crop registries standards to be implemented across centres and crops and expanded to national and regional collections	M1.1.4.2.1 (2011) Definition of common way to identify cross reference between collections M1.1.4.2.2 (2012) Crop Registry file completed by partners genebanks of RTB crops M1.1.4.2.3 (2013) Promoting use of Crop Register Template for exchange of information between collections M1.1.4.2.4 (2014) Lead centers of RTB crop implementing databases/softwares to record the	Research Outcome: Genebank curators use the Crop Registry: to identify duplicates and gaps, to solve identification problems Development outcome: Global RTB Crops Conservation Strategies implemented and validated. Increased access information (e.g. where is the material conserved and what are its main characteristics)	RTB relevant growing countries	Bioversity, CIAT, CIP, IITA and RTB GR collection networks
1.1.4.3 Information systems linked to global platforms	M1.1.4.3.1 (2011) Definition of a protocol for exchanging data with SINGER, GENESYS, Crop Register M1.1.4.3.2 (2012) Definition of a protocol for exchanging data with GBIF and other global platform M1.1.4.3.3 (2013) Develop tools to help compile data from different information system such as GIS and eco-geographic/climate data	Research outcome: Genebanks data integrated in global initiatives to increase visibility among the users communities. Global systems enhanced with data up-to-date. Development outcome: users have access to integrated data about RTB in global systems (with climatic data, cross-crops etc.). Study and ordering of germplasm with the latest knowledge is available	Global	Bioversity, CIP, CIAT, IITA USDA, GBIF, Consortium for Spatial Information (CGIAR-CSI)

1.1.4.4 Linking morphological characters to molecular markers and genetic maps	M1.1.4.4.1 (2012) Standards for exchange of data between molecular markers data and morpho-taxonomic data developed M1.1.4.4.2 (2014) Tools for exchange of data between molecular databases and morpho-taxonomic database developed M1.1.4.4.3 (2016) Links established between markers data and morpho-taxonomic data	Research outcome: Researchers and breeders are able to link phenotypes to genotypes. Improved knowledge on traits and their genetics. Speed up the breeding process Development outcome: More improved varieties available to end users	Peru, Colombia, Nigeria, Belgium, France	Bioversity,CIP, CIAT, IITA CIRAD
R&D PRODUCT LINE 1.1.5: Safe exchange of RTB genetic resources: cross-cutting products				
Next users:	Genebank curators			
End users:	Genebanks curators, extensionists, general public, farmers			
Expected impact:	Exchange of germplasm amongst the RTB communities or researchers and curators and delivery of germplasm to farmers eased by the reinsurance that the material is disease and virus free.			
Products	**Milestones**	**Outcomes**	**Target region & key countries**	**Key partners**
1.1.5.1 Efficient germplasm health monitoring and certification system to facilitate safe conservation and distribution	M1.1.5.1.1 (2012) Barcoding in an agreed format and used in genebank management M1.1.5.1.2 (2013) Fulfill FAO-IPPC quarantine requirements M1.1.5.1.3 (2014) Implement a certification system to facilitate safe conservation and distribution (internal or external)	Research Outcome: Genebanks curators can obtain certification system Development outcome: RTB genetic resources can be safely distributed in the world	Global	Bioversity, CIP, CIAT, ITA
1.1.5.2 Harmonization of sanitary and phytosanitary protocols for international exchange of germplasm	M1.1.5.2.1 (2011) Agree on pathogens to be targeted for indexing in RTB M1.1.5.2.2 (2013) Protocols for indexing and cleaning specific pathogens M1.1.5.2.3 (2016) Validated and harmonized protocols and system	Research Outcome: RTB genebanks are clean of pathogens Development outcome: RTB genetic resources can be safely distributed in the world	Global	Bioversity, CIP, CIAT, ITA
1.1.5.3 Socioeconomic survey on germplasm use	M1.1.5.3.1 (2011) Compilation of germplasm distribution by the centers and report done M1.1.5.3.2 (2012) Survey form on germplasm use formulated and survey initiated M1.1.5.3.3 (2013) Result analysis and report done	Research outcome: Support decisions on material to be kept only in cryopreservation conditions (less used germplasm) for more cost effective genebanks Development outcome: Distribution of RTB genetic resources more targeted and user-oriented	Global	Bioversity, CIP, CIAT, ITA

1.1.5.4. Germplasm safe duplication, multiplication, sanitation and distribution platform	M1.1.5.4.1 (2012) Optimal locations for platform development identified M1.1.5.4.2 (2014) At least 2 platforms in 2 priority regions developed M1.1.5.4.3 (2016) At least 2 additional platforms in 2 additional regions developed	Research outcome: Accerelrated germplasm distribution following international quarantine requirements based on FAO-IPPC recommendations and national quarantine requirements Development outcome: National and international germplasm exchange facilitated	Africa, Latin America and Asia	IITA, CIP, CIAT, Bioversity

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.2.1: Ex-situ and in-situ conservation methodologies optimised: banana				
Next users:	All curators of genebanks / institutions involved in the conservation of Musa genetic resources.			
End users:	Agronomists, farmers, extension agents who receive Musa genetic resources for evaluation or direct use.			
Expected impact:	Increased income through markert diversity; more productive agrobiodiverse farming systems with resilience to climate shocks; improved nutrition through consumption of more micronutrients dense RTB.			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Key partners**
1.2.1.1 Improved methods for in-situ conservation developed	M1.2.1.1.1 (2012) Predictive mapping tools applied to identify species and clones with interesting traits in centers of secondary diversity M1.2.1.1.2 (2013) Cluster/subgroup-linked distribution models developed/validated for landraces.	Research outcome: NARS can better target collecting missions or identify areas to set up in situ conservation where landraces germplasm with interesting traits are conserved. Development outcome: Farmers accessing more diversity as landraces and incorporating into cropping systems	South East Asia, South Pacific Islands East African Coastal ranges	Bioversity, Key NARS in targeted regions (e.g. ARD - Tengeru (Tanzania), KARI - Thika (Kenya))
1.2.1.2 Improved methods for banana botanical seed conservation available	M1.2.1.2.1 (2012) In vitro germination protocol developed (zygotic embryo) M1.2.1.2.2 (2014) Cryopreservation protocol for Musa zygotic embryo developed M1.2.1.2.3 (2014) In vivo germination protocol developed (seed) M1.2.1.2.4 (2015) Musa seed storage under non-cryopreserved condition (low moisture/low temperature) protocol developed. M1.2.1.2.5 (2016) Musa seed cryopreservation	Reseach outcome: - Better understanding of Musa seed physiology - Wild species can be safely conserved in germplasm collections - Increased choice of parent lines used by conventional breeders Development outcome: - Increased improved plant material used by farmers	Belgium, France, Uganda, banana growing countries in South East Asia	Bioversity, IITA, IRD, Millenium seed bank, key Partners in South East Asia
1.2.1.3 Improved methods for Musa medium-term storage (In vitro)	M1.2.1.3.1 (2013) Study on storage potential of different genotypes M1.2.1.3.2 (2016) Study on in vitro storage conditions to increase storage time and reduce costs	Reseach outcome: - More cost-effective conservation of Musa germplasm Development outcome - Safe conservation of Musa germplasm	Global	Bioversity, IITA

1.2.1.4 Improved methods for safety back-up of Musa conservation	M1.2.1.4.1 (2011) Improved methods for safety duplication in vitro standardized in national and regional collections M1.2.1.4.2 (2012) Standardized methods for safety back-up implemented at the Global Musa Collection (ITC) M1.2.1.4.3 (2013) Cryopreserved "Black box material" (deposited at IRD) tested for its post-thaw regeneration.	Research outcome: - All Musa accessions maintained ex situ are backed-up in vitro in national collections and / or at the ITC global Musa collection Development outcome: - Wider range of germplasm stored in genebanks and available for distribution	Belgium, Nigeria, France, banana growing countries	Bioversity, IITA, IRD and collaborating Musa collections (MusaNet)
1.2.1.5 In-vitro induced somaclonal variation assessed	M1.2.1.5.1 (2012) Morphological variation assessed after optimum number of subcultures under medium term storage conditions at ITC global Musa collection M1.2.1.5.2 (2014) Cytogenetic and molecular tools developed to detect DNA aberrations M1.2.1.5.3 (2016) Epigenetic tools to detect DNA methylation in vitro induced in Musa	Research outcome: - Better understanding on the parameters that influence the appearance of somclonal variants Development outcome: - Users are provided with true to type accessions	Global	Bioversity, IITA, IEB,CIRAD, IAEA, major Musa collections
PRODUCT LINE 1.2.2: Increased coverage of gene pools in global genebanks+A20: banana				
Next users:	Breeders, curators of genebanks keeping collections of Musa genetic resources and researchers (molecular biologists, taxonomists, conservationists)			
End users:	Farmers and producers who can benefit from more diverse varieties of RTB.			
Expected impact:	Farmers have access to more diversity of germplasm and therefore have more chances of getting cultivars adapted to their needs			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Key partners**
1.2.2.1 Inventory of the Global Musa genepool maintained in ex-situ collections performed	M1.2.2.1.1 (2012) Inventory of all accessions maintained in regional and national field collections obtained M1.2.2.1.2 (2013) Gaps of material maintained in ex situ collections (field and in vitro) identified	Research outcome: Knowledge of material maintained ex-situ accross all field and in vitro collections Development outcome: Inventory of musa genepool available through databases to all users	Global	Bioversity, IITA, partners with Musa collections (Global Musa Genetic Resources Network: MusaNet)

1.2.2.2 Threatened status of Musa genetic resources established	M1.2.2.2.1 (2012) Tools for determining red listing of cultivars validated M1.2.2.2.2 (2013) Clones (and species at greatest risk identified)	Research outcome: - NARS adapt and use tools for determining red lists. - Plans developed for protection of cultivars at highest risk. Development outcome: Farmers accessing more diversity as landraces and incorporating into cropping systems	South East Asia Great lakes region of East Africa and forested Central Africa South West Asia	Bioversity, IITA, partners with major collections in Asia and in Africa
1.2.2.3 Maximum genetic variability and relative trait contribution of wild species and landraces in primary and secondary centres of diversity established	M1.2.2.3.1 (2012) Molecular and morphological tools validated M1.2.2.3.2 (2014) Relative positions of cultivar/species in the taxonomic structure of Musa established	Research outcome: - Classification of wild and land races revised - More targeted crop improvement strategies developed Development outcome: Farmers accessing more diversity as landraces and incorporating into cropping systems	Pacific, South East Asia, Great lakes region of East Africa, Forested regions of Central Africa (Plantains) and South East Africa	Bioversity, IITA, partners with major collections in Asia and in Africa
1.2.2.4 Rationalization of genepool sampling	M1.2.2.4.1 (2012) GIS-based mapping of gene pools M1.2.2.4.2 (2013) Effective sampling tools tested and validated M1.2.2.4.3 (2014) Musa pathogens collected during Musa collecting missions (when ever possible)	Research outcome: - Gene pools are effectively explored. - Gene pools effectively represented in ex-situ gene banks . - Better understanding on plant and diseases interaction over time and areas. Development outcome: Farmers accessing more diversity as landraces and	Melanesian Islands IndoChina Indonesia/Philippines South India Great lakes region of East Africa and Central Africa	Bioversity, IITA, partners with major collections in Asia and in Africa
1.2.2.5 Targeted explorations and collecting missions	M1.2.2.5.1 (2012) exploration and targeted collecting missions for traits related to nutritional quality of cultivars M1.2.2.5.2 (2013) exploration and target collecting missions in areas where useful traits are likely to be found (tolerance to cold, drought, …) M1.2.2.5.3 (2014) exploration and target collecting missions for threathened wild species and cultivars	Research outcome: Increase diversity available to breeders (theme 2) but to other MPs (e.g. MP4 and MP7) Development outcome: Increase diversity of Musa germplasm in genebanks available for future generation.	Philippines/Indonesia/ Melonesia. Great lakes of East Africa. Rainforests of Central Africa, South West Asia.	Bioversity, IITA, MusaNet (and more especifically the Taxonomy Advisory Group (TAG) and partners with major collections in Asia and in Africa
PRODUCT LINE 1.2.3: Collections of RTB evaluated, genotyped, and phenotyped for important traits: banana				
Next users:	Musa breeders and agronomists having access to genetic resources with documented traits, genebanks curators			
End users:	Breeding communities, intermediaries collections, farmers			
Expected impact:	Genetic resources in genebanks documented and characterized for added value for their utilization by the breeding communities or to provide directly to Musa dependent population.			

Products	Milestones	Outcomes	Target region and key countries	Key partners
1.2.3.1 Characterization and identification morpho-taxonomic tools for characterization and identification of clones optimized and standardized	M1.2.3.1.1 (2011) Establishement of the most important characters to record for characterization and / or identification (stable and unstable characteristics). M1.2.3.1.2 (2012) Guidelines for characterization improved. M1.2.3.1.3 (2013) Reference accessions characterized. M1.2.3.1.4 (2014) Curators trained in using morphological characterization tools in genepool-specific	Research outcome: - Tools for characterizing / identifying Musa accessions improved and widely used by the Musa research community. - Descriptors revised. - Duplications sorted out and core collections established Development outcome: Increased knowledge on Musa diversity	Global	Bioversity, IITA, CIRAD, collaborating genebank curators
1.2.3.2 Genetic diversity characterized by re-sequencing for candidate loci	M1.2.3.2.1 (2012) SNP discovery and allele frequency in Musa genotypes determined. M1.2.3.2.2 (2013) Nucleotide polymorphism using Ecotilling. M1.2.3.2.3 (2016) Musa Gene Chip available to rapidly screen the Global Musa collection	Research outcome: Tools for characterizing / identifying Musa accessions improved and widely used by the Musa research community.	Global	Bioversity, IITA, JCVI, IAEA, CIRAD, University of California
1.2.3.3 Musa Genotyping platform fully operational	M1.2.3.3.1 (2011) Validation of the Musa genotyping platform using Flow cytometry for ploidy determination and SSR markers for genomic constitution of cultivated species. M1.2.3.3.2 (2012) Musa genotyping platform operational and used by the Musa research community. M1.2.3.3.4 (2013) All accessions acquired by ITC characterized using flow cytometry, SSR, and/or other markers such as ITS markers. M1.2.3.3.3 (2014) Musa germplasm distributed in MLS, characterized for ploidy, genome constitution and sub-species/sub-group belonging	Research outcome: - Ploidy and genome constitution of accessions maintained in Musa ex situ collections determined using molecular markers Development outcome: - service to determine the genomic constitution of Musa germplasm available for the Musa community	Global	Bioversity, IEB

1.2.3.4 Musa genetic resources characterized	M1.2.3.4.1 (2012) 5 Musa collections provided characterization data (identification and use descriptors) M1.2.3.4.1 (2014) 10 Musa collections (including international collections) provided characterization data (identification and use descriptors)	Research outcome: Data of characterization: for identification, and for use provided to the Musa research community Development outcome: Users are certified to receive material they are ordering	Global	Bioversity, IITA, NARS partners
1.2.3.5 Musa genetic resources evaluated for agronomic performance, stress response and post-harvest traits	M1.2.3.5.1 (2012) Pre-evaluation of wide range of accessions in collections for nutritional quality traits M1.2.3.5.2 (2014) Pre-evaluation of wide range of accessions in collections for tolerance to disease such as black leaf streak and Fusarium wilt M1.2.3.5.3 (2015) Pre-evaluation of wide range of accessions in collections for drought tolerance	Research Outcome: Breeders, pathologists and physiologists target the accessions for specific traits, to incorporate in their research programs Development outcome: More germplasm developed with traits of interest and more rapidly accessible for farmers	Global	Bioversity, IITA and collaborating Musa field collections
PRODUCT LINE 1.2.4: Collections of RTB documented and information freely accessible to users: banana				
Next users:	Musa breeders and agronomists having access to information of different genetic resources, genebanks curators			
End users:	Genebanks curators, extensionists, general public, farmers			
Expected impact:	Data about accessions stored in genebanks shared within the Musa communities for research and breeding. More users of the general public reached and looking for a specialized knowledge about genetic resources.			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Key partners**
1.2.4.1. Improve cross-reference of accessions among the Musa collections using Musa Crop registry	M1.2.4.1.1 (2011) Contact 10 new relevant collections for participation to Musa Crop Registry M1.2.4.1.2 (2012) Procedure in place for yearly up to date crop registry M1.2.4.1.3 (2013) Include in the Musa Crop Registry, new Musa collections using routine procedure developed in 2012 M1.2.4.1.4 (2016) 50% of known Musa collections registered and with up to date passport data involved in Musa Crop Registry project	Research Outcome: Collections can identify duplicates and gaps in their collection Development outcome: Up-to-date information on passport data and status of Musa genetic resources available in collections around the world can be provided	Musa growing countries	IITA, Bioversity NARS collection

1.2.4.2. Develop interface for access to evaluation data	M1.2.4.2.1 (2013) Structure to host raw evaluation data in the Musa Germplasm Information System developed M1.2.4.2.2 (2014) Interface for uploading raw evaluation data into MGIS M1.2.4.2.3 (2015) Interface for downloading raw evaluation data from MGIS for analysis purpose M1.2.4.2.3 (2016) Access to online evaluation data analysis	Research outcome: Evaluation data available to the Musa research community and in particular to breeders Development outcome: Evaluation data available for the Musa community, and in particular for producers	Musa growing countries	IITA, Bioversity NARS collection
1.2.4.3 Improved access to Musa GR information	M1.2.4.3.1 (2012) Develop online update feature M1.2.4.3.2 (2014) Develop exchange of data with Global platform such as Genesys M1.2.4.3.3 (2016) Develop interoperability with global platform such as GBIF	Research Outcome: Capture information of majority of Musa Collections worldwide Development outcome: Data on Musa available to wider communities of users - beyond Musa projects	Musa growing countries	IITA, Bioversity NARS collection, GBIF
PRODUCT LINE 1.2.5: Safe exchange of RTB genetic resources: banana				
Next users:	genebank curators			
End users:	genebank curators, farmers			
Expected impact:	Exchange of germplasm amongst the Musa communities or researchers and curators and delivery of germplasm to farmers eased by the reinsurance that the material is disease and virus free.			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Key partners**
1.2.5.1 Virus detection and eradication	M1.2.5.1.1 (2012) Technical guidelines for safe exchange of Musa germplasm updated M1.2.5.1.2 (2013) Virus eradication techniques for 5 banana viruses (CMV, BBTV, BSV, BBrMV and BanMMV) are available. M1.2.5.1.3 (2016) Rapid (Molecular) in vitro screening techniques for viruses developed	Research outcome: Guidelines available to genebanks curators Development outcome: Healthy Musa germplasm available for exchange	Global	Bioversity, IITA, Ulg (Gembloux)
1.2.5.2 Increase exchange of bananas with B genome by better controling BSV expression	M1.2.5.2.1 (2013) 200 eBSV patterns of B genome containing banana genotypes characterized M1.2.5.2.2 (2016) additional 300 eBSV patterns of B genome containing banana genotypes characterized	Musa germplasm containing B genome held at ITC available for exchange with limited risk of eBSV activation	Global	Bioversity (ITC), CIRAD

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.3.1: Ex-situ and in-situ conservation methodologies optimised: cassava				
Next users:	Institutions keeping collections of cassava genetic resources, genebanks.			
End users:	Agronomists, farmers, extension agents who receive cassava genetic resources for evaluation, direct use, etc.			
Expected impact:	Increased efficiencies in ex situ and in situ conservation, and hence larger sets of genetic resources conserved.			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.3.1.1 Botanic seed conservation methodology operational	M1.3.1.1.1 (2012) Cassava seed behavior towards dehydration and low temperature studied M1.3.1.1.2 (2014) Cassava geneflow studied M1.3.1.1.3 (2016) Cassava botanic seedbanking initiated	Cassava biodiversity further secured for future users.International collections conservation further optimised	Sub Sahara Africa, Amazonia, South East Asia; Nigeria, Brazil, Thailand.	CIAT, IITA, ARIs involved in seedbanking
1.3.1.2 In vitro induced somaclonal variation assessed	M1.3.1.2.1 (2013) Cassava germplasm stability after in vitro storage assessed at molecular and agromorphological level	Cassava biodiversity further secured for future users.International collections conservation further optimised	Sub Sahara Africa, Amazonia, South East Asia; Nigeria, Brazil, Thailand.	CIAT, IITA, ARIs involved in seedbanking
1.3.1.3 Efficient cryopreservation process	M1.3.1.3.1 (2011) High performance cryopreservation process developed for cassava meristem M1.3.1.3.2 (2012) Cryobanking initiated at IITA and CIAT	Cassava germplasm conservation further rationalised; safety back-ups of the in-trust collections saved in third country institutions.	Sub Sahara Africa, Amazonia, South East Asia; Nigeria, Brazil, Thailand.	CIAT, IITA, ARIs involved in seedbanking
1.3.1.4 Improved in vitro conservation under slow growth	M1.3.1.4.1 (2012) In vitro seedling maintenance cost further reduced	Cassava germplasm conservation further optimised, with possibility to enrich the collections.	Sub Sahara Africa, Amazonia, South East Asia; Nigeria, Brazil, Thailand.	CIAT, IITA, ARIs involved in seedbanking
1.3.1.5 Establishment of a DNA bank	M1.3.1.5.1 (2012) DNA extraction, purification, and conservation protocols established M1.3.1.5.2 (2014) one third of the in-trust collections have a copy representation in the DNA bank. M1.3.1.5.3 (2016) two third of the in-trust collections have been DNA banked.	Research outcome: Germplasm identification made possible. DNA available for distribution and future genotyping increased, faster service towards cassava geneticists.	Sahelian Africa, South and Central America; Brazil, Nigeria.	Bioversity, CIAT, IITA, CENARGEN, national universities.
PRODUCT LINE 1.3.2: Increased coverage of gene pools in global genebanks: cassava				
Next users:	Curators of genebanks keeping collections of cassava genetic resources.			
End users:	Cassava breeders and agronomists having access to a wider genetic diversity of cassava.			
Expected impact:	Cassava elite varieties produced with novel traits (e.g. starch characterisitcs) or new resistances against pests and diseases.			

Products	Milestones	Outcomes	Target region and key countries	Lead institution and key partners
1.3.2.1 Collections of cassava enriched	M1.3.2.1.1 (2012) Priority regions for cassava germplasm collection or recollection identified based on GIS and/or diversity analysis M1.3.2.1.2 (2016) Negociation with national partners for germplasm collection and/or inclusion into the international collections M1.3.2.1.3 (2016) Acquisition of new germplasm via exploration missions and/or direct transfer from national collections	1. Increase diversity of germplasm available for future generation 2. Irreversible loss of agrobiodiversity prevented	Central and South America, Sahelian Africa+A7	CIAT, IITA, CENARGEN, CATIE, NARS
1.3.2.2 Major factors responsible for cassava genetic erosion assessed	1.3.2.2.1 Agro-socio- economical analysis of cassava genetic erosion performed	Genetic erosion threat better understood - Collection prioritization rationalised	Central and South America, Sahelian Africa; Brasil, Nigeria	CIAT, IITA, IFPRI, Universities, NARS
PRODUCT LINE 1.3.3: Collections of RTB evaluated, genotyped, and phenotyped for important traits: cassava				
Next users:	Cassava breeders and agronomists having access to genetic resources with well documented traits, and thus fast progressing breeding.			
End users:	Farmers and agroindustries using cassava varieties with well known specific traits.			
Expected impact:	Performant cassava varieties in different well characterized environments and for specific markets.			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.3.3.1 Molecular based diversity analysis of common collections	M1.3.3.1.1 (2013) International collections of cassava fingerprinted. M1.3.3.1.2 (2014) Diversity of cassava germplasm maintained in the multilateral system assessed M1.3.3.1.3 (2013) Duplicates identified in international collections	Comprehensive information of the global diversity of cassava available to breeders	Africa/Latin america	CIAT, IITA, CENARGEN (and cassava common registry).
1.3.3.2 Trait based reference set developed	M1.3.3.2.1. (2014) Trait based reference sets amalgated with diversity reference set M1.3.3.2.2 (2014) Cassava germplasm evaluated for selected abiotic stress tolerance, disease and pest resistance, nutrition and post-harvest utilization traits	Cassava reference set identified, conserved and distributed, facilitated use of intra-specific and interspecific variation for key breeding traits	Africa/Latin america	CIAT, IITA, CENARGEN (and cassava common registry, and respective cassava breeders).

1.3.3.3 Allele and/or candidate gene discovery by next generation sequencing and next generation genotyping for diversity analysis and marker-trait association	M1.3.3.3.1 (2012) Array- or bead-based resources developped for discovery and genotyping of SNPs M1.3.3.3.2 (2013) Genome wide SNP discovered and validated M1.3.3.3.3 (2016) High throughput genotyping of germplasm performed for allele profiling in core (or any subset) collections and association mapping	Genomic resources and tools for genetic characterization of cassava accessions made available and widely used; Genes/alleles underlying desirable traits tagged.	Africa/Latin america	CIAT, IITA, CENARGEN (and cassava common registry, and respective cassava breeders).
1.3.3.4 Evaluation for cyanide content for pending accessions	M1.3.3.4.1 (2013) half the in-trust collections in key major genebanks are evaluated for cyanide content; M1.3.3.4.2 (2016) the whole in-trust collections in such genebanks are evaluated for cyanide content.	Distribution of nutritionally safe cassava germplasm accessions; knowledge about bitter cassava clones for agroindustry.	Africa, Latin america, South East Asia.	CIAT, IITA, CENARGEN through the Cassava Common Registry.
1.3.3.5 Evaluation of pending accessions for reaction to mites	M1.3.3.5.1 (2013) half the in-trust collections in key major genebanks are evaluated for reaction to mites (1 or 2 species, depending on users' feedback); M1.3.3.5.2 (2016) the whole in-trust collections in such genebanks are evaluated for reaction to mites.	Identified sources of resistances or susceptibility that can be used in cassava breeding efforts.	Latin America, Africa, South East Asia.	CIAT, IITA, CENARGEN.
PRODUCT LINE 1.3.4: International collections of RTB documented and information freely accessible to users: cassava				
Next users:	Cassava breeders, cassava users' communities, consortiums and networks such as CLAYUCA.			
End users:	Cassava farmers, producers for food, feed, and industrial products (e.g. starch industries).			
Expected impact:	Uses of appropriate cassava germplasm in specified environments for cassava production and consumption (better information towards producers and customers).			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.3.4.1. Registry expanded to major national and international collections of cassava	M1.3.4.1.1 (2011) Cassava inventory and passport data harmonised amongst main national germplasm holders M1.3.4.1.2 (2014) Inventory and passport data uploaded into a common portal	Access to germplasm related information and germplasm facilitated	Central and South America, Sahelian Africa, and South East Asia; Brasil, Nigeria, Thailand.	CIAT, IITA, CENARGEN (and cassava common registry, and SINGER), National genebank

1.3.4.2 Transfer of digital images from characterization activities into web sites	M1.3.4.2.1 (2011) Selected botanical and agromorphological descriptors digitalised M1.3.4.2.2 (2013) Digital information available on line	Access to germplasm related information and germplasm facilitated	Central and South America, Sahelian Africa, and South East Asia; Brasil, Nigeria, Thailand.	CIAT, IITA, CENARGEN (and cassava common registry, and SINGER), National genebank
PRODUCT LINE 1.3.5: Safe exchange of RTB genetic resources: cassava				
Next users:	Cassava farmers, extensionists and scientists who receive cassava germplasm free of diseases of quarantine importance.			
End users:	Local and regional economies depending on cassava are not affected by seed borne diseases of cassava.			
Expected impact:	Cassava production and cassava-based business can continue unaffected by seed borne diseases.			
1.3.5.1 Protocol for establishing virus free germplasm	M1.3.5.1.1 (2013) Cryotherapy tested for virus of quarantine importance M1.3.5.1.2 (2013) Adjustment of in vitro conservation process	International collection maintained clean Germplasm distribution facilitated	Potentially all regions where cassava is grown but specially Central and South America, Sahelian Africa, and South East Asia; Brasil, Nigeria, Thailand.	CIAT (and CLAYUCA) and IITA.
1.3.5.2 Diagnostic tools for pathogen indexing in vitro collections	M1.3.5.2.1 (2013) Development diagnostic tools for virus of quarantine importance present in in vitro stored tissues M1.3.5.2.2 (2014) Development of diagnostic tools for bacteria of quarantine importance present in in vitro stored tissues	Pathogen diffusion prevented	Potentially all regions where cassava is grown but specially Central and South America, Sahelian Africa, and South East Asia; Brasil, Nigeria, Thailand.	CIAT (and CLAYUCA) and IITA.
1.3.5.3 Protocol for the detection and identifcation of endophytic contaminants	M1.3.5.3.1 (2012) The endophytic contaminants have been identified, and their importance quantified for the in-trust collections. M1.3.5.3.2 (2014) A protocol for the fast detection has been tested. M1.3.5.3.3 (2016) The in-trust collections have been cleaned against these endophytic contaminants	Access to germplasm of the in-trust collections made safer, and cryoconservation of the in-trust collections made more reliable.	Potentially all countries/regions of the world where cassava is grown.	CIAT, IITA, CIP, Bioversity (ITC), ARIs.

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.4.1: Ex-situ and in-situ conservation methodologies optimised: potato				
Next users:	Genebank currators of global (ex-situ) potato collections and institutions involved in promoting on-farm conservation in the Andes			
End users:	Breeders, farmers, NARI, rural communities, consumers among other end-users			
Expected impact:	Efficient conservation of the global potato collection (ex-situ) and resilience in the face of climate change in Andean communities through on-farm conservation of potato cultivar diversity			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.4.1.1 Dynamic in-situ & ex-situ conservation strategy and methodology fully developed	M1.4.1.1.1 (2015) Implemented at 10 benchmark sites in Argentina, Bolivia, Chile, Colombia, Ecuador, Peru and Venezuela M1.4.1.1.2 (2015) Evaluation of 2 past sites and 1 training manuel on dynamic conservation published M1.4.1.1.2 (2016) Capacity strengthening program on dynamic conservation implemented in 7 countries	Research outcomes: Novel conservation model available for wider testing Development outcomes: Cultivar collections at 10 benchmark sites fully documented and conserved, > 1000 accessions repatriated, better livelihoods in Andean communities, ongoing field evolution to face climate change	LAC - Peru, Bolivia, Ecuador, Columbia, Argentina, Chilie and Venezuela	CIP, NARS, farming communities, NGOs, local universities
1.4.1.2 Next generation of cryopreservation protocols for accessions that do not respond to the current protocol	M1.4.1.2.1 (2013) Protocols for viability monitoring M1.4.1.2.2 (2013) Protocols for genetic stability evaluation and analysis M1.4.1.2.3 (2016) New protocols to cryopreserve accessions that cannot be accomplished using the current protocol	Research outcomes: New protocols fully tested and available for distribution, Additional 20% of the native potato collection cryopreserved with the new protocols	Global	CIP, Bioversity (ITC)
1.4.1.3 Optimized MTS in vitro slow growth	M1.4.1.3.1 (2014) Protocols for genetic stability evaluation and analysis M1.4.1.3.2 (2016) New slow-growth media added to the current single medium for testing	Research outcomes: New protocols fully tested and available for distribution, new slow-growth media developed Development outcomes: adoption of new protocols by genebanks	Global	CIP
1.4.1.4 Optimized field genebank in term of sanitory quality	M1.4.1.4.1 (2013) 50% of field genebank with clean planting material M1.4.1.4.2 (2016) 100% of field genebank with clean planting material	Research outcomes: Stabilized and healthy field collection preserved under optimal conditions	Global	CIP

1.4.1.5 Optimized seed generation, storage and viability monitoring protocols in both cultivated and wild species	M1.4.1.5.1 (2014) Seed production protocols for wild species by photoperiod groups in greenhouse M1.4.1.5.2 (2016) Seed multiplication and later generation regeneration strategy and protocols M1.4.1.5.3 (2016) Seed storage and seed viability specification for different species groups	Research outcomes: New protocols fully tested and available for distribution, Seed of 75% of wild potato accessions available for distribution to researchers	Global	CIP
1.4.1.6 Complete DNA collection of all the cultivated species and Herbarium species	M1.4.1.6.1 (2012) Protocol for the standardization for quality and concentration DNA M1.4.1.6.2 (2012) Protocol and standards in labelling of vials and boxes M1.4.1.6.3 (2012) Standardized protocol for herbarium specimen preparation, labelling and storage M1.4.1.6.4 (2013) Standardized taxonomic naming and subsequent reconfirmation of name M1.4.1.6.5 (2016) Database on management of the collection M1.4.1.6.6 (2016) Database on management of the herbarium collection	Research outcomes: Stablized DNA genebank where 100% of cultivated potato collection are conserved, Stablized herbarium where 100% of both cultivated and wild potato species collection are preserved	Global	CIP
PRODUCT LINE 1.4.2: Increased coverage of gene pools in global genebanks: potato				
Next users:	Genebank curators and potato breeders globally through conservation, pre-breeding and gene discovery			
End users:	NARI, farmers, consumers and other end-users of new potato varieties incorporating novel genetic diversity			
Expected impact:	Novel genetic diversity from vulnerable habits sustainably conserved and used for germplasm enhancement			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.4.2.1 Complete representations of wild species in the world with at least 3 accessions each	M1.4.2.1.1 (2011) First phase on the implementation of global conservation strategy M1.4.2.1.2 (2012) exploration and collection in Peru M1.4.2.1.3 (2013) 2nd phase on the implementation of the global conservation strategy M1.4.2.1.4 (2016) exploration and collection in other Andean and American countries	Research outcome: Species coverage of the ex-situ collection increased and properly documented Development outcome: All the known wild potato species are available for use (assuming that all the new collected accessions have the permits for IT)	LAC	CIP, NARs, local universities

1.4.2.2 Complete representations of all the cultivated species in the countries of origin (native) and from other countries (landraces)	M1.4.2.2.1 (2011) First phase of the implementation of global conservation strategy with Global Crop Diversity Trust and NARS and local communities M1.4.2.2.2 (2014) All native potato collections in Peru characterized and compared using DNA and morphological characters, duplicates eliminated, unique accessions consolidated at CIP (under IT); Solanum hydrothermicum collected and conserved M1.4.2.2.3 (2013) 2nd phase of the implementation of the global conservation strategy with Global Crop Diversity Trust and NARS and local communities and the accessions of all released cultivars of developing countries M1.4.2.2.4 (2016) Exploration in and introduction from other Andean and American countries	Research outcomes: Genetic (cultivar) coverage of the CIP ex-situ collection increased and compared for duplicates at the population level Development outcomes: All the know cultivated potato species are available for use (assuming that all the new collected accessions have the permits for IT except Solanum phureja which is not in Annex 1)	Andean countries	CIP, NARs, local universities
PRODUCT LINE 1.4.3: Collections of RTB evaluated, genotyped, and phenotyped for important traits: potato				
Next users:	Genebank curators and potato breeders globally through pre-breeding and gene discovery			
End users:	NARI, farmers, consumers and other end-users of new potato varieties incorporating novel genetic diversity			
Expected impact:	Novel genetic diversity documented and available for germplasm enhancement			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.4.3.1 A SNP marker kit available for both cultivated and wild species	M1.4.3.1.1 (2013) SNP markers evaluated and applicability defined M1.4.3.1.2 (2016) A standard SNP marker kit established for potato (applying for both wild and cultivated)	Research outcomes: New range of DNA markers tested and available for characterizing potato	Global	CIP, UCDavis, ARIs
1.4.3.2 A refined SSR marker kit for both cultivated and wild species	M1.4.3.2.1 (2013) New SSR markers evaluated and applicability defined M1.4.3.2.2 (2016) A standard SSR marker kit established for potato (applying for both wild and cultivated)	Research outcomes: Comprehensive (updated) SSR marker kit available for characterizing potato genetic diversity	Global	CIP
1.4.3.3 Hub for the conservation and distribution of reference set of specific traits, core collection, DNA mapping populations	M1.4.3.3.1 (2013) A core collection, reference set and mapping populations for potato established M1.4.3.3.2 (2016) The core and reference collection and mapping populations indexed and cleaned for international distribution	Research outcomes: A well documented core collection representing the total genetic diversity availble for global use Development outcome: 25% increase distribution and utilization of the collection	Global	CIP, ARIs, universities and NARS

1.4.3.4 Protocols to identify major and minor genes for late blight, bacterial wilt, nematodes and key viruses	M1.4.3.4.1 (2013) Protocols for screening LB (minor genes) in greenhouse, laboratory and field compared and established M1.4.3.4.2 (2013) Protocols for screening BW in greenhouse, laboratory and field compared and established M1.4.3.4.3 (2013) Protocols for fast screening of nematodes in greenhouse, laboratory and field compared and established M1.4.3.4.4 (2013) Mass screening protocols (deep-sequencing methods) for potato viruses validated with conventional protocols M1.4.3.4.5 (2015) DNA marker protocols for screening LB (minor genes) established M1.4.3.4.6 (2015) DNA marker protocols for screening BW established M1.4.3.4.7 (2015) DNA marker protocols for screening nematodes established M1.4.3.4.8 (2015) Mass screening protocols (deep-sequencing methods) for potato viruses established M1.4.3.4.9 (2013) Establishment of international trial nursreies for these traits	Research outcomes: Screening and DNA marker protocols fully tested, Collection with useful information on important biotic traits available for researchers, 20% increase in distribution of documented sources of resistance	Global	CIP, ARIs, universities and NARS

1.4.3.5 Protocols to evaluate for heat, drought, frost and salinity tolerance and candidate genes identified	M1.4.3.5.1 (2013) Protocols for heat tolerance evaluation in greenhouse, laboratory and field compared and established M1.4.3.5.2 (2013) Protocols for drought evaluation in greenhouse, laboratory and field compared and established M1.4.3.5.3 (2013) Protocols for frost evaluation in greenhouse, laboratory and field compared and established M1.4.3.5.4 (2013) Protocols for salinity evaluation in greenhouse, laboratory and field compared and established M1.4.3.5.5 (2013) Establishment of international trial nurseries for these traits M1.4.3.5.6 (2016) DNA marker protocols for heat tolerance screening established M1.4.3.5.7 (2016) DNA marker protocols for drought tolerance screening established M1.4.3.5.8 (2016) DNA marker protocols for frost tolerance screening established	Research outcomes: Screening and DNA marker protocols fully tested, Collection with useful information on important abiotic traits available for researchers, 20% increase in distribution of documented sources of resistance	Global	CIP, ARIs, universities and NARS
1.4.3.6 High nutrient early-bulking accessions for iron, zinc, beta-carotene and Vit C, total phenolic value with good table quality identified	M1.4.3.6.1 (2013) 50% of collection evaluated for iron, zinc, betacarotene and total phenolic value M1.4.3.6.2 (2013) 50% of collection evaluated for earliness in tuberization (70 days) and eating quality M1.4.3.6.3 (2013) Establishment of international trail nurseries for these traits M1.4.3.6.4 (2016) Reminding 50% of collection evaluated for iron, zinc, betacarotene and total phenolic value M1.4.3.6.5 (2016) Reminding 50% of collection evaluated for earliness in tuberization (70 days) and eating quality	Research outcomes: Collection with useful information on nutrient, table quality and early tuberization available for researchers, 20% increase in distribution of accesions with documented nutrition and early bulking traits	Global	CIP, ARIs, universities and NARS
PRODUCT LINE 1.4.4: Collections of RTB documented and information freely accessible to users: potato				
Next users:	Genebank curators and direct user of potato genetic resources, principally breeders			
End users:	NARI and universities			
Expected impact:	Globally shared information enhances the cost-efficient and rational conservation of potato genetic resources			

Products	Milestones	Outcomes	Target region and key countries	Lead institution and key partners
1.4.4.1. Improve cross reference acessions among the potato collections using Potato Crop registry	M1.4.4.1.1 (2013) Potato Crop Register (both cultivated and wild species) is functioning and being actively used online M1.4.4.1.2 (2016) All significant potato collections are included in the registry	Research outcomes: Rationalization of the conservation of potato under the Global Potato Conservation Strategy	Global	CIP, ARIs, universities and NARS
1.4.4.2 Improved access to potato GR information based in the GIGA project	M1.4.4.2.1 (2013) All the database fields and respective data at CIP are aligned with the international standards based on GIGA M1.4.4.2.2 (2016) CIP database is linked to GIGA and available for wider international viewing	Research outcomes: Rationalization of the conservation of potato under the Global Potato Conservation Strategy	Global	CIP, ARIs, universities and NARS
PRODUCT LINE 1.4.5: Safe exchange of RTB genetic resources: potato				
Next users:	Genebanks, NARI, breeders and direct users of potato genetic resources			
End users:	Farmers, consumers, NGO's and other actors using new potato cultivars and varieties			
Expected impact:	More efficient, rapid and quality guaranteed global distribution of potato genetic resources			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**

1.4.5.1 Improved endophyte detection, identification and cleaning protocols (both viruses and bacteria) to include all quarantined diseases	M1.4.5.1.1 (2013) Mass screening protocols (deep-sequencing methods) and virus micro-array for potato viruses validated with conventional protocols with a wide range of germplasm and viruses M1.4.5.1.2 (2016) Replacement of indicator plants with deep-sequencing methods and virus micro-array and application of the protocols on the collection to prove their stability and cost effectiveness M1.4.5.1.3 (2013) Mass screening protocols for detection and identification of potato bacteria and validated with conventional protocols M1.4.5.1.4 (2016) Application of the bacteria protocols on a wide range of diversity of the collection to prove their stability and cost effectiveness M1.4.5.1.5 (2013) Protocols with the combination of thermotherapy with cryotherapy in the cleaning of viruses M1.4.5.1.6 (2013) Protocols for cleaning germplasm of endophyte bacteria and phytoplasma M1.4.5.1.7 (2016) Application of the cleaning protocols from endophytic bacteria on the collection to prove their stability and cost	Research outcomes: Fulfill international quarantine requirements based on FAO-IPPC recommendations and national quarantine requirements of individual countries, protocols fully documented Development outcomes: 10% increase in global distribution	Global	CIP, ARIs, universities and NARS
1.4.5.2 Improved mass propagation and safe distribution system	M1.4.5.2.1 (2011-13) Protocols for in vitro micro-tuberlet production M1.4.5.2.2 (2014-16) The quarantine quality of the micro-tuberlets validated and cost analysis of in vitro plantlet vs in vitro tuberlet system	Research outcomes: Fulfill international quarantine requirements based on FAO-IPPC recommendations and national quarantine requirements of individual countries, protocols fully documented Development outcomes: 10% increase in global distribution	Global	CIP, ARIs, universities and NARS

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.5.1: Ex-situ and in-situ conservation methodologies optimised: sweetpotato				
Next users:	Genebank currators of global (ex-situ) sweetpotato collections and institutions involved in promoting on-farm conservation in centers of origin and			
End users:	Breeders, farmers, NARI, rural communities, consumers among other end-users			
Expected impact:	Efficient conservation of the global sweetpotato collection (ex-situ) and food security in communities through on-farm conservation of sweetpotato cultivar diversity			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.5.1.1 Dynamic in situ-ex situ conservation strategy methodologies	M1.5.1.1.1 (2012) Atlas of related wild species of sweetpotato published M1.5.1.1.2 (2012) Proposal for in situ-ex situ conservation of sweetpotato in PNG and Indonesia M1.5.1.1.3 (2013) In situ conservation of Ipomea species in Peru national park system M1.5.1.1.4 (2014) Dynamic in situ-ex situ conservation field sites in PNG/Irian Jaya implemented M1.5.1.1.5 (2014) Geneflow between cultivated and wild species	Research outcomes: Better understanding on the ancestry of sweetpotato and the related wild species and consequent targeting of conservation in both in-situ and ex-situ conditions	LAC, Peru and Papua New Guinea and Indonesia (Irian Jaya)	CIP, NARS in LAC, Ministry of Environment of Peru, NARS in PNG and Indonesia
1.5.1.2 Improved cryopreservation methods	M1.5.1.2.1 (2012) Protocol for the cryopreservation of sweetpotato developed M1.5.1.2.2 (2013) Protocol for genetic stability evaluation and analysis developed M1.5.1.2.3 (2016) New protocols to cryopreserve accessions that cannot be conserved using the current protocol	Research outcomes: New protocols fully tested and available for distribution, Cryopreservation as the long-term conservation method of sweetpotato clones	Global	CIP, Bioversity (ITC)
1.5.1.3 Optimized MTS in vitro slow growth	M1.5.1.3.1 (2011-2014) New slow-growth media added to the current single medium M1.5.1.3.2 (2013-2016) Protocols for genetic stability evaluation and analysis M1.5.1.3.3 (2013-2016) New slow-growth media and genetic stability protocol proven	Research outcomes: Sub-culture extended to 2 years, new protocols fully tested and available for distribution, new slow-growth media developed Development outcomes: Adoption of new protocols by genebanks	Global	CIP, Global Crop Diversity Trust, ARIs
1.5.1.4 Optimized field genebank in term of sanitory quality	M1.5.1.4.1 (2013) Implementation of aphid-proof screenhouse and protocol for conserving field collection in clean condition M1.5.1.4.2 (2016) 50% of field genebank with clean planting material	Research outcomes: 50% of field collection in clean status in sweetpotato and preserved under optimal conditions	Global	CIP

1.5.1.5 Optimized seed generation, storage and viability monitoring protocols in both cultivated and wild species	M1.5.1.5.1 (2014) Seed production protocols for wild species by photoperiod groups in greenhouse M1.5.1.5.2 (2016) Seed multiplication and later generation regeneration strategy and protocols M1.5.1.5.3 (2016) Seed storage and seed viability specification for different species groups	Research outcomes: 100% of wild species with sufficient seed for long-term storage and blackbox at another site of different risk	Global	CIP
1.5.1.6 Complete DNA collection of all the cultivated species and Herbarium species	M1.5.1.6.1 (2012) Protocol for the standardization for quality and concentration DNA M1.5.1.6.2 (2012) Protocol and standards in labelling of vials and boxes M1.5.1.6.3 (2016) Database on management of the collection M1.5.1.6.4 (2012) Standardized protocol for herbarium specimen preparation, labelling and storage M1.5.1.6.5 (2013) Standardized taxonomic naming and subsequent reconfirmation of name M1.5.1.6.6 (2016) Database on management of the herbarium collection	Research outcomes: 100% of collection in DNA genebank, 100% of both cultivated and wild species have samples in CIP herbarium	Global	CIP
PRODUCT LINE 1.5.2: Increased coverage of gene pools in global genebanks: sweetpotato				
Next users:	Genebank curators and sweetpotato breeders globally through conservation, pre-breeding and gene discovery			
End users:	NARI, farmers, consumers and other end-users of new sweetpotato varieties incorporating novel genetic diversity			
Expected impact:	Novel genetic diversity from vulnerable habits sustainably conserved and used for germplasm enhancement			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.5.2.1 Good representations of wild species in the world with at least 3 accessions each	M1.5.2.1.1 (2012) Gaps in CIP in-trust collection identified M1.5.2.1.2 (2013) Exploration and collection in Peru M1.5.2.1.3 (2015) Seed of collected germplasm regenerated and conserved M1.5.2.1.4 (2016) Exploration in other LAC countries especially in Central America	Research outcomes: Species coverage of the ex-situ collection increased and properly documented Development outcomes: All the known wild sweetpotato species are available for use	LAC, Peru	CIP, NARS and universities in LAC

1.5.2.2 Good representations of all landraces in international collections	M1.5.2.2.1 (2012) Top priority collections in the world identified and comparison with CIP in-trust collection implemented (1st phase of the implementation of global conservation strategy with the Global Crop Diversity Trust) M1.5.2.2.2 (2016) 75% of the studied material in 2nd phase of the implementation of the global conservation strategy	Research outcomes: 75% of all landraces and useful improved lines from the whole world are safely conserved and available for distribution	Global	CIP, NARS in the world, SENASA
PRODUCT LINE 1.5.3: Collections of RTB, evaluated, genotyped,A30 and phenotyped for important traits: sweetpotato				
Next users:	Genebank curators and sweetpotato breeders globally through pre-breeding and gene discovery			
End users:	NARI, farmers, consumers and other end-users of new sweetpotato varieties incorporating novel genetic diversity			
Expected impact:	Novel genetic diversity documented and available for germplasm enhancement			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.5.3.1 SSR and AFLP marker kits for both cultivated and wild species	M1.5.3.1.1 (2013) Standard SSR and AFLP marker kits established for potato (applying for both wild and cultivated) M1.5.3.1.2 (2015) Kits tested with a wide range of cultivated and wild germplasm	Research outcomes: Comprehensive SSR and AFLP marker kit available for characterizing sweetpotato by researchers	Global	CIP
1.5.3.2 CIP in trust sweetpotato collection consolidated with only unique accessions	M1.5.3.2.1 (2012) All the duplicates of Peru collection in CIP (~1800 accessions) eliminated M1.5.3.2.2 (2013) All the duplicates of LAC collection in CIP (~1200 accessions) eliminated	Research outcomes: Costs to conserve Peru and LAC collections reduced by half and the formulation of core and reference collections improved	Global	CIP
1.5.3.3 Hub for the conservation and distribution of reference set of specific traits, core collection, DNA mapping populations	M1.5.3.3.1 (2013) A core collection, reference set and mapping populations for sweetpotato established M1.5.3.3.2 (2016) 50% of the core and reference collection and mapping populations indexed and cleaned for international distribution	Research outcomes: A well documented core collection representing the total genetic diversity availble for global use Development outcome: 20% increase distribution and utilization of the collection	Global	CIP, NARS and ARIs and universities

1.5.3.4 Protocols to identify major and minor genes for key viruses and weevils	M1.5.3.4.1 (2011-13) Protocols for screening SPVD in greenhouse, laboratory and field compared and established M1.5.3.4.2 (2011-13) Protocols for screening sweetpotato weevil (Cylas spp.) in greenhouse, laboratory and field compared and established M1.5.3.4.3 (2011-13) Protocols for fast screening of root-knot nematode in greenhouse, laboratory and field compared and established M1.5.3.4.4 (2011-13) Mass screening protocols (deep-sequencing methods) for sweetpotato viruses validated with conventional protocols M1.5.3.4.5 (2013) Establishment of international trial nurseries for these traits M1.5.3.4.6 (2014-16) DNA marker protocols for screening SPVD established M1.5.3.4.7 (2014-16) DNA marker protocols for screening sweetpotato weevil (Cylas spp.) established M1.5.3.4.8 (2014-16) DNA marker protocols for screening root-knot nematodes established M1.5.3.4.9 (2014-16) Mass screening protocols	Research outcomes: Screening and DNA marker protocols fully tested, Collection with useful information on important biotic traits available for researchers, 20% increase in distribution of documented sources of resistance	Global	CIP, NARS and ARIs and universities

1.5.3.5 Protocols to evaluate for heat, drought, frost and salinity tolerance and candidate genes identified	M1.5.3.5.1 (2013) Protocols for heat tolerance evaluation in greenhouse, laboratory and field compared and established M1.5.3.5.2 (2013) Protocols for drought tolerance evaluation in greenhouse, laboratory and field compared and established M1.5.3.5.3 (2013) Protocols for frost tolerance evaluation in greenhouse, laboratory and field compared and established M1.5.3.5.4 (2013) Protocols for salinity tolerance evaluation in greenhouse, laboratory and field compared and established M1.5.3.5.5 (2013) Establishment of international trial nurseries for these traits M1.5.3.5.6 (2016) DNA marker protocols for heat tolerance screening established M1.5.3.5.7 (2016) DNA marker protocols for drought tolerance screening established M1.5.3.5.8 (2016) DNA marker protocols for frost tolerance screening established M1.5.3.5.9 (2016) DNA marker protocols for salinity tolerance screening established	Research outcomes: Screening and DNA marker protocols fully tested, Collection with useful information on important abiotic traits available for researchers, 20% increase in distribution of documented sources of resistance	Global	CIP, ARIs, universities and NARS
1.5.3.6 High nutrient accessions for iron, zinc, beta-carotene and Vit C, total phenolic value with good table quality and early bulking identified	M1.5.3.6.1 (2013) 50% of collection evaluated for iron, zinc, betacarotene and total phenolic value M1.5.3.6.2 (2013) 50% of collection evaluated for early bulking and table quality M1.5.3.6.3 (2013) Establishment of international trial nurseries for these traits M1.5.3.6.4 (2016) Remaining 50% of collection evaluated for iron, zinc, betacarotene and total phenolic value M1.5.3.6.5 (2016) Remaining 50% of collection evaluated for early tuberization in wet condition and eating quality	Research outcomes: Collection with useful information on nutrient, table quality and early tuberization available for researchers, 20% increase in distribution of accesions with documented nutrition and early bulking traits	Global	CIP, ARIs, universities and NARS

1.5.3.7 Genome sequencing of Ipomea trifida (2x) and sweetpotato (6x)	M1.5.3.7.1 (2012) Monoploid plants of I. trifida produced M1.5.3.7.2 (2013) Genome of I. trifida sequenced M1.5.3.7.3 (2015) Genome of sweetpotato sequenced	Research outcomes: Map of the sweetpotato genome made available	Global	CIP, ARIs, universities and NARS
PRODUCT LINE 1.4.4: Collections of RTB documented and information freely accessible to users: sweetpotato				
Next users:	Genebank curators and direct user of potato genetic resources, principally breeders			
End users:	NARI and universities			
Expected impact:	Globally shared information enhances the cost-efficient and rational conservation of sweetpotato genetic resources			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.5.4.1. Improve cross reference of accessions among the sweetpotato collections using sweetpotato Crop registry	M1.5.4.1.1 (2013) A sweetpotato registry (both cultivated and wild species) is functioning and being actively used online M1.5.4.1.2 (2016) All significant sweetpotato collections are included in the registry	Research outcomes: Rationalization of the conservation of sweetpotato under the Global Potato Conservation Strategy	Global	CIP, ARIs, universities and NARS
1.5.4.2 Improved access to sweetpotato GR information based on the GIGA project	M1.4.4.2.1 (2013) All the database fields and respective data at CIP are aligned with the international standards based on GIGA M1.4.4.2.2 (2016) CIP database is linked to GIGA and available for wider international viewing	Research outcomes: Rationalization of the conservation of sweetpotato under the Global Potato Conservation Strategy	Global	CIP, ARIs, universities and NARS
PRODUCT LINE 1.5.5: Safe exchange of RTB genetic resources: sweetpotato				
Next users:	Genebanks, NARI, breeders and direct users of sweetpotato genetic resources			
End users:	Farmers, consumers, NGO's and other actors using new sweetpotato cultivars and varieties			
Expected impact:	More efficient, rapid and quality guaranteed global distribution of sweetpotato genetic resources			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**

1.5.5.1 Improved endophyte detection, identification and cleaning protocols (both viruses and bacteria) to include all quarantined diseases	M1.5.5.1.1 (2013) Mass screening protocols (deep-sequencing methods) and virus micro-array for sweetpotato viruses validated with conventional protocols with a wide range of germplasm and viruses M1.5.5.1.2 (2016) The replacement of indicator plants with deep-sequencing methods and virus micro-array and application of the protocols on the collection to prove their stability and cost effectiveness M1.5.5.1.3 (2013) Mass screening protocols for detection and identification for sweetpotato latent bacteria and validated with conventional protocols M1.5.5.1.4 (2016) Application of the bacteria protocols on a wide range of diversity of the collection to prove their stability and cost effectiveness M1.5.5.1.5 (2013) Protocols with the combination of thermotherapy with cryotherapy in the cleaning of viruses M1.5.5.1.6 (2013) Protocols for the cleaning of endophyte bacteria and phytoplasma M1.5.5.1.7 (2016) Application of the endophytic cleaning protocols on the collection to prove their	Research outcomes: Fulfill international quarantine requirements based on FAO-IPPC recommendations and national quarantine requirements of individual countries, protocols fully documented Development outcomes: 20% increase in global distribution	Global	CIP, ARIs, universities and NARS
1.5.5.2 Improved mass propagation and safe distribution system	M1.5.5.2.1 (2013) Protocols for fast propagation of in vitro plantlets for distribution	Research outcomes: Fulfill international quarantine requirements based on FAO-IPPC recommendations and national quarantine requirements of individual countries, protocols fully documented Development outcomes: 10% increase in global distribution	Global	CIP

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.6.1: Ex-situ and in-situ conservation methodologies optimised: yams				
Next users:	All Institutions involved in yam germplasm conservation and use and biotechnologists			
End users:	Agronomists, extentionists, farmers			
Expected impact:	Increased efficiency of yam conservation systems, yam genetic resources secured for future generations			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.6.1.1 In vitro technology-induced somaclonal variation assessed	M1.6.1.1.1 (2013) Yam germplasm stability after in vitro storage assessed at molecular and agromorphological levels	Yam biodiversity further secured for future users	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, JIRCAS, IRD, CIRAD
1.6.1.2 Efficient cryopreservation process	M1.6.1.2.1 (2012) High performance cryopreservation process developed for yam meristem M1.6.1.2.1 (2013) Cryobanking of yam initiated at IITA	Cryopreservation as the long-term conservation method of yam clones	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, JIRCAS, IRD, CIRAD
1.6.1.3. Improved in vitro conservation under slow growth	M1.6.1.3.1 (2014) In vitro maintenance cost further reduced	Yam conservation further rationalised	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, JIRCAS, IRD, CIRAD
1.6.1.4 DNA banking	M1.6.1.4.1 (2012) DNA extraction, purification, and conservation protocols established. M1.6.1.4.2 (2014) DNA bank for international collections completed	Germplasm identification made possible. Increased and fast service towards yam geneticists.	Sahelian Africa, South and Central America; Brazil, Nigeria.	IITA
1.6.1.5. Supporting in vitro conservation (following meristem culture) of clean stocks of selected varieties as backup for field and screenhouse maintenance	M1.6.1.5.1 (2011) Elite genotypes for target countries identified. M1.6.1.5.2 (2014) Plantlets of selected yam varieties conserved in vitro at IITA and in national programs.	Development: Clean stocks of elite yam varieties safeguarded for the future	West & Central Africa (East Africa) / Nigeria, Ghana, Corte d'Ivoire & Cameroon	IITA, ISTRC, regional CG centers outside of Africa; national programs; NGO's; private enterprise for input and markets
1.6.1.6. Participatory on farm conservation strategies	M1.6.1.6.1 (2014) Strategy for cultivated landraces of D. alata and D. rotundat developed. M1.6.1.6.2 (2015) Strategy for other Dioscorea spp in domestication process with other taxas developed	Farmers agroecological knowledge, and on-farm Yam diversity and variability provide key elements to complement in-situ and ex-situ conservation strategies; National breeding Programs and Genetic Resources Units are able to plan on farm yam conservation	West Africa (Benin, Nigeria, Togo, Ghana, Cote D'Ivoire)	IITA-CIRAD-Bioversity (NARs)
PRODUCT LINE 1.6.2: Increased coverage of gene pools in global genebanks: yams				
Next users:	Yam genetic resources users communities including scientists, farmers and consumers			
End users:	Yam genetic resources users communities including scientists, farmers and consumers			

Expected impact:	Increased used of yam genetic resources to fight poverty			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.6.2.1 International collection of yam enriched	M1.6.2.1.1 (2012) Priority regions for yam germplasm collection or recollection identified based on GIS and/or diversity analysis M1.6.2.1.2 (2016) Negociation with national partners for germplasm collection/acquisition and inclusion into the international collections. M1.6.2.1.3 (2016) Acquisition of new germplasm via collections and/or transfer from national	- Increased diversity of germplasm available for future generation - Irreversible loss of agrobiodiversity prevented	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, National programs in Sub Sahara Africa,
1.6.2.2 Major factors responsible for yam genetic erosion assessed	1.6.2.2.1 (2014) Agro-socio- economical analysis of yam genetic erosion performed	Genetic erosion threat better understoods; Collection prioritization further rationalized	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, National programs in Sub Sahara Africa,
PRODUCT LINE 1.6.3: Collections of RTB, evaluated, genotyped and phenotyped for important traits: yams				
Next users:	Yam collection holders, breeders, biotechnologists, agronomists			
End users:	Farmers and industry			
Expected impact:	Increased used of yam genetic resources to fight poverty via variety release and new use of yam germplasm to regenerate revenue			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.6.3.1 Molecular based diversity analysis of common collections	M1.6.3.1.1 (2013) International collections of yam fingerprinted M1.6.3.1.2 (2013) Diversity of yam germplasm maintained in the multilateral system assessed M1.6.3.1.3 (2014) Duplicates identified in international collections	Comprehensive information of the global diversity of yam available to breeders	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, major national collection's holders partners
1.6.3.2 Trait based reference set developed	M1.6.3.2.1 (2014) Yam germplasm evaluated for speficic traits (reaction to mites, drought tolerance, virus resistance, secondary metabolite). M1.6.3.2.2 (2015) Trait-based sets defined.	Yam reference set identified, conserved and distributed	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, major national collections
1.6.3.3. Yam association with other plant taxa	M1.6.3.3.1 (2012) Potential beneficial associations identified for yam M1.6.3.3.2 (2015)Yam evaluation for specific trait performed in association with another taxa	Yam potential further explore	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA, National programs in Sub Sahara Africa,
PRODUCT LINE 1.6.4: Collections of RTB documented and information freely accessible to users: yams				
Next users:	Yam genetic resources conservation and improvment community			
End users:	Farmers and industrials			

Expected impact:	Increased used of yam genetic resources to fight poverty			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.6.4.1. Registry expanded to major national and international collections of yam	M1.6.4.1.1 (2012) Yam inventory and passport data harmonised amongst main germplasm holders. M1.6.4.1.2 (2013) Inventory and passport data uploaded into a common portal	Access to germplasm related information and germplasm facilitated; Germplasm use increased	Sub Sahara Africa, Asia, Carribean, Pacific Island	IITA
PRODUCT LINE 1.6.5: Safe exchange of RTB genetic resources: yams				
Next users:	Yam genetic resources conservation and improvment community			
End users:	Farmers and industrials			
Expected impact:	Accelerated use of elyte germplasm, reduced risk disease diffusion within and accross continents			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.6.5.1 Improved mass propagation system	M1.6.5.1.1 (2012) Review of existing mass propagation for accelerated seedlings production	Faster delivery of germplasm to breeders/end users	Sub-Sahara Africa, Carribeans, Asia, Pacific Islans	IITA, JIRCAS
1.6.5.2 Protocol for establishing virus free germplasm	M1.6.5.2.1 (2012) Cryotherapy tested for virus of quarantine importance M1.6.5.2.2 (2013) Adjustment of in vitro conservation process for clean germplasm maintenance	International collection maintained clean Germplasm distribution facilitated	Sub-Sahara Africa, Carribeans, Asia, Pacific Islans	IITA
1.6.5.3 Diagnostic tools for pathogen indexing in vitro collections	M1.6.5.3.1 (2012) Molecular tools developed for fast and reliable detection of virus in in vitro seedling. M1.6.5.3.2 (2012) Fast and efficient diagnostic tools developed for endophyte bacteria detection in in vitro seedlings	Pathogen diffusion prevented	Sub-Sahara Africa, Carribeans, Asia, Pacific Islans	IITA

THEME 1: Conserving and accessing genetic resources

PRODUCT LINE 1.7.1: Ex-situ and in-situ conservation methodologies optimised: other RTB				
Next users:	Genebank currators of ARTC collections and institutions involved in promoting on-farm conservation in the Andes			
End users:	Farmers, NARI, rural communities, consumers among other end-users			
Expected impact:	Efficient conservation of ARTC collections (ex-situ) and resilience in the face of climate change in Andean communities through on-farm conservation of ARTC cultivar diversity			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.7.1.1 Dynamic in situ-ex situ conservation strategy methodologies	Olluco, Oca and Mashua (companion crops of native potato and will be implemented with the potato as shown in M1.4.1.1): M1.7.1.1.1 (2012) Implemented 2 benchmark sites in Peru and methodology tested M1.7.1.1.2 (2014) Implemented 1 additional benchmark site in Peru, Ecuador and Bolivia M1.7.1.1.3 (2016) 1 field manuel prepared and 1 capacity strengthening program implemented	Research outcomes: Novel conservation model available for wider testing Development outcomes: Cultivar collections at benchmark sites fully documented and conserved, better livelihoods in Andean communities, ongoing field evolution to face climate exchange	LAC - Peru, Ecuador and Bolivia	CIP, INIA Peru, INIAP, INIA Bolivia and PROINPA
1.7.1.2 Cryo protocols for Andean root and tuber crops	M1.7.1.2.1 (2013) Protocols for the cryopreservation of olluco, oca and mashua developed M1.7.1.2.2 (2013) Protocols for genetic stability evaluation and analysis of these crops established M1.7.1.2.3 (2016) Protocols for the cryopreservation of yacon, achira and arracacha developed	Research outcome: Cryopreservation established as the long-term conservation method of Andean root and tuber cropsResearch outcomes, New protocols fully tested	Global	CIP, Bioversity (ITC)
1.7.1.3 Optimized MTS in vitro slow growth	Olluco, Oca, Mashua, Achira, Yacon, Arracacha and Mauka: M1.7.1.3.1 (2014) New slow-growth media added to the current single medium M1.7.1.3.2 (2016) Protocols for genetic stability evaluation and analysis M1.7.1.3.3 (2016) New slow-growth media and genetic stability protocol proven	Research outcomes: In vitro collection of Andean root and tuber crops stabilized, new protocols fully tested, new slow-growth media developed	LAC - Peru, Ecuador, Bolivia, Colombia, Argentina	CIP, NARS, Universities

1.7.1.4 Optimized field genebank in term of sanitory quality	M1.7.1.4.1 (2013) Lists of viruses and other systemic micro-organism for Andean root and tuber crops M1.7.1.4.2 (2014) 10% of the collection cleaned M1.7.1.4.3 (2016) 50% of the collection cleaned	Research outcomes: Stabilized and healthy field collection of Andean root and tuber crops preserved under optimal conditions	LAC - Peru, Ecuador, Bolivia, Colombia, Argentina	CIP, NARS, universities
1.7.1.5 Optimized seed generation, storage and viability monitoring protocols in both cultivated and wild species	M1.7.1.5.1 (2013) Seed production protocols for maca and ahipa and wild species of other ARTC in greenhouse M1.7.1.5.2 (2016) Seed multiplication and regeneration strategy and protocols M1.7.1.5.3 (2016) Seed storage and seed viability specification for different species groups	Research outcomes: Stablized seed genebank of ARTCs	LAC - Peru, Ecuador, Bolivia, Colombia, Argentina	CIP, NARS, universities
1.7.1.6 Complete DNA collection of all the cultivated species and Herbarium species	M1.7.1.6.1 (2012) Protocol for the standardization for quality and concentration DNA M1.7.1.6.2 (2012) Protocol and standards in labelling of vials and boxes M1.7.1.6.3 (2016) Database on management of the collection M1.7.1.6.4 (2012) Standardized protocol for herbarium specimen preparation, labelling and storage M1.7.1.6.5 (2013) Standardized taxonomic naming and subsequent reconfirmation of name M1.7.1.6.6 (2016) Database on management of the herbarium collection	Research outcomes: Stabilized DNA genebank of ARTCs, Stabilized herbarium of ARTCs of both cultivated and wild species	LAC - Peru, Ecuador, Bolivia, Colombia, Argentina	CIP, NARS, universities
PRODUCT LINE 1.7.2: Increased coverage of gene pools in global genebanks: other RTB				
Next users:	Genebank curators, NARI and NGO's involved in conservation of ARTC's			
End users:	Farmers and consumers, among other endusers			
Expected impact:	Novel genetic diversity from vulnerable habits sustainably conserved			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.7.2.1 Good representations of wild species in the world with at least 3 accessions each	M1.7.2.1.1 (2013) Gaps in different collections in Peru identified M1.7.2.1.2 (2015) Exploration and collection in Peru M1.7.2.1.3 (2016) Collected germplasm regenerated and conserved	Research outcomes: Species coverage of the ex-situ collection increased and properly documented Development outcomes: Selected set of the known wild RTAs species are available for use	Peru	CIP, Peru NARS and universities

1.7.2.2 Good representations of all landraces in international collection (Note: lack representation of a tetraploid species)	M1.7.2.2.1 (2014) Important collections in Peru identified and comparison with CIP collection implemented M1.7.2.2.2 (2016) Missing gaps identified and joint exploration mission initiated	Research outcomes: Genetic (cultivar) coverage of the CIP ex-situ collection increased and compared for duplicates at the population level Development outcomes: All the know cultivated ARTC accessions consolidated and are available for use	Peru	CIP, Peru NARS and universities
1.7.2.3 International collection of cocoyam assembled	M1.7.2.3.1 (2016) 75% of the studied material in 2nd phase on the implementation of the global conservation strategy M1.7.2.3.2 (2012) Survey completed on the existing collections in the new world and an exploration proposal completed especially on the Xanthosoma species in the new world M1.7.2.3.3 (2016) Exploration and conservation of important diversity completed in new world.	Research outcomes: World cocoyam genepool conserved and available for distribution	Global	IITA, CIP, SPC and NARS
PRODUCT LINE 1.7.3: Collections of RTB evaluated, genotyped, and phenotyped for important traits: other RTB				
Next users:	Genebank curators, NARI and NGO's involved in conservation of ARTC's			
End users:	Farmers, consumers and other end-users of ARTC varieties			
Expected impact:	Novel genetic diversity documented and available for use			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.7.3.1 A refined SSR and AFLP marker kit for both cultivated and wild species	M1.7.3.1.1 (2013) A standard SSR and AFLP marker kit established for olluco, oca, mashua, yacon M1.7.3.1.2 (2015) The kit tested with a wide range of cultivated germplasm proven	Research outcomes: Comprehensive SSR and AFLP marker kit available for characterizing olluca, oca, mashua, yacon	Peru	CIP, Peru NARS and universities
1.7.3.2 Standard descriptors of the Andean root and tuber crops and collections characterized	M1.7.3.2.1 (2013) Standard crop descriptives formulated and published for yacon, arracacha and ahipa M1.7.3.2.2 (2015) Standard crop descriptives formulated and published for mashua, maca and achira	Research outcomes: Standard descriptor lists for morphological charaterization of RTAs available	Peru	CIP, Peru NARS and universities

1.7.3.3 ARTC value as high value functional food analysed and accessions with gret potential identified	M1.7.3.3.1 (2013) 25% of ARTC collections selectively evaluated for functional food value M1.7.3.3.2 (2016) 50% of ARTC collections selectively evaluated for functional food value	Research outcomes: Novel neutriceutical traits documented Development outcomes: High-value income generation for Andean smallholder households (fair trade) niche markets	Peru	CIP, Peru NARS and universities
PRODUCT LINE 1.7.4: Collections of RTB documented and information freely accessible to users: other RTB				
Next users:	Genebank curators and direct user of ARTC genetic resources			
End users:	NARI, NGO's and universities			
Expected impact:	Shared information enhances the cost-efficient and rational conservation of ARTC genetic resources			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.7.4.1 Collections of ARTCs in Andean countries documented	M1.7.4.1.1 (2013) Collections of ARTCs in Andean countries documented M1.7.4.1.2 (2016) Shared database of ARTC's collections	Research outcomes: Documented genetic diversity of ARTCs shared among genebanks and NARI	LAC - Peru, Ecuador, Bolivia, Colombia, Argentina	CIP, NARS and local universities
PRODUCT LINE 1.7.5: Safe exchange of RTB genetic resources: other RTB				
Next users:	Genebanks, NARI, NGO's and direct users of ARTC genetic resources			
End users:	Farmers, consumers, NGO's and other actors using ARTC cultivars			
Expected impact:	More efficient, rapid and quality guaranteed distribution of ARTC genetic resources			
Products	**Milestones**	**Outcomes**	**Target region and key countries**	**Lead institution and key partners**
1.7.5.1 Improved endophyte detection, identification and cleaning protocols (both viruses and bacteria) to include all quarantined diseases	M1.7.5.1.1 (2013) A list of important viruses and bacteria published M1.7.5.1.2 (2016) Protocols and anti-sera for major viruses of olluco, oca, mashua, yacon and mashua available for germplasm cleaning M1.7.5.1.3 (2016) Mass screening protocols (deep-sequencing methods) and virus micro-array validated with conventional protocols with a wide range of germplasm and viruses M1.7.5.1.4 (2016) 30% of collections of the ARTCs cleaned of major viruses	Research outcomes: Major viruses and bacteria identified and documented, 30% of CIP ARTC germplasm collections cleaned	Peru	CIP, INIA Peru and local universities
1.7.5.2 Improved mass propagation and safe distribution system	M1.7.5.1.1 (2011) Resume distribution of 'in trust' ARTCs at CIP M1.7.5.1.2 (2013) Protocols for mass propagation of different ARTCs available	Research outcomes: Protocols for mass propagation fully developed and available for distribution, the in trust ARTC collections at CIP are distributed and used in the world	PERU	CIP, INIA Peru and local universities