



RICE Flagship project 4:

Global Rice Array

Rationale and scope

Climate variability explains around 33% of rice yield variation globally (Ray et al 2015). Current rice yields are projected to decline with climate change, for example, by 45% for zones in sub-Saharan Africa (Adhikari et al 2015). To meet the challenges of climate change, new rice varieties are needed that are adapted to projected future climates, including the consequences for pest and disease pressures. This calls for accelerating the discovery of new genes and traits and optimizing the use of genetic diversity under different environments and climate scenarios. A clear understanding of the complexity of interactions between genotypes (G), environments (E), and crop management (M) is necessary. The E factor includes weather, soils, and pest and disease patterns. Conventional methods to quantify $G \times E$ interactions rely on a limited number of multi-environment evaluations of breeding materials. With the exception of a few large multinational companies, there is no systematic strategy to exploit $G \times E \times M$ to enhance crop performance in major cereals. A significant investment in understanding the environments under climatic change and discovering adaptive traits and genes and their E- and M-dependent expression is much needed to accelerate genetic gain in breeding.

Advances in genomics and high-throughput phenotyping tools provide a unique opportunity to discover new genes targeted at each $G \times E \times M$ relationship. Germplasm can now be sequenced at low cost to reveal genetic diversity in fine molecular detail. GIS allows the integration of geographic information with environment and crop data. Missing are multi-environment and multitrait phenotypic data to rapidly

discover gene-phenotype relationships and their $G \times E \times M$ dependency that determines crop performance in diverse environments.

A main goal of Flagship Project (FP) 4 is to provide rice breeders worldwide with the phenomics, genomics, and environmental information, as well as target ideotypes, in order to generate better adapted varieties at a faster rate. A Global Rice Array will be established consisting of high-throughput (HTP) field phenotyping sites to evaluate genetic populations, including diversity panels, mapping, and breeding populations. Complementary HTP platforms will be used for precision phenotyping of physiological, biochemical, and architectural traits. Smaller but diverse “diagnostic” populations at different sites of the Global Rice Array will also serve as biological “antennae” to characterize and diagnose the diversity and dynamics of a changing climate “through the eye of the crop.” This “sensing” of the effects of climate variability on rice crops globally will provide useful information to policymakers, agronomists, and scientists studying the impacts of climate change.

Crop models such as [ORYZA2000](#) will be used to analyze and extrapolate data from the Global Rice Array in predicting the effects of climate variability and change on the rice crop. Conversely, crop models will help translate the phenotypic diversity and factor responses into ideotypes adapted to changing environments. In-depth research on $G \times E \times M$ effects on gene/trait expression will reveal genetic networks that condition adaptive traits, providing genomic markers that are effective across major rice production environments.

The data will be integrated in a Big Data user-friendly platform to allow data mining and use by the global community.

FP4 products will increase the efficiency and efficacy of the breeding programs of FP5.

The Global Rice Array will engage many partners in phenotyping and gene discovery for both common and site-specific traits using genotyped genetic populations. Partners will include NARES, ARIs, and the private sector as appropriate. FP4 will collaborate strongly with CCAFS, which will provide downscaled climate change scenarios for the sites of the Global Rice Array and link FP4 rice efforts with those on other crops.

Objectives and targets

The production constraints associated with environmental changes and the current yield ceiling for improved rice varieties are global and a challenge to all rice improvement programs. Generating genomics and phenomics data resources for multiple environments and climatic conditions, and understanding the genetic control of crop adaptation/performance constitute a strategic bottleneck. The large dataset generated by the Global Rice Array of FP4 will be open to benefit public rice breeding and provide the information needed to tailor the use of rice diversity to meet future needs. Moreover, the Global Rice Array will involve rice improvement and research programs from all major rice-growing environments across the globe, including international and national institutions from the public and private sector.

FP4 intends to accelerate gene and trait discovery in order to help optimize the use of genetic diversity under different climate scenarios. It will use knowledge from partners worldwide, including CCAFS, to select climate change sentinel sites in key rice production environments across the globe and assess the impact of climatic variation on rice crops. The use of populations of diverse genetic background as biological antennae to sense the environment under different climate scenarios will provide a head start in developing climate-smart technologies in FP3 (Sustainable rice farming systems) and FP5 (New rice varieties). FP4 will collaborate

closely with CCAFS to make use of predictive tools such the analogue approach (Rameris et al 2011) to identify adaptive germplasm for different locations. At a regional level, the rice array will enhance preparedness for deploying adapted technologies based on good knowledge of specific features of future rice production environments.

FP4 will collaborate extensively with NARES to capture local knowledge and expertise. Each phenotyping site will serve as a research capacity development site for young rice scientists, both men and women, in NARES and equip them with skills in modern breeding, phenotyping, computational science, and informatics. Phenotyping, genotyping, and climatic data will be integrated in a rice data hub publicly available and connected to other Big Data platforms.

FP4 will deliver the following research outcomes to selected sub-IDOs, IDOs, SLOs, and cross-cutting issues of the SRF (see also the performance indicators matrix):

Impact pathway and theory of change

Fig. 4.1 presents the impact pathway and theory of change, with assumptions, risks, and associated enabling actions of FP4. Impact is generated on food security, productivity, producers, and environmental resilience. It will be achieved through better adapted germplasm (via FP5) and improved regional/national mitigation strategies (via FPs 1, 2, and 5). Anticipated risks are mainly related to (1) the efficiency and timeliness of the various interdependent actions in FP4 and FP5, (2) effective coordination and choices in methodology, (3) potentially inaccurate predictions of representative sites and ideotypes, (4) weak testing network deficient in environmental characterization, (5) inadequate agronomic and breeding capacity at action sites, and (6) selected sites not being representative of key constraints and climate change.

Within FP4, achieving targets will depend on (1) good trait expression at selected sites; (2) easy germplasm

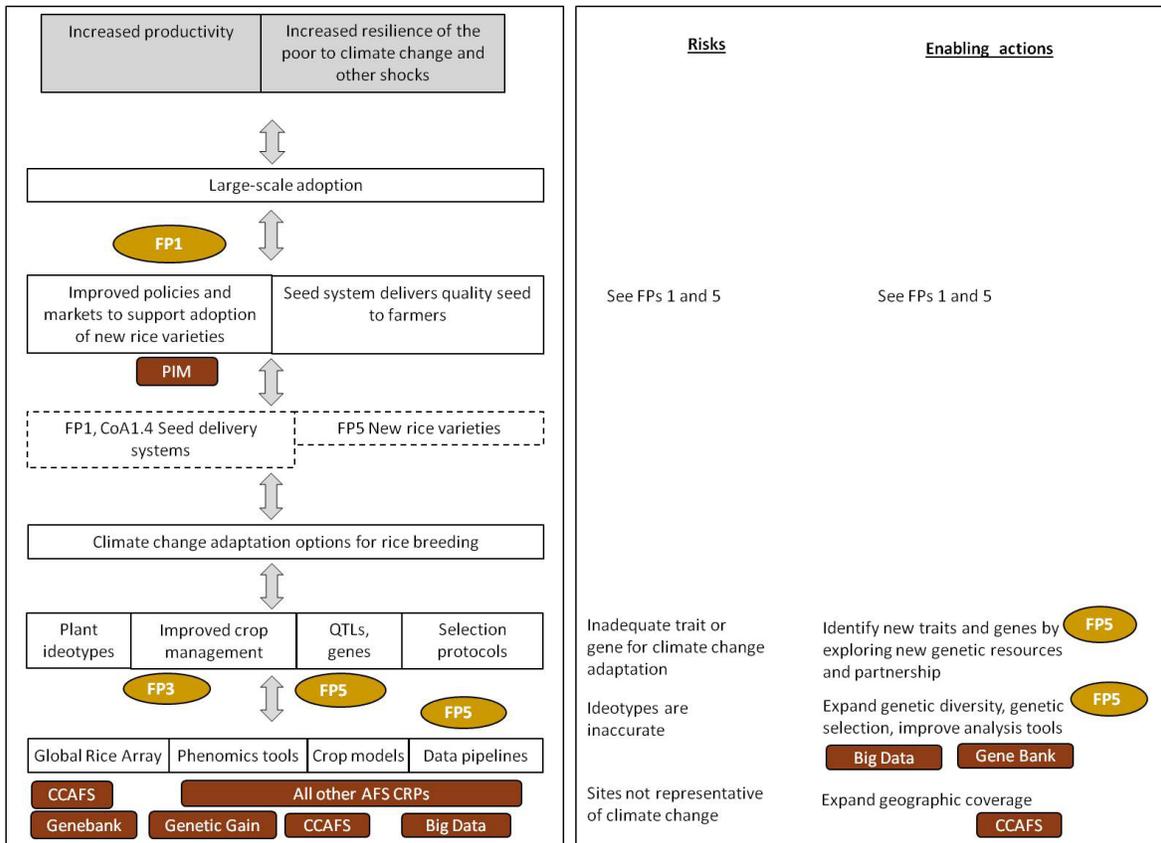


Fig. 4.1. Impact pathway (left) and theory of change (right) of FP4. Grey boxes are IDOs, ovals (with FP x) refer to links with other FPs, and the dark boxes refer to links with other CRPs (see Annex 14.2 for abbreviations).

exchange across countries and availability of sufficient seed; (3) existing genomic data and efficient genome-wide association studies (GWAS) pipelines; (4) availability of robust prediction models for the rice crop, pathogens, and future climate scenarios; and (5) a well-structured database and rapid data-analysis pipelines for large datasets. The enabling actions will include upgrading agronomic and breeding capacity as well as data handling, and regular re-analysis of the Global Rice Array sites using additional data in consultation with CCAFS. Use of consistent metadata and agri-semantics in the Big Data platform will allow efficient contextual searches, including links between genetic, environmental, and gender aspects, enabling highly targeted use of the data. Although breeders will be the most frequent direct users of FP4 outputs, agronomists, economists, and policymakers will also benefit from such outputs as risk and impact maps.

Science quality

The revolution in knowledge and methodology in genomics and informatics has opened up vast opportunities for accelerated and more effective crop improvement. However, optimizing the use of genetic diversity under different environments and climatic conditions remains a major challenge in plant breeding. Large-scale phenotyping in multiple environments offers tremendous power to understand the complex interactions among $G \times E \times M$. Such knowledge is critical for the identification of combinations of genes and traits that are adaptive to changing climatic regimes. By exposing a common set of genetic populations to a range of climate conditions, FP4 will reveal the genetic networks that condition adaptive traits across major rice production environments. The diagnostic genetic populations placed in different locations serve as “biological

FP4 research outcome	Sub-IDO	IDO	SLO or cross-cutting issue
Predicted global rice production risks used to guide development and targeting of climate change-adapted technologies at least for the most vulnerable rice agroecosystems	Enhanced adaptive capacity to climate risks	More sustainably managed agroecosystems	Improved natural resource systems and ecosystem services
A functional global phenotyping network composed of 30% non-CRP partners (including self-sponsored), and genetic donors (>10) and ideotypes (2-4) adopted by breeding programs to develop climate-smart rice varieties	Enhanced genetic gain	Increased productivity	Reduced poverty Improved food and nutrition security for health
Characterized pathogen populations and diversity used to predict varietal deployment for at least 3 major rice diseases	Enhanced capacity to deal with climatic risks and extremes	Mitigation and adaptation achieved [to climate change]	Climate change
At least 5 major QTLs/genes that are stable across environment and management, for all rice mega-environments, integrated in the respective varietal development pipelines	Enhanced genetic gain	Increased productivity	Reduced poverty Improved food and nutrition security for health
A functional rice data hub providing open access phenotypic and genotypic information and data analysis tools for users worldwide	Increased conservation and use of genetic resources	Increased productivity	Reduced poverty Improved food and nutrition security for health
Increased capacity for innovation in pre-breeding and Big Data in partner research organizations	Increased capacity for innovation in partner research organizations	National partners and beneficiaries enabled	Capacity development

antennae” assessing the response of genetic resources to climate change in a much shortened timeframe, thus enabling better preparation for future climatic scenarios.

FP4 will provide a large store of genetic potential for rice improvement. State-of-the-art HTP phenomics technology will be deployed and partners will be trained to exploit the data resources to empower many breeding programs worldwide.

The novelty of the proposed project comes from the integration of the best advances in several disciplines. The new genetic resources underpinning the Rice Array are specially designed to have high genetic diversity for sensing the environment. The range of scientific expertise assembled has the depth and scope needed, covering genetics, breeding, physiology, crop modeling, GIS, and computational science.

The team involved in the project has a track record of publishing on genetic resources, large-scale phenotyping, crop modeling, and GIS applications. These attributes ensure a high probability of success in implementing the work plan.

As recommended by the IEA review of the science quality of GRiSP (recommendation #2, IEA report, p xvi), FP4 management will foster strong research collaboration with partners in ARIs (see section on Partnerships). FP4 will aim for jointly authored, high-quality publications in high-quality international journals.

Lessons learnt and unintended consequences

FP4 and the establishment of a Global Rice Array are completely new; however, the

project builds on elements and learning from GRiSP Theme 1 (Harnessing genetic diversity to chart new productivity, quality, and health horizons). In particular, the existing global phenotyping network of GRiSP has provided valuable lessons: (1) ensure that populations are genotyped before engaging many partners in costly phenotyping efforts; (2) take phenotyping/GWAS closer to the breeding process by giving sufficient emphasis to recombinant populations (as opposed to gene discovery in exotic accessions, which is complementary); (3) ensure timely availability of data infrastructure and tools to avoid a backlog, which could cause disorder; and (4) ensure that the implementation of crucial actions, in terms of timeliness for the Global Rice Array, is controlled by network management to avoid potential disruptions to the collective workflow. FP4 will develop a Big Data platform based on the work of the International Rice Informatics Consortium (IRIC) created under GRiSP.

FP4 mainly engages in upstream research, and its (intended or unintended) consequences for the CGIAR SLOs are mostly realized through FP5, which takes up and uses the outputs and outcomes of FP4. A specific risk of unintended consequences is that FP4 genetic or trait discoveries are not widely shared and thus do not reach a large number of beneficiaries (e.g., breeders in national programs). To minimize this risk, FP4 will be as inclusive as possible by partnering with diverse stakeholders, who will define their needs in terms of phenotyping and target traits.

Clusters of activity (CoA)

FP4 will establish field sites using GIS, climatic analogue tools (Ramírez-Villegas et al 2011), FP1 (Accelerating impact and equity) mapping data, and extensive consultation with NARES partners and CCAFS. Phenotyping of reference genetic populations and local breeding materials will be conducted at each site. Through FP4, investment will be made to upgrade phenotyping capacity by improving

infrastructure and the technical skills of researchers, and by deploying phenotyping systems.

Through GWAS, the phenotyping and genotyping data will be analyzed to discover new genes underlying traits relevant to adaptation. FP4 will use the Global Rice Array sites as regional observatories for pathogen populations of major diseases. The pathogen population data will provide a guide to effective deployment of disease-resistant varieties.

A data integration platform will be established to store and analyze the large dataset generated from genotyping and phenotyping. The project will provide support and provide incentives to key site operators to ensure that high-quality data are collected. The potential benefits of the dataset should attract participation of many national programs. For countries with large breeding programs, FP4 will mobilize financial support from national governments. Together, the outputs of the CoAs will be channeled to FP5 where varietal development will be accelerated through new understanding of the adaptive traits and the interactions of G x E x M. Especially the understanding of G x E x M interactions is critical to the improvement of rice based systems - because G x E x M interactions for rice (e.g. direct seeded short duration varieties) are critical for complex rotations. The genetics required for the rice components of such systems will be dissected in FP4.

4.1 Establishing a worldwide field laboratory

CoA4.1 establishes the Global Rice Array, a physical array (network) of field laboratories and trial sites, characterizes and monitors the environments (e.g., through “antenna” experiments), conducts crop/pathogen trials, and develops models to quantify and map the impact of abiotic/biotic factors on yield. The scale and scope of phenotyping will depend on the function of a site within the network and on breeders’ requirements for regional or global data.

Sites will be selected based on geographic location, climatic pattern, local rice production systems, and infrastructure criteria such as proximity to breeding and laboratory facilities. As much as possible, marginal/low-lying areas that are usually left to women rice producers will be captured in the Global Rice Array. Existing trial sites of IRRI, AfricaRice, and CIAT and of other CRPs, notably CCAFS, will be included as appropriate. Linking with CCAFS, site selection will be guided by both current and future climates using such approaches as the [analog-site principle](#) (Ramírez-Villegas et al 2011) and [the Target Prone Environment principle](#).

Besides the analog site analysis, CoA4.1 will work with CCAFS on areas of mutual interest. CCAFS has expertise on past, present, and future environments and their impact on yield, as well as on characterizing breeding programs' target populations of environments. CoA4.1 will use the data to identify priority constraints and traits, define extrapolation domains, and design ideotypes to feed into FP5. Risk, climate impact, and varietal performance maps generated by CoA4.1 in collaboration with CCAFS will be provided to agronomists, economists, and policymakers (through FP3 and FP1).

The key products of this CoA will be (1) a Global Rice Array consisting of equipped and well-characterized field laboratories and trial sites, (2) information on yield potential and biotic/abiotic factor contributions to yield variability by environment and varietal type, and (3) risk management database and maps for policymakers.

4.2 Global phenotyping

Phenotyping, in the sense of measuring trait expression in large populations, is a necessary step for gene discovery, marker development, and breeding. In GRiSP, a Global Rice Phenotyping Network was established to characterize subspecies diversity for yield potential and abiotic-stress-related traits in different environments. GWAS led to the identification of many putative genes/alleles that breeders can potentially use. Building on this, as well as on available genome sequences and SNP maps,

a new concept for global phenotyping will be implemented in CoA4.2. It will integrate environmental characterization, gene discovery, and marker development and validation.

In the initial stage of CoA4.2, phenotyping capability will be increased to enable each site to measure a common set of agronomic traits from the reference populations. These include measurements of plant growth and yield-related traits. Response to environmental stresses will be measured at sites where stresses are present. Depending on the locations and local capability, additional phenotyping methods will be implemented. For selected sites, HTP phenotyping in the field will be implemented using tractor-based and drone-based technologies. At sites with laboratory capability, a HTP, low-cost, analytical pipeline, based on Fourier transform infrared spectroscopy technology for rice tissue and grain chemistry (including nutrition and consumer health aspects), will be deployed. This will help expand the scope of phenotyping to traits that were previously too costly to screen or characterize genetically. The phenotypic data collected from field and laboratory at multiple sites will provide an assessment of the response of rice diversity to specific environmental and climatic conditions.

The genetic populations to be phenotyped will include (1) subsets of the 3,000 rice genomes already sequenced, (2) the PRAY panel that was characterized in the GRiSP New Frontier Project, (3) nested association mapping (NAM) populations produced by CIAT and AfricaRice, and (4) multiparent advanced generation intercross (MAGIC) populations produced at IRRI. The NAM populations were developed from 20 diverse crosses (4,000 lines total). NAM is a powerful design that allows ultra-fine mapping of QTLs. The NAM populations are being sequenced under FP5. The MAGIC populations were derived from 16 founder elite parents and recombined by intercrossing to generate high genotypic diversity (Bandillo et al 2013).

An important feature of these populations is that they represent genetic diversity from both landrace and elite varieties. Further, these populations have been densely genotyped and are ready for phenotype-genotype association analysis. Additional training populations designed for genomic selection in FP5 can be evaluated in selected sites. Besides these genetic populations, CoA4.2 will encourage NARES partners to put their elite breeding populations in the same site to enable comparative analysis.

The phenotypic information on trait diversity and variable expression obtained from the Global Rice Array will be used to predict better-adapted ideotypes. This will make use of rice growth models to simulate trait-trait and $G \times E \times M$ interactions, including morphological traits. Ideotypes, in terms of specific trait combinations that improve resilience and yield, will be proposed as guidance to breeders.

An important aspect of this CoA is the speed of data acquisition, analysis, and sharing to accelerate data transfer from phenotyping to breeders and geneticists, as well as the rapid shuttling of populations and data between phenotyping, GWAS (CoA4.4), and breeding (FP5). Through partly automated data acquisition and data processing (CoA4.5), users will have timely access to multisite results. The Global Rice Array will actively engage NARES and other partners to participate when appropriate with their own sites or facilities, and with joint methodology development and technology transfer.

4.3 Genetics of rice plant interaction with the biotic environment

Rice is susceptible to many fungal, bacterial, and viral diseases. Because of climate change and changing production systems, previously minor diseases such as sheath blight and false smut have become new threats. The dynamic nature of host-pathogen interaction requires a constant search for diverse resistance mechanisms and deployment strategies to manage disease epidemics.

The impact of rice disease depends largely on pathogen population diversity, climatic conditions, and the genetic background of varieties. The interactions between pathogens, host, and environment (including cultural practices) will ultimately determine the effectiveness and durability of resistance. The Global Rice Array offers the opportunity to develop a long-term observatory of disease impacts on representative sets of genetic diversity. CoA4.3 includes pathogen monitoring at key breeding sites, characterizing the pathogen virulence spectrum and genetic diversity, and hot-spot screening of breeding material for new resistance. Results of CoA4.3 will feed into FP5 for breeding new varieties with enhanced resistance to diseases.

There is growing evidence that soil microbiomes can improve plant health. In collaboration with the University of California-Davis, initial experiments are being designed to compare microbiomes under different cropping environments at IRRI. The Global Rice Array can provide a range of diverse sites for examining the potential of microbiomes in sustaining rice production.

4.4 Discovery of genomic associations

Since all phenotypic information delivered by CoA4.2 will be on populations that have been genotyped by either re-sequencing or genotyping-by-sequencing, QTLs can be readily identified by GWAS. Most available QTLs for rice have unknown environment interactions. CoA4.4 will therefore combine QTL discovery with characterization of the stability of their effects ($G \times E$ and $G \times E \times M$) across the Global Rice Array sites. CoA4.4 will apply GWAS methods to identify trait-loci associations and will build linear mixed models and apply machine-learning techniques for predicting phenotypes from genotypes and environment. Improved GWAS pipelines and tools will be used to conduct multienvironment and multitrait analyses to identify QTLs and underlying candidate genes. Confidence in these discoveries will be strengthened by the $G \times E$ and $G \times E \times M$ information on their effects.

Cross-species searches for synteny and gene function will further strengthen them (engaging other CRPs). This information will be fed into FP5 for further validation (e.g., on different genetic backgrounds), marker development, and use in breeding. Meta-analysis of multiple gene-trait associations will be conducted to identify co-localizations and to explore potential cross-adaptations, which may be physiological or controlled by a network of genes of particular interest for breeding.

In the GRiSP New Frontier Project, the PRAY panel was characterized in different locations and GWAS were undertaken. Data analysis pipelines and tools developed in CoAs 4.4 and 4.5 can be trained on these datasets and be rapidly validated. Consolidated genetic associations in the PRAY panel can then quickly move to gene discovery and marker development in FP5 while the other populations are progressively moving in the phenotyping and GWAS pipelines.

4.5 Big Data integration platform

A large amount of data has been generated by GRiSP and will continue to be generated by RICE through the work of FPs 4 and 5. A cross-cutting Big Data platform is essential to connect the different FPs. Specifically, FP4 needs a platform for fast genotypic-phenotypic analysis and generation of markers for breeding in FP5.

CoA4.5 will create a Big Data integration platform to integrate such data as well as create linkages to databases of other CRPs and the proposed Genetic Gain Platform. The Big Data integration platform will provide an efficient mechanism for data sharing and communication not only within RICE but also with other rice researchers and the plant research community in general.

The development of the Big Data platform will build on the work of IRIC, in which many research institutions from the public and private sector already participate, for example, Cirad, University of Arizona, University of Queensland, The Genome Analysis Center, and Bayer Crop Science. The Big Data platform will expand such partnerships.

The platform will support the Global Rice Array by integrating the following activities:

- (1) *Automated phenotyping data capturing.* This activity will result in building a new or adopting an existing tool for mobile devices to ensure accurate, easy, and quick processing of phenotypic data collection, minimize errors in data collection, and provide initial quality control on the data.
- (2) *Data storage.* Phenotypic data have a complex structure, which should be properly reflected in the relational database. Data curation will adopt existing crop, trait, and other ontologies. Data structures for genotyping and sequencing data with gene ontologies have already been developed and will be used in this project. CoA4.5 will establish sufficient storage space for digital images.
- (3) *Data analysis.* CoA4.5 will apply statistical description analysis to the phenotypic data to ensure data quality and to identify outliers. It will also apply methods of quantitative genetics to estimate environmental and genetic contributions to the phenotypes.
- (4) *Data sharing.* All data from this project will be publicly available and CoA4.5 will develop user-friendly web interfaces for browsing, searching, and downloading the results.

Partnerships

RICE is uniquely positioned to lead a global program using well-characterized genetic populations, multiple locations, and different agronomic practices ($G \times E \times M$) as a platform for discovering new traits needed for climate change adaptation. Most of its partners can be categorized as partners at the discovery research level. Following the IEA review recommendations of GRiSP to “encourage and incentivize stronger research collaboration with partners in advanced research institutes for further improving the overall quality of the scientific output”

(IEA review recommendation #2, IEA report, p xvi), FP4 will partner with such ARIs as Cornell University, University of Arizona, University of Queensland, The Genome Analysis Center, and Bayer Crop Science. In addition, NARES partners are involved, especially through the establishment of the Global Rice Array. The rice phenotyping network of GRiSP already involves many partners from Africa, Asia, Australia, Europe, Latin America, and the US, each of which brings in a particular expertise. RICE will aim to expand this network with additional partners from countries that have a large investment in rice research, such as China, India, Indonesia, and Vietnam. RICE will continue GRiSP's coordination of a global rice modeling team (part of AgMIP: Agricultural Model Intercomparison Program) and will use the rice simulation model ORYZA2000. This model is integrated in the DSSAT (Decision-Support Systems for Agrotechnology Transfer) suite that is used in CCAFS and PIM, connecting the crop modeling work of these CRPs with RICE.

The comparative advantage of RICE (as opposed to actions of individual centers) resides in (1) distributing research that surpasses an individual center's capacity, (2) gaining access to the necessary range of environments globally, and (3) using increased power of analysis resulting from the large amount of data on any given panel of genotypes.

Climate change

Climate change is central to FP4. Existing climate variability will be used to identify proxy (analog) sites for future conditions. By combining the RICE rice growth model with climate prediction models generated by CCAFS, FP4 will evaluate the resilience of breeding materials (FP5) and develop ideotype concepts. These will guide breeding strategies for adaptation to anticipated climate change, particularly where current varieties are poorly adapted. The identification of traits (associated genes) related to nutrient- and water-use efficiency will contribute to the development of rice

varieties with reduced needs for these inputs and that can be grown under management systems with reduced emissions of GHGs (in collaboration with FP3 and FP5).

Gender

FP4 will follow the overall gender strategy of RICE, and will have the following specific elements:

- FP4 will strive for gender balance in the leadership roles at flagship project and CoA levels.
- FP4 is uniquely positioned to train a new generation of scientists equipped with the skills set needed in modern plant breeding and agronomy. To promote women's careers in plant sciences, FP4 will actively recruit female candidates to participate in training courses and degree programs (MS and PhD) with affiliated universities.
- FP4 will facilitate the development of climate-resilient varieties in FP5 and will work closely with FP5 to target traits that can benefit women such as drought tolerance, labor-saving, cooking and eating quality.
- By making its data an open resource, FP4 ensures that all rice stakeholders independently of their age and sex are given an equal right to access and use the data.

Capacity development

The overall capacity development strategy of RICE is given. FP4 will specifically strengthen research capacity in its partner organizations. The Global Rice Array sites are well suited for practical training sites. These sites will act as focal points to develop locally adapted technologies, providing technical support, and demonstrating technology to partners and adopters. As they emerge, new research methodologies will be shared with NARES and other CRPs through workshops, short-term training, and degree training. Sandwich/joint training programs with ARIs will be favored whenever possible to tap into expertise available outside RICE.

In a gap analysis of capacity, GRiSP identified important areas for capacity development, including bioinformatics to ensure an intelligent use of tools for GWAS; genotyping-by-sequencing; genetic mapping; new phenotyping methods for disease scoring; remote sensing; instrumentation; development of sound experimental protocols; experimental error tracking; data management; and modeling to accurately account for G x E x M and climate change.

Phenotyping sites hosted by NARES partners will provide ideal locations for training in these areas. Training will be on the use of measurement equipment, including climate stations and diagnostics kits; and data collection, management, and analysis. FP4 will explore sandwich programs with universities for training PhD and MS students to enable them to work in each of the five CoAs. Active interactions with stakeholders—breeders, geneticists-physiologists, and other users—will be crucial for application of Global Rice Array results.

2.4.1.11 Intellectual asset and open access management

FP4 follows the RICE policies and strategies on intellectual asset management, open access, and data management, which are in line with the [CGIAR Principles on the Management of Intellectual Assets](#) and their [Implementation Guidelines](#), and with the CGIAR [Open Access and Data Management Policy](#) and its [Implementation Guidelines](#). FP4 intellectual assets/research data include (1) readily accessible data on novel genes/alleles for rice adaptation and productivity in different environments and future climates, along with donor materials and selection tools for them; (2) knowledge of environment profiles, risk factors associated with climate change scenarios, and varietal adaptation; (3) ideotype concepts as blueprints for breeding strategies; and (4) a public database for phenomics, genomics, environment profiles, and trait–G x E x M interactions.

Data are made widely and publicly accessible through various pertinent and

dedicated websites such as the [International Rice Information System](#) (providing access to structured information on rice germplasm pedigrees, field evaluations, structural and functional genomic data—including links to external plant databases and environmental [GIS] data), and the [Rice SNP-Seek Database](#) (providing genotype, phenotype, and variety information based on the [3,000 Rice Genomes Project](#)). FP4 will develop public-/private-sector partner agreements for the use of discovered genes/materials in order to ultimately reach as many farmers and national breeding programs as possible. Access to data and germplasm will be guided by customized Material Transfer Agreements and specific collaborative agreements.

Flagship Project management

FP4 is a network of partners, in particular NARES. Thus, management of the project must involve stakeholders who participate in the Global Rice Array. The essential elements of a management plan for FP4 will include the FP leaders Dr. Camilla Rebolledo (CIAT) and Dr. Hei Leung (IRRI), and formation of an inclusive committee for developing governance mechanisms that will include representatives of different institutes and network stakeholders and users such as breeders, geneticists, and Big Data managers. The committee will nominate leaders for individual CoAs and will develop consensus and recommend activities matching the common interests of the network. Each CoA is co-led by a team of senior scientists (focal persons) consisting of one or more representatives from each center.

The FP4 coordinator and management team will organize workshops, using the FP4 leader's coordination budget. Also, the team will facilitate communication across the participating centers and institutes to enhance information and knowledge sharing. Developing an integrated platform with collaborating groups from different organizations requires regular communication, using commonly accepted tools for project management and common source control repositories (for example, BitBucket).