For pragmatic reasons, 2013 Annual Report has been split and published in 10 sections as follows:

1. Overview on the CGIAR Generation Challenge Programme
2. Cassava Research Initiative
3. Legumes Research Initiative
4. Maize Research Initiative
5. Rice Research Initiative
6. Sorghum Research Initiative
7. Wheat Research Initiative
8. Comparative Genomics Research Initiative
9. Integrated Breeding Platform
10. Capacity Building

All the reports are available online at [www.generationcp.org/communications/programme-publications/annual-reports-and-workplans](http://www.generationcp.org/communications/programme-publications/annual-reports-and-workplans)

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**Edited by:** Robert Koebner and Larry Butler

**Cover illustration:** Extracts from original artworks by Rhoda Okono entitled *Bountiful African Madonna* and *Marketplace at dawn*, and by Durga Bernhard entitled *World harvest* recomposed by Eliot Sánchez P

**Art direction:** Eliot Sánchez P, CIMMYT
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## Acronyms

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<th>Description</th>
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<tbody>
<tr>
<td>AI</td>
<td>aluminium</td>
</tr>
<tr>
<td>EMBRAPA</td>
<td>Empresa Brasileira de Pesquisa Agropecuária (Brazil)</td>
</tr>
<tr>
<td>GCP</td>
<td>Generation Challenge Programme</td>
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<tr>
<td>GY</td>
<td>grain yield</td>
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<tr>
<td>ICABIOGRAD</td>
<td>Indonesian Center for Agricultural Biotechnology and Genetic Resources</td>
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<tr>
<td>ICRISAT</td>
<td>International Crops Research Institute for the Semi-arid Tropics (India)</td>
</tr>
<tr>
<td>INRAN</td>
<td>Institut National de la Recherche Agronomique du Niger</td>
</tr>
<tr>
<td>IRRI</td>
<td>International Rice Research Institute (The Phillipines)</td>
</tr>
<tr>
<td>JIRCAS</td>
<td>Japan International Research Center for Agricultural Sciences</td>
</tr>
<tr>
<td>KARI</td>
<td>Kenya Agricultural Research Institute</td>
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<tr>
<td>MAS</td>
<td>marker assisted selection</td>
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<tr>
<td>NIL</td>
<td>near isogenic line</td>
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<td>P</td>
<td>phosphorus</td>
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<tr>
<td>PAE</td>
<td>P acquisition efficiency</td>
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<td>PUE</td>
<td>P use efficiency</td>
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<tr>
<td>PUTIL</td>
<td>P internal utilization</td>
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<tr>
<td>QTL</td>
<td>quantitative trait locus</td>
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<tr>
<td>RIL</td>
<td>recombinant inbred line</td>
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<tr>
<td>SNP</td>
<td>single nucleotide polymorphism</td>
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<tr>
<td>USDA-ARS</td>
<td>United States Department of Agriculture-Agricultural Research Service</td>
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Comparative Genomics Research Initiative

Introduction

Comparative genomics is predicated on the assumption that phylogenetically related species share much of their genome sequence and organization, so that genetic inferences made in one species have a high probability of successful application in another. While the technical difficulty of gene isolation and identification of gene function has eased considerably over recent years with the development of high throughput DNA sequencing and improved transgenic technology, it remains the case that substantial savings in time and effort can be gained by taking advantage of the comparative approach when dealing with closely related sets of species such as the tropical cereals rice, maize and sorghum. Crop productivity over a large proportion of arable land in the tropics is compromised by soil acidity, which both solubilizes aluminium (Al) to potentially toxic levels and immobilizes phosphorus (P) to create deficiency problems. Genetic variation for tolerance to Al toxicity and P deficiency is documented in plant species which have evolved in such environments. The question is whether a gene which has arisen in, say, sorghum, has an effective homologue in rice and/or maize. In some cases, the answer to this question is that an effective homologue is indeed present, but in others, it may be present but ineffective, or less effective because there are in fact several homologue genes, while in a few cases no homologue is present at all. A number of GCP research programmes have adopted the comparative genomics approach for the identification and subsequent exploitation of key genes determining Al tolerance and P uptake and use efficiency in the tropical cereals, building on the successful cloning of a major gene for phosphorus uptake efficiency in rice (Pstol1) and major gene for aluminium tolerance in sorghum (AltSb1). The achievements made in the relevant projects within this theme are detailed below.
G3008.04: Drought from a different perspective: improved tolerance through phosphorus acquisition

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Achievements

The Final Technical Report for this project was submitted in 2013. The Pup[P uptake]1 gene (now denoted PSTOL1), the presence of which enhances P uptake efficiency, was positionally cloned in rice. The candidate genomic region in the high P use efficiency (PUE) cultivar Kasalath proved to harbour a sequence absent from either of the two reference genome sequences (cvs. Nipponbare and 9311); part of this sequence consists of the gene OsPSTOL1, which encodes a serine/threonine protein kinase. The constitutive expression of PSTOL1 in cvs. IR64, IR74 (indica types) and cv. Nipponbare (japonica) enhanced root growth and grain yield (GY) in various environments, including those in which the availability of soluble P was non-limiting; meanwhile RNAi-based knockout lines constructed in cv. Kasalath were compromised with respect to the development of the crown root. Follow-on transcriptomic experiments identified a number of genes responsive to changes in the transcript abundance of PSTOL1, and some of these have been shown to co-localize with known drought or root-related quantitative trait locus (QTL). PSTOL1 is uncommon among modern irrigated rice cultivars, but is frequently found in accessions adapted to drought-prone environments. Many BC2F7 PSTOL1 selections tested for yield performance in Indonesia out-performed their recurrent parent with respect to GY under medium input rainfed conditions, and some cv. IR64-PSTOL1 lines tested in India yielded more than their non-PSTOL1 sister lines. Finally, the gene also appeared to support productivity under drought conditions, presumably via its effect on root architecture, since two cv. IR74-PSTOL1 lines out-yielded their non-PSTOL1 sister lines under both well-watered and droughted P limiting conditions. Field trials have been able to confirm the beneficial effect of PSTOL1 in certain genetic backgrounds. Much of this research has been published, including, in particular, a paper in Nature (Gamuyao et al. 2012, Nature 488:535-541.) All data have been published in peer reviewed journals and additional manuscripts are in preparation.

G4008.10: Assessment of the breeding value of superior haplotypes for AltSB, a major Al tolerance gene in sorghum: linking upstream genomics to acid soil breeding in Niger and Mali

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Achievements

The Final Technical Report for this project was submitted in 2013. Given the known effectiveness of the *Alt*$_{59}$ gene in promoting the Al tolerance of sorghum, the initial aim of the project was to correlate its presence with greater Al tolerance in a collection of Sahelian germplasm. The frequency of landraces from Niger showing tolerance to Al toxicity (measured as root regrowth in a hydroponics-based environment) was only 1%, but some 9% of those from Mali (mostly belonging to the predominant guinea race) showed considerable tolerance. A marker assisted back crossing programme was then based on two elite Al sensitive accessions from Niger 90SN-7 and IRAT-204, combining foreground selection for *Alt*$_{59}$ with some background selection. Fixed lines at BC$_2$ from both recipient parents were provided for field validation in Africa in late 2011 and 2012, but these experiments were hindered by difficulties in identifying suitable (Al toxic) sites, since Sahelian soils tend to vary spatially for Al toxicity, and field trials in this region are frequently affected by drought stress. However, successful validation of the positive effect of *Alt*$_{59}$ on GY (20-60%) was carried out in Brazil. There was no evidence for any yield penalty caused by linkage drag in the absence of Al toxicity, while GY in the presence of Al toxicity was enhanced by up to 1 t/ha. The tolerance of selections from the Malian germplasm was high enough not to require any improvement through backcrossing, and seven entries have since been recommended for use by farmers where Al toxicity may be a problem. Germplasm is being maintained by the participants and is available on request from Embrapa and ICRISAT.

G7009.07: Cloning, characterization and validation of *AltSB*/Al tolerance in rice

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Achievements

The Final Technical Report for this project was submitted in 2013. The rice genome harbours five *MATE* homologues, all of which lie in the vicinity of a known Al tolerance QTL. Related research, however, was able to demonstrate that rice, unlike the other cereals, does not release organic acid from its roots as a means of preventing the uptake of Al into the root meristem; rather it tolerates the presence of a certain level of Al in its cell wall and symplasm. As a result, no attempt was made to characterize any of the five *OsMATE* knockout lines. Instead, a phenotype/genotype association approach was adopted, taking advantage of current high throughput genotyping platforms able to expose single nucleotide polymorphism (SNP) variation. The extensive genomic coverage which can be achieved in this way was exploited to genotype a rice germplasm panel using a one million feature SNP chip. This experiment highlighted a number of genomic regions associated with Al tolerance. One of these led to the identification and subsequent positional cloning of the *ART1* transcription factor, a master regulator of the Al-induced expression of a number of downstream Al tolerance genes. A second significant locus lay on chromosome 2, in which the putative Al uptake transporter *Nrat1* resides. Heterologous expression studies using yeast suggested a process in which the *Nrat1* product moves Al from the cell wall to the cytoplasm, where a second Al transporter ALS1 sequesters the absorbed Al into the vacuole. The heterologous expression of contrasting *Nrat1* alleles in *A. thaliana* showed that the presence of either the sensitive or the tolerant allele conferred a significant increase in Al tolerance, but the expression of the tolerant haplotype conferred the greater level of tolerance. Two contrasting *Nrat1* alleles proved to be highly predictive of Al tolerance in *aus* germplasm. Since the maize genome also harbours an *Nrat1* homologue, this discovery offers a potential opportunity to apply the comparative genomics approach in maize (and presumably in other related cereals such as sorghum and the millets). Meanwhile, a QTL approach has identified four independent Al tolerance QTL, and near isogenic lines (NILs) for each QTL have been generated in two genetic backgrounds for future field evaluation. Analysis of the NILs has shown that the most likely candidate for the largest effect Al tolerance QTL on chromosome...
12 (Alt12.1) is ART1, which encodes a transcription factor known to regulate at least 30 other genes, including several already implicated in the Al response. This hypothesis is currently being tested using a transgenic approach. Data have been lodged at the IGD database (http://cbsuss03.cs.cornell.edu/sorghum/index.html) and will subsequently be transferred to the GCP Central Registry.

G7010.03.01: Cloning, characterization and validation of PUP1/P efficiency in maize

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Achievements
A set of maize recombinant inbred lines (RILs) was developed from a cross between the P efficient line L3 and the P inefficient line L22. Analysis of root morphology traits expressed by the RILs demonstrated the presence of wide-ranging genetic variation, with L3 showing a superior phenotype to L22 for all the traits, and some RILs out-performing L3. There was however no correlation between any of the root traits and PUE. The six PSTOL homologues in maize (sharing at least 55% amino acid sequence identity with the rice sequence) proved to be distributed over three chromosomes. A QTL mapping exercise based on the RIL population demonstrated that four of the ZmPSTOL loci lay close to genes determining various combinations of multiple or single traits expressed under low P conditions. Two were transcribed preferentially in the roots of L22 and a third in the roots of L3. Six QTL were mapped for PUE, six for P acquisition efficiency (PAE) and five for P internal utilization (PUTIL). Most of the PUE loci overlapped PAE ones, so that PUE and PAE were highly correlated with one another; both tended to be correlated to GY under low P conditions. The PUTIL QTL were, however, clearly distinct. Four genomic regions were highlighted: one on chromosome 1 harboured QTL for PUE, PAE and PUTIL measured from field-grown material, as well as for root morphology and PAE in hydroponics; a second on chromosome 3 harboured QTL for PUE and PAE expressed in low P soils, PAE in hydroponics and root morphology; a third on chromosome 7 harboured QTL for PUE and PAE expressed in low P soils and root diameter, and a final one on chromosome 8 harboured QTL for PUE and PAE expressed in low P soils and PAE, root length and root surface in hydroponics. Of the ZmPSTOL genes, only ZmPSTOL1 co-localized with a PUE or PAE QTL. A study of the inheritance of root morphology under high and low P showed that dominance effects predominated over additive ones, implying that breeding for PUE should focus on the exploitation of heterosis. Data have been lodged at the IGD database (http://cbsuss03.cs.cornell.edu/sorghum/index.html) and will subsequently be transferred to the GCP Central Registry.

G7010.03.02: Validation of ZmMATEs as genes underlying major Al tolerance QTL in maize

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S Gudu: Moi University, Eldoret, Kenya

Achievements
The Final Technical Report for this project was submitted in 2013. This project was a follow-up to G3008.02 (see above). A set of 118 RILs derived from the cross Cateto Al237 x L53 was saturated with SNPs to map Al tolerance, as measured by seedling root growth after five days exposure to Al³⁺. The chromosome 6 QTL qALT6 explained around a quarter of the phenotypic variance and co-localized with the ZmMATE1 locus. Around 84% of the variance for ZmMATE1 transcript abundance was associated with the
structural gene, reflecting the presence of three copies of the gene in the tolerance allele. NILs for ZmMATE1 and the parents used for their production were also evaluated in the field at sites where three different levels of Al saturation prevailed in the first 20 cm of the soil profile. The GY of Cateto Al237 was low but stable, while L53 yielded well in limed soil, but poorly in untreated soil. The qALT6 NILs yielded at least as well as L53 in the limed soil and out-performed it in untreated soil. In the context of implementing a marker assisted selection (MAS) strategy based on ZmMATE1, an unfortunate consequence of this form of genetic polymorphism is that it hinders the development of a satisfactory DNA marker for the effective allele, since all three copies are identical in sequence to one another. A second locus, qALT5, which also explained a significant proportion of the genetic variance for Al tolerance, co-localized with ZmMATE2; however, in this case, the genetic basis of transcript abundance was not associated with the structural gene, nor were NILs for the gene any less Al sensitive than the recipient cultivar. ZmNrat1, a homologue of rice Nrat1, was mapped in the vicinity of qAlt5, so is considered to be a possible candidate gene underlying Al tolerance in maize. Although Al tolerance is widespread among Kenyan landrace germplasm, the frequency of the effective ZmMATE1 allele is low, so their tolerance clearly must have a different genetic basis. Certain Kenyan lines carrying the superior allele of ZmMATE1 have been identified as suitable donors in a marker assisted backcrossing programme. In the context of a MAS strategy based on ZmMATE1, a suite of DNA-based markers flanking qALT6 is now available for use. These data have been assembled in a forthcoming publication in BMC Genomics. The SNP genotypic data will be uploaded in the near future into the IBP maize SNP fingerprinting database.

G7010.03.03: Establishing a molecular breeding programme based on the aluminum tolerance gene AltSB and the P efficiency gene PSTOL1 for increasing sorghum production in sub-Saharan Africa

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Achievements
Parental lines of random mating populations facilitated by the use of the genetic male sterile gene ms, have been genotyped to assess the frequency of lines carrying AltSR. The attempt to generate random mating populations in Niger was thwarted by consecutive poor seasonal conditions, so the Niger team has been forced to re-focus on the evaluation of a set of backcrossed lines involving two recurrent parents sensitive to Al. A set of 80 lines adapted to Malian conditions were evaluated in five locations under high P and...
low P growing conditions, but few associations between the target traits and the specific marker alleles were evident. A genome-wide association study based on around 200,000 SNP loci, however, did generate a number of associations with plant height, heading date and GY under low P conditions. A set of 188 entries were exposed to P stress for 38 days in a pot trial, in an experiment designed to study diversity for crown root angle and colonization of the roots with mycorrhizae, and to determine whether these traits were related to P uptake and plant performance. However, neither of the traits proved to be sufficiently reliable. The same 188 lines were also used to re-sequence a set of candidate genes for P efficiency (PHR2, SIZ1, PHO2, SPX1, PHT1 and Ph1;6). The number of SNPs per gene varied from zero to nine; the entries were, in addition, SNP genotyped for eight sorghum candidate genes based on PSTOL1. The latter analysis generated a set of 31 SNPs, but few significant SNP/trait associations emerged. Of the 188 lines, 17 carried \textit{Alt}_{SB} and 16 of these were either pure Guinea types or had been derived from Guinea type x Caudatum crosses. Due to the small sample size, no significant phenotype/genotype associations with adaptation to low P soils have been uncovered so far. At ICRISAT Samanko (Mali), the third and last random mating of the population generated by inter-mating lines identified as being well adapted to low P soils was conducted. This has generated a set of lines currently being multiplied for testing and genotyping.

EMBRAPA has based a selection programmer on two random mating populations for tolerance to Al toxicity. So far, 200 S1 selections have been exposed to Al stress in a hydroponics situation and 200 S2 progenies are in the process of being phenotyped in a P deficient field site, while and root morphology is being recorded to validate the molecular markers for \textit{Alt}_{SB} and the PSTOL1 homologues. All the data will be made freely available to all partners by the end of the project.

G7010.03.04: Developing rice with dual tolerance of phosphorus deficiency and aluminium toxicity: Marker-assisted pyramiding of PSTOL1 with novel tolerance QTL

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\textbf{Achievements}  
In India, the effect of introgressing PSTOL1 into both IR64 and IR74 is being tested in the field in two locations. IR64-PSTOL1 lines out-performed sister lines lacking the gene, while IR74-PSTOL1 lines were superior to their respective non-PSTOL1 sister lines when tested in low P soil, both when well-watered and when drought stressed. The relevant markers have been made available to local breeders. In Africa, the same materials are being tested in Benin and a novel set of markers has been developed for use in African germplasm. PSTOL1 has also been introgressed into adapted Indonesian cultivars, and a number of BC$_2$F$_2$ selections have been successfully yield trialled; most of the material outperformed the recurrent parent with respect to GY under medium input, rainfed conditions. In India, in an attempt to combine PSTOL1 with two major drought QTL (DTY2.2 and DTY4.1), homozygotes for all three genes/QTL have now been advanced to the F$_3$ generation for field testing. A similar effort to combine PSTOL1 with genes for Al tolerance is at the stage of elaborating the necessary markers. The mapping of Al tolerance QTL harboured by the Indonesian cultivar Dupais has exposed several minor effect QTL on chromosomes 1, 3 and 6. Markers for these are currently being developed for use in a screen for dual tolerance to P defiency and Al toxicity. Over-expressing the gene \textit{PupK20-2}, thought to act downstream of PSTOL1, was shown to have a positive effect on plant performance under low P conditions. Simultaneously introducing both tolerance of P deficiency and of Al toxicity into African rice is an ongoing activity; however, as yet no suitable field site has been identified. Data are available upon request, and will appear as part of two forthcoming PhD theses.
**G7010.03.05: Marker-assisted breeding for improving phosphorus-use efficiency and tolerance to aluminum toxicity in maize**

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**Achievements**

A collection of Kenyan maize germplasm has been screened for Al tolerance and the transcription of the ZmMATE1 gene which underlies the major tolerance QTL qALT6 profiled. The screen identified that some 15% of the lines were highly tolerant, but none of the material derived from the highly Al tolerant Kenyan landraces 203B, K4 and CONS showed the pronounced abundance of ZmMATE1 transcript characteristic of the Brazilian landrace Cateto Al237. This demonstrated that the genetic basis of their tolerance does not rely on qALT6. The pedigree of the few tolerant Kenyan lines which did carry the superior allele of ZmMATE1 included Cateto Al237. Selections from the Kenyan germplasm have been used to generate ten highly Al tolerant inbred lines. A similar screen for P efficiency among the Kenyan material has identified ten P efficient inbred lines. As part of an ongoing effort to combine Al tolerance and PUE, the ten Al tolerant and ten high PUE lines have been intercrossed with one another, and the hybrids are currently being evaluated for tolerance to low P. A marker assisted backcrossing programme to introduce the superior allele of ZmMATE1 into Kenyan germplasm has been initiated, based on three recipient Al sensitive lines and a tolerant line. A similarly approach is being taken to introduce the Al tolerance gene into four elite Brazilian lines. A Kenyan Al tolerant line displaying a low abundance of ZmMATE1 transcript has been crossed to a line carrying qALT6 in an attempt to combine these two sources of tolerance, but relevant phenotypic data are not yet available. Two mapping populations have been constructed; one involves a contrast for PUE and the other for Al tolerance. QTL detection based on SNP markers in the latter population has identified four tolerance loci and a number of marker/trait associations, some relating to genomic locations which have not been observed in other populations. The former population has been genotyped but the collection of phenotypic data is ongoing. Two synthetic populations based on Al tolerant and P efficient parents have been entered into
national trials, and others are at an earlier stage in the registration process. Open pollinated varieties exploiting both Kenyan and Brazilian sources of Al tolerance along with P efficient lines should be well adapted to acidic soils. Data have been uploaded to the GCP Central Registry.

G7010.03.06: Improving phosphorus efficiency in sorghum by the identification and validation of sorghum homologues for PSTOL1, a major QTL underlying phosphorus uptake in rice

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Achievements
Seven putative PSTOL1 homologues have been identified in the sorghum genome, and trait/gene associations of varying strengths have been detected for all the loci. A standard QTL mapping strategy was therefore implemented, based on 400 RILs bred from a cross between parental lines contrasting in their root morphology. The RILs were genotyped using genotyping by sequencing, and classified with respect to their root morphology. On chromosome 3, a QTL determining shoot dry weight accumulation was found to co-locate with one SbPSTOL locus, and second QTL (affecting average root diameter) mapped within 4 Mbp of this locus; a third QTL (total root length) was separated by just 12 Mbp from a cluster of SbPSTOL homologues. Consistent results for the allelic effect on P uptake traits have been obtained for some of the SbPSTOL1 homologues. For this same set of SNPs, there was a consistent association with GY under deficient P conditions in Brazil and with biomass yield under deficient P conditions in Africa. An initial survey of root architecture among a set of landraces and selected members of the US sorghum association panel uncovered plenty of diversity; some of the plants form shallow and bushy roots, others narrow and deep ones. The current consensus is that the former type is the better adapted for low P soils. The PSTOL1 markers have been converted into KASPar assays and are available through the IBP. A forthcoming publication will include the phenotypic data related to the characterization of the association panel, but are available upon request.

Capacity building
Within the context of project G7010.03.03, a hydroponic facility for testing Al tolerance, modeled on one established in Brazil, was successfully commissioned at ICRISAT Samanko (Mali). Two graduate students from Kenya have been trained in molecular breeding techniques. W Leiser is continuing his PhD studies and M Olatoye submitted his thesis during 2013.

Major accomplishments, challenges & lessons learnt
The Research Initiative has recorded a number of significant scientific and technical advances. Notable in the former category are the Mendelization of the qALT6 locus in maize; the isolation in rice of PSTOL1 (encoding a serine/threonine protein kinase, and proven to be a major determinant of PUE); the recognition of the important contribution of the ART1 transcription factor and the Nrat1 gene to Al tolerance in rice; the identification of QTL for Al tolerance in rice present in the Indonesian local variety Dupa;
the implementation of GWAS in sorghum, which has highlighted a genomic region harbouring a gene(s) controlling both PUE and Al tolerance; the identification of the likely maize homologue of rice PSTOL1 which appears to contribute to early root development as well as to PUE; a demonstration that PSTOL1 homologues support P uptake in sorghum by enhancing early root growth, just as in rice; and the development of maize lines carrying novel genetic determinants of Al tolerance. As is increasingly the case, the ability to genotype on a large scale, once seen as a bottleneck, has now far out-stripped the capacity to phenotype with accuracy. A major challenge in testing gene candidates and validating QTL remains the elaboration of robust field testing protocols and the identification of reliable field sites. Sandy soils in the semi-arid tropics typically contain inadequate amounts of organic matter and consequently have a poor soil cation exchange capacity. As a result, spatial variability in soil Al tends to be high, complicating the choice of an appropriate field site. Thus while it is recognized that the seedling root regrowth assay is predictive of the plant response to Al toxicity, it cannot fully reproduce the stress experienced by the field-grown plant throughout its life cycle, either in time or in space. Field trials are also necessarily subject to the vagaries of climate: a combination of terminal drought conditions in one season, followed by high rainfall and flooding in the subsequent season resulted in a major loss of materials and time in the project aiming to establish a MAS-based sorghum improvement programme based on Alₜ₈ and SbPSTOL. Although some exciting developments in phenotyping methodology, particularly with respect to root architecture, are in train, the ultimate and necessary test will always remain field performance.

While the comparative genomics approach has been productive for determining the genetic basis of a number of traits (most notably perhaps for the major developmental traits flowering time and dwarfing) and in several plant groups, it remains one of the tools in the breeding toolbox. The efficiency of that approach depends on the nature of the trait, mainly the level of polygeny, and the nature of the crop. One problem, as well illustrated by the experience with both the MATE and the PSTOL sequences, was that scanning a whole genome for homology with a heterologous sequence produces multiple hits, none of which is even a near-perfect match. Determining which (if any) of these putative homologues is effective can be a lengthy process unless (as is the case in rice) extensive sets of knock-out lines are available. Nevertheless, the strategy will retain its value for at least as long as the genomic resources (sequence, mutants etc.) available in the target plant species have not reached the level attained in leading species such as rice.
Conclusions & perspectives

The comparative genomics strategy has proved its worth for identifying key genes determining tolerance to low P and high Al soils. The approach is efficient in crops like rice and sorghum but more challenging with maize, As the genomic resources of all of the mandate crop species continue to expand, it will ultimately be replaced by targeted gene discovery within each species, as illustrated by the examples of rice ART1 and Nrat1. The challenge of the approach is exemplified by the example of the Kenyan Al tolerant maize landraces, which do not generate the high abundance of ZmMATE1 transcript as does the Brazilian line Cateto Al237. Provided that the reliability of phenotyping assays can be improved, current intraspecific gene discovery methodology (via either biparental QTL mapping or genotype/phenotype association analysis) allied to high density, high throughput SNP genotyping, will offer a very powerful means of determining the genetic basis of important agronomic traits.