

# GCP Fellowships 2008

Applications are invited from developing country crop science researchers working in developing country research institutions. Priority will be given to scientists already involved in GCP research projects.

**Rationale:** To facilitate innovative research related to GCP's central theme — unlocking genetic diversity of crops for the resource-poor.

**Target:** Scientists wishing to broaden their skills by conducting research outside their home countries/institutions

**Duration:** Determined by research subject—minimum four months, maximum one year.

**Themes:** Research in any of GCPs four thematic subprogrammes: 1) genetic diversity of global genetic resources, 2) comparative genomics for gene discovery, 3) trait capture for crop improvement, and 4) genetic resources, genomic, and crop information systems

**Eligibility:** Minimum Master of Science degree (MSc), or equivalent, in a relevant subject area (see research subject)

**Conditions:** Applicants must demonstrate they are engaged in a related ongoing research activity in their home country. Applicants are expected to return to their home institution and contribute to its research and education programmes.

No of fellowships: 8

**Award:** Up to US\$25,000<sup>1</sup> per fellow to cover travel, living expenses, accommodation, laboratory consumables and conference participation, where applicable

Application procedures and deadlines Pre-proposals, 31<sup>st</sup> December, 2007; Full proposals 31 January 2008,

Successful applicants will be informed by **1<sup>st</sup> March 2008** and **will be required** to take up their Fellowships by **31<sup>st</sup> July, 2008**.

## Research subjects

GCP is seeking candidates who elaborate a sound proposal to be trained in the subjects described below. Minimum qualifications and proposed duration are given for each subject:

1.

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| <b>Title:</b> | Translation of SNPs underlying drought tolerance in wild barley into |
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<sup>1</sup> This is the maximum award a fellow may receive. It varies depending on factors such as duration of the fellowship period and host country, among others. *Note: The fellowship award does not represent a salary but support for a learning experience, thus it must be used only for the items described above. Living expenses and accommodation need to be calculated in consultation with the host institute(s).*

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|   | high-throughput low technology markers.                           |
| <p><b>Description of research proposed:</b> The main aim of this project is to translate SNP assays that define chromosomal regions underlying drought tolerance in wild barley into high sample throughput low technology single marker assays such as Cleaved Amplified Polymorphic Sequences (CAPS) that can be routinely deployed in MAS programmes. These assays are simple, accurate and cost-effective, and can be implemented in laboratories that do not have access to sophisticated equipment. CAPS markers are based on the detection of a polymorphism by restriction endonuclease digestion of a PCR amplified DNA fragment. Polymorphism is revealed when the enzymes recognition sequence has been destroyed or created by a SNP. CAPS are simply analysed as a single locus marker on agarose gels. This research and training project will focus on converting the SNPs identified in the ongoing project '<a href="#">Genomic dissection of tolerance to drought stress in wild barley</a>'. into CAPS markers that will therefore have direct utility in barley breeding programmes. The project will focus on using informatics approaches to identify and concert SNPs to CAPS and molecular approaches to assess and track molecular diversity in germplasm and defined plant populations using the defined assays.</p> <p>The project will identify QTL originating from wild barleys that have been introgressed into cultivated North American germplasm. These QTL will be defined by a number of SNPs on the OPA marker platform used to conduct the genetic analysis in this project. Information from each locus will be enhanced by allele survey resequencing using a collection of barley landraces that will reveal haplotype diversity at each locus. In this training project, collections of aligned sequences spanning the identified QTL, will be interrogated by different SNP conversion programs (dCAPS Finder 2.0 (Neff <i>et al.</i>, 2002 Trends Genets 18: 613-615) and SNP2CAPS (Thiel <i>et al.</i>, 2004, NAR 32: e5) to identify primer-enzyme combinations that reveal CAPS markers. These primer-enzyme combinations will be experimentally verified using a standard set of barley accessions including those from which the allelic repertoire and locus haplotypes were originally determined. PCR will be performed using these DNAs according to standard protocols and digested with the designated enzyme, analysed using agarose gel electrophoresis and assessed for suitability as robust CAPS markers.</p> |   |
| <b>Related GCP project:</b>   | Genomic dissection of tolerance to drought stress in wild barley. |
| <b>Principal Investigator/host scientist(s):</b>  | Prof Robbie Waugh/ Joanne Russell                                 |
| <b>Host institution:</b>  | Scottish Crop Research Institute (SCRI)                           |
| <b>Country:</b>   | Scotland, United Kingdom  |
| <b>Duration<sup>2</sup>:</b>  | 9 months  |
| <b>Qualifications of the candidate<sup>3</sup>:</b>   | Basic laboratory skills   |
| <b>Crop:</b>  | Barley  |

## 2.

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| <b>Title:</b>   | Multi-Trait Analysis for Agronomical Performance on Acid Soils. |
| <p><b>Description of research proposed:</b> Crops cultivated on acid soils, which occupy large portions of agricultural lands in developing countries, are subjected to numerous stress factors such as aluminum (Al) toxicity, phosphorus (P) and nitrogen (N) deficiency; in addition to drought stress. Therefore, superior and stable agronomical performance therein is the result of adaptation to the whole acid soil complex rather than to any single stress factor alone. On acid soils, Al toxicity inhibits root growth, making crops more prone to drought stress. Phosphorus diffusion to the roots in water-limited soils is dramatically reduced, resulting in severe P deficiency, which in turn results in N stress and concomitant severe yield losses. <a href="#">EMBRAPA</a> Maize and Sorghum has a single sorghum RIL population that has been phenotyped for root growth inhibition caused by Al in nutrient solution (a more direct measure of Al tolerance), agronomical performance on acid soils</p> |   |

<sup>2</sup> The project activities must be planned within this timeframe.

<sup>3</sup> Qualifications describe the expected applicant's profile.

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| <p>(one-year data), tolerance to drought stress (two-year data), and phenotyping for P efficiency is underway. In addition, a genetic map with approximately 70 SSRs is now being saturated with DArT technology. Here we propose to use multi-environment / multi-trait QTL analysis using a mixed model framework to (1) account for plot heterogeneity in QTL analysis based on field data, (2) identify QTLs for single stress factors that are stable across environments (accounting for QTLx E effects), (3) by multi-trait QTL mapping, dissect acid soil responses into its genetic components elucidating individual QTL effects on overall acid soil performance. The results are expected to shed light on the actual role of AI tolerance estimated in controlled conditions for yield performance on acid soils, concurrently directing molecular breeding efforts toward other component traits important for yield stability.</p> |  |
| <b>Related GCP project:</b>   | <p><i>An Eco-Physiological-Statistical Framework for the Analysis of GxE and QTLxE as Occurring in Abiotic Stress Trials</i> (please see page 59 of the <a href="#">2007 Project Mid-year and final reports: Competitive and commissioned projects</a>) and <a href="#">Tailoring Superior Alleles for Abiotic Stress Genes for Deployment into Breeding Programmes</a></p>                            |
| <b>Principal Investigator/host scientist(s):</b>  | Dr Jurandir Magalhaes  |
| <b>Host institution:</b>  | EMBRAPA Maize and Sorghum  |
| <b>Country:</b>   | Brazil   |
| <b>Duration:</b>  | 6 months   |
| <b>Qualifications of the candidate:</b>   | <ul style="list-style-type: none"> <li>• General background: PhD in Genetics and Plant Breeding or strong background in those fields</li> <li>• Specific background: strong background in statistical and quantitative genetics and biometry with emphasis on QTL mapping</li> <li>• Knowledge on generally used mapping software and statistical computing packages (SAS and R)</li> <li>•</li> </ul> |
| <b>Crop:</b>  | Sorghum  |

### 3.

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| <b>Title:</b>   | Data analysis of a network of field trials involving a population of recombinant inbred lines: dissecting the genotype x environment interaction. |
| <p><b>Description of research proposed:</b> The genetic determinism of tolerance to water deficit is often analysed via the identification of quantitative trait loci (QTLs) of yields, which are unstable because of the climatic variability. This GCP project has generated two types of information on a common mapping population of 220 recombinant inbred lines of maize: (i) QTLs of sensitivity of leaf growth rate to water deficit and evaporative demand, obtained on a phenotyping platform, (ii) final area of leaves, together with environmental data, in 8 field experiments in Mexico, Kenya and India. Yield components have also been collected in this network of experiments. Field experiments allow testing to what extent the genetic variability of responses to environmental conditions, collected in semi-controlled conditions, translate into genetic differences in leaf area and biomass accumulation in field conditions. The work will consist in a re-analysis of the whole set of field data (i) consistency of data in the different experiments (e.g. ranks between genotype, size of the studied leaves, range of water balance across treatment x location), (ii) A model-assisted reanalysis of the whole dataset to identify relationships between traits or between traits and environmental conditions in the field data, and between traits obtained in controlled conditions and in the field. (iii) A multi-environment QTL analysis, in order to identify QTLs of leaf area or yield components common to several fields, and QTLs associated to specific environmental conditions as source for adaptation. A QTL x Environment analysis might be carried out at the end of the period if time allows it.</p> |   |
| <b>Related GCP project:</b>   | Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes.                    |
| <b>Principal</b>  | Dr Francois Tardieu   |

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| <b>Investigator/host scientist:</b>     |  |
| <b>Host institution:</b>                | Institut National de la Recherche Agronomique (INRA-Montpellier)   |
| <b>Country:</b>                         | France   |
| <b>Duration:</b>                        | 7 months   |
| <b>Qualifications of the candidate:</b> | <ul style="list-style-type: none"> <li>• Reasonable training in the common tools of data processing (excel or R, statistical packages) and a minimum mathematical or statistical base</li> <li>• Bases of crop physiology, ecophysiology or quantitative genetic will be appreciated but not required</li> <li>• An interest for field data analyses using improved methods</li> </ul> |
| <b>Crop:</b>                            | Maize  |

#### 4.

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| <b>Title:</b>                                 | Studying the influence of genetic correlations between environments on the power to detect QTLs and QTLxE.   |
| <b>Description of research proposed:</b>      | A common experiment in plant breeding is to evaluate a set of genotypes under different environmental conditions. For example, in breeding for abiotic stresses, genotypes can be evaluated under different water or nitrogen regimes. On the one hand, some degree of genetic correlation between the performances in the different environments is expected because the same set of genotypes is used across the experiments. On the other hand, lack of genetic correlation between environments is expected because of the ubiquitous and well known phenomenon of genotype by environment interaction (GxE). If genotypes come from a designed cross (e.g. F2 or RIL population), the data can be used in QTL mapping to detect QTLs and QTLxE (QTL by environment interaction). To improve the tests for the detection of QTLs and to estimate QTL effects realistically, the genetic correlations between environments need to be considered. In this project, we propose to use simulation studies based on real-life CIMMYT experiments on maize and wheat to evaluate the importance of considering the genetic correlations across environments in contrast to ignoring such correlations. The latter case, that is, ignoring genetic correlations, is what most of the currently used QTL mapping methods are doing. The evaluation will be on capacity to detect main effect QTLs and QTL by environment interaction (power of the method) and the accuracy of the estimated QTL effects. |
| <b>Related GCP project:</b>                   | QTL mapping methodology for multi-trait, multi-cross, multi-environment drought stress trials in tropical maize and bread wheat  |
| <b>Principal Investigator/host scientist:</b> | Dr Fred van Eeuwijk  |
| <b>Host institution:</b>                      | <a href="#">Wageningen University and Research Centre (WUR)</a>  |
| <b>Country:</b>                               | The Netherlands  |
| <b>Duration:</b>                              | 9 months   |
| <b>Qualifications of the candidate:</b>       | <ul style="list-style-type: none"> <li>• Plant breeders/biologists with interest in quantitative genetics and good background in statistics, or</li> <li>• Statisticians with good knowledge of plant genetics and physiology</li> </ul>   |
| <b>Crops:</b>                                 | Maize and Wheat  |

#### 5.

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| <b>Title:</b>                            | The use of relatedness information in linkage disequilibrium mapping: pedigree information versus molecular marker information   |
| <b>Description of research proposed:</b> | Linkage disequilibrium (LD) mapping is an alternative strategy to map QTLs to conventional QTL mapping. LD mapping is more attractive for breeders as it does not require spending time and resources in developing crosses, and it allows the use of germplasm that is more relevant to the breeding programme. For example, elite breeding material and germplasm collections can be directly used to map QTLs, exploiting the data that has been historically accumulated. Unlike populations used for conventional QTL mapping, populations used |

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| <p>for LD mapping are composed of genotypes that do not have the same degree of parentage. Ignoring the degrees of parentage between genotypes can dramatically increase the rate of false QTL detection. One solution is to incorporate pedigree information in the LD mapping procedure to reduce false positives. However, such pedigree information is not always available or accessible, so molecular marker information can be used as an alternative. The objective of the present proposal is to compare the efficiency of LD mapping strategies using genetic relationships based on molecular marker information with those using direct pedigree information. Various datasets are available.</p> |  |
| <b>Related GCP project:</b>   | Design and analysis of marker-trait association studies, with special attention on genetically challenging crops.  |
| <b>Principal Investigator/host scientist(s)</b>   | Dr Fred van Eeuwijk  |
| <b>Host institution:</b>  | Wageningen University and Research Centre (WUR)  |
| <b>Country:</b>   | The Netherlands  |
| <b>Duration:</b>  | 9 months   |
| <b>Qualifications of the candidate:</b>   | <ul style="list-style-type: none"> <li>• Plant breeders/biologists with interest in quantitative genetics and statistics</li> <li>• Direct contact with a breeding programme is desirable</li> </ul> |
| <b>Crop:</b>  | NA   |

## 6.

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| <b>Title:</b>  | Marker-based estimation of coancestry measures in genebank collections   |
| <p><b>Description of research proposed:</b> Many estimators have been proposed inferring the coancestry (the degree of relatedness) for pairs of individuals using molecular marker data. The performance of these estimators depends strongly on assumptions, e.g. about the allelic frequencies in the presumed populations under study (e.g., Bink <i>et al.</i> 2007). In many important crop species accurate estimates of allele frequencies are not available for the datasets at hand. In this project we will study the possibility of obtaining information about allele frequencies by analyzing genebank collections. We will aim at incorporating knowledge of the breeding history of the crop species, which may involve many deviations from model assumptions (genetic bottlenecks, selection, recurrent backcrossing).</p> |  |
| <b>Related GCP project:</b>  | Design and analysis of marker-trait association studies, with special attention to genetically challenging crops   |
| <b>Principal Investigator/host scientist(s)</b>  | Dr Fred van Eeuwijk  |
| <b>Host institution:</b>   | Wageningen University and Research Centre (WUR)  |
| <b>Country:</b>  | The Netherlands  |
| <b>Duration:</b>   | 9 months   |
| <b>Qualifications of the candidate:</b>  | <ul style="list-style-type: none"> <li>• Plant breeders/biologists with interest in quantitative genetics and statistics</li> <li>• Direct contact with a breeding programme is desirable</li> </ul> |
| <b>Crop:</b>   | NA   |

## 7.

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| <b>Title:</b>  | Estimation of genetic parameters in autotetraploid |
| <p><b>Description of research proposed:</b> Polyploidisation has played an important role in plant evolution. The majority of polyploids exhibit disomic inheritance. They are presumed to be amphidiploid species hybrids (allopolyploids) which in the past have developed genetically controlled, preferential pairing between homologous chromosomes. Usually, they can be treated as diploids. However, a few important crop species are autopolyploid, exhibiting polysomic inheritance (e.g. potato, coffee, alfalfa and some grass species); most of them are tetraploids. All</p> |  |

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| <p>autopolyploids are outbreeders and show marked inbreeding depression (Breese, 1989). As a consequence, it is not possible to use breeding strategies requiring pure lines. The genetic dissection of quantitative traits in autotetraploids has been hampered by the complexity of models and associated analyses as compared to diploids. A few attempts have been made in the areas of map construction and QTL analysis. Currently, methods and software for calculating population genetic parameters such as coancestry coefficients and linkage disequilibrium measures are not available, as in many cases useful marker data. This project aims at making a start with developing such methodology and software to support breeders and geneticists in the genetic improvement of autotetraploid crops.</p> |  |
| <b>Related GCP project:</b>  | Design and analysis of marker-trait association studies, with special attention to genetically challenging crops   |
| <b>Principal Investigator/host scientist(s):</b>   | Dr Fred van Eeuwijk  |
| <b>Host institution:</b>   | Wageningen University and Research Centre (WUR)  |
| <b>Country:</b>  | The Netherlands  |
| <b>Duration:</b>   | 9 months   |
| <b>Qualifications of the candidate:</b>  | <ul style="list-style-type: none"> <li>• Plant breeders/biologists with interest in quantitative genetics and statistics</li> <li>• Direct contact with a breeding programme is desirable</li> </ul> |
| <b>Crop:</b>   | NA   |

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| <b>Title:</b>   | Data mining approach to assessing biotic constraints   |
| <p><b>Description of research proposed:</b> Major advances in assessing impact of crop improvement technology have been made the last five to 10 years. Survey, census and spatial data and tools have benefited greatly from the information technology revolution. Researchers can better evaluate obstacles to crop production, especially soil- and climate-related abiotic constraints. However, information on the impacts of biotic constraints such as pests and pathogens are less well-known. These constraints can vary widely across landscapes and through time. They tend to be more crop-specific, and more difficult to generalise. Surveys of these constraints are difficult and costly to carry out over large areas. Reliance on experts in a given region is often required, which can sometimes be biased by professional and institutional agendas. Data mining provides an alternative approach to collecting information on the impact of pests and pathogens. A research project is proposed to collect information on biotic constraints using a data mining approach. A research fellow would use Internet search techniques, Google Alerts, RSS feeds and other data mining methods to collect the information. Sources would include the CABI database, PRO-MED disease reports and similar resources. The information would be geographically referenced using digital and hard-copy gazetteers and managed in a geographic information system. The fellow will produce a global assessment of the main pests and pathogens constraining crop production, from the perspective of information on the Internet and specialised sources.</p> |  |
| <b>Related GCP project:</b>   | Targeting and impact analysis of Generation Challenge Programme (GCP) technologies. ( <a href="#">please see page 175 in 2007 Project mid-year and final reports: Competitive and commissioned projects</a> )              |
| <b>Principal Investigator/host scientist(s):</b>  | Dr Glenn Graham Hyman  |
| <b>Host institution:</b>  | International Center for Tropical Agriculture (CIAT)   |
| <b>Country:</b>   | Colombia   |
| <b>Duration:</b>  | 9 months   |
| <b>Qualifications of the candidate:</b>   | <ul style="list-style-type: none"> <li>• University degree in agricultural, biological or environmental science</li> <li>• Fluency in English</li> <li>• Strong computer skills, preferably with GIS experience</li> </ul> |

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|              | • Interest in biotic constraints to agricultural production a plus |
| <b>Crop:</b> | NA   |

### **IMPORTANT NOTES:**

1. **Applications on subjects other than the ones above will not be considered.**
2. The proposal should present evidence that **the fellowship will be oriented towards training of the candidate and improving capacity at the home institution, rather than to provide extra funding for ongoing projects.**
3. GCP Fellowship awards can be held concurrently with other sources of support, but such sources **must be** mentioned in the application.

### **Host Institution and application procedure**

The host institution must be the one described on each research subject (above) and the larger party of the proposed research must be done at the host institution.

The 2008 GCP Fellowships will have a two-step procedure:

1) *Pre-proposal requirements*

- a) A covering letter indicating applicant's current position, a brief description of research work in which s/he/ is involved and the expected benefits for the applicant as well as the research at the home institution, if selected
- b) Duly filled [application form](#) for pre-proposals),
- c) Full *curriculum vitae* of candidate (please see CV template)
- d) A letter of support from the home institute: i) endorsing the application; and, ii) specifying how the proposed research will benefit the institute and/or country, and
- e) Two professional recommendations from individuals familiar with the applicant's scientific ability.

*Note: In all cases, accompanying letters must be on official stationery. They need to be signed, scanned and submitted via email as a JPEG, GIF or PDF attachment.*

*Selection and notification*

A Fellowship Committee constituted by the GCP Management Team and including the Principal Investigator (PI) of the related GCP project will assess applications and select the ones to submit a full proposal. Criteria for selection are: scientific suitability of the applicant and likelihood of application of the learning experience to further GCP-related work at the home institution or country.

Candidates qualified for the second stage will be contacted by e-mail on January

10<sup>th</sup> 2008 and requested to prepare a full proposal.

### *Language*

Applications may be in English, French or Spanish.

### *2) Full proposal requirements:*

- a) A research proposal, which must be elaborated in collaboration with the PI (host) of the related GCP project, as reflected in the research subjects. The proposal must also adhere to the [Fellowship guidelines](#).
- b) Duly filled application form for full proposals (to be sent by e-mail), and
- c) A letter of acceptance and commitment from the proposed host institute and endorsement by the host researcher confirming the proposal is acceptable, ie, has been mutually agreed upon by the host researcher, applicant and applicant's home institution.

### **Important notes:**

1. Submitting a full proposal does not guarantee a fellowship award.
2. **Bench fees will not be covered for [Consortium](#) member institutions.**
3. All applications and full set of supporting documents must be submitted as e-mail attachments to Ms. Laura Ruiz, SP5 Programme Assistant, at [l.ruiz@cgiar.org](mailto:l.ruiz@cgiar.org).
4. Deadline for submitting Full proposals: **31<sup>st</sup> January 2008.**
5. The Fellow may be invited to participate in the Annual Research Meeting of the Generation Challenge Programme.
6. The Generation Challenge Programme reserves the right not to select a fellow if applicants do not meet the criteria for the fellowship.

### **Reporting requirements**

1. *Technical reports:* The fellow will be required to submit an interim progress report halfway through the fellowship and a full final report at the termination of the Fellowship. Both interim and final reports must be accompanied by a duly completed [Appendix A](#)<sup>4</sup> in each case.
2. *Finances:* *Financial statements, certifying funds have been spent on intended purpose, must accompany both the interim and final technical reports.*
3. *Supervisor approval:* The supervisor (hosting scientist) must endorse the technical and financial reports by either signing them, or by submitting them directly to GCP.

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<sup>4</sup> For reporting purposes, Appendix A must be updated as the project produces new outputs.