ERA-NET PLANT GENOMICS

ERA-PG Research Programme

Report 2007

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Publication prepared by
Catarina Resende, FCT, Portugal
Paul Beckers, NGI, The Netherlands
Christine Bunthof, NGI, The Netherlands

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ERA-PG managing office
C/o Netherlands Genomics Initiative
P.O. Box 93035
2509 AA The Hague
The Netherlands
Tel. +31 70 3440672
E-mail office@erapg.org

More information about the ERA-NET Plant Genomics is available at the ERA-PG website:
www.erapg.org

Foreword

This booklet is issued on the occasion of ERA-PG's first Grantholders Meeting to be held in Tenerife on October 2nd, 2007.

ERA-NET Plant Genomics (ERA-PG) is a network of currently eighteen research funding organisations from sixteen countries, supported by the European Commission under the ERA-NET scheme of the 6th Framework Programme. ERA-PG was established in 2004 with the mission to build a European Research Area in plant genomics by creating a stimulating and fruitful environment for European plant genomics together with the scientific community. By bringing together national programmes, ERA-PG tries to build a strong knowledge base to strengthen European competitiveness.

Aiming at collaboration, scientific excellence, synergy and cohesion, ERA-PG launched its first joint call for proposals in the beginning of 2006 under the title 'Structuring Plant Genomics Research in Europe'. With a substantial budget of over 35 M€ it is one of largest coordinated transnational research programmes in the ERA-NET scheme.

This booklet describes the process of the first call and presents abstracts of the 29 projects that finally have been rewarded on the basis of scientific excellence and consortium strength. The ERA-PG network congratulates its first group of grantholders with the high quality of these collaborative projects. With the first call of ERA-PG widely perceived to be a great success, we are convinced that the projects as well as the networks formed between researchers and between funding organisations will further contribute to the achievement of true coordination of European national ambitions.

With a second joint call in preparation to be launched in the beginning of 2008, ERA-PG will continue to build solid and sustainable transnational collaborative partnerships, aiming towards integrating plant genomics research even at a global level.

ERA-NET Plant Genomics
September 2007

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1. Summary

ERA-PG is a collaborative network of currently eighteen funding organisations initiated under the ERA-NET instrument of the sixth Framework Programme of the European Commission. The goal of the network is to contribute to the development of the European Research Area and to build a strong knowledge-base in Europe to strengthen the competitiveness in plant genomics.

Aiming towards collaboration, scientific excellence, synergy and cohesion, ERA-PG developed its first joint call for research '***Structuring Plant Genomic Research in Europe***'. The call, launched on February 1st, 2006, was addressed to plant genomic researchers in Belgium (Flanders), Denmark, Finland, France, Germany, Italy, The Netherlands, Norway, Portugal, Spain and United Kingdom. With a budget of over 35 million euros this is one of the largest coordinated multinational research programmes in the ERA-NET scheme.

The call was divided into two sub calls. Sub Call A; '*Broad Call for Publicly Funded Research in Plant Genomics*', and Sub Call B; '*Trilateral Partnership and beyond; the Future for European Public-Private Partnerships in Plant Genomics*'. Under Sub Call A, 70 proposals were submitted, by consortia of three to eight institutes, involving in total 342 applicants. 15 Projects were selected and granted with in total 21 M€. Under Sub Call B, 36 project proposals were submitted, by consortia up to 16 partners, involving in total 247 applicants, of which one out of three were companies. 14 Projects were selected and granted with in total 17 M€.

Grants were awarded using a jointly administrated pot model. In this model there is one central secretariat. Evaluation and selection are centrally organized following commonly agreed procedures, and consortium agreements and IPR conditions are developed transnationaly. The grants do not cross borders; the consortium members are awarded according to national funding rules by the agency from their own country.

New to many was the opportunity given to the applicants to provide a rebuttal to the (anonymous) peer review reports. The research projects started from March 2007 onwards and the first grantholders meeting is held during PlantGEMs, on 2nd October 2007, at Tenerife, Canary Islands, Spain.

Developing an ERA-PG call with minimal bureaucracy and maximum transparency with twelve different funding agencies and ministries participating was a challenge. Implementing the first call was a valuable experience and the success of the process provides a strong basis for continued collaboration. The network now aims to further establish a transnational funding programme in plant molecular science, transcending

national and where appropriate European boundaries, as efficiently as possible.

2. ERA-NET Plant Genomics

The development of the first call was a major activity of the ERA-NET Plant Genomics, a Coordination and Networking Action supported by the Sixth Framework Programme of the European Commission. The creation of a European Research Area (ERA) was launched as a major strategic goal by European heads of state and government at the Lisbon Council in March 2000. A major element of the specific FP6 programme '*Integrating and strengthening the European Research Area*' is the ERA-NET scheme, designed to provide targeted support for the coordination and co-operation of national and regional research programmes. The productive experience of bilateral and trilateral cooperative European projects in plant genomics provided a strong basis for extending the activity under this new scheme, and the ERA-NET Plant Genomics (ERA-PG) was one of the first of these coordination actions to be funded. It started in 2004 as a network of twelve national and regional funding organisations. In 2005 five more members joined the network. For further details see www.erapg.org. ERA-PG has been very successful in unifying its members and also in providing information for scientists and policy makers in the area of plant genomics research. It is now in the remit of ERA-PG to continue this coordination and cooperation by implementing joint calls. The ultimate goal of the network is to have a fully integrated European plant genomics programme where all partners can participate on an equal footing.

3. Purpose of the Call

The ERA-NET Plant Genomics' first call for proposals, *Structuring Plant Genomic Research in Europe*, came into effect on February 1st 2006. Twelve funding organisations jointly provide funds in the order of 35 million euros to support the call. The joint ambition of the funders is to increase synergies between research teams around Europe and to increase the quality as well as the competitiveness of plant genomics research in Europe. In order to achieve the ambitions of ERA-PG, both scientifically and in terms of funding agency cooperation, the call had overarching themes described in section 5, which address the common priorities identified in the ERA-PG Planning Workshop (June 2005, Norwich) and the ERA-PG survey in 2004 described in the report

'*Plant Genomics Research in Europe*' (2005). The topics are also clearly in alignment with the objectives of other strategic groups in plant science currently active in Europe, including the European Technology Platform Plants for the Future. There is no central EU funding support for collaborative research between national genomics programmes. The ERA-PG network aims to establish a transnational funding programme in plant genomics, transcending national boundaries, as efficiently as possible and with minimal bureaucracy.

4. Call Structure

The ERA-PG network consisted at the beginning of 2006 of seventeen funding organisations, of which twelve participate in the call (Table 1). These twelve funding organisations (of eleven countries) preliminary allocated a budget in the order of 30 million Euros to support the call. Individual country commitments and specific national procedures to complement the information in the Call Notice were published in National Annexes. Each national funding organisation only awarded grants to the project participants from its own country.

Structurally, the call was divided into two Sub Calls:

- Sub Call A: Broad Call for Publicly Funded Research in Plant Genomic;
- Sub Call B: Trilateral Partnership and beyond; the Future for European Public-Private Partnerships in Plant Genomics.

This is in order to satisfy the diversity of priorities and strategic ambitions of the partner countries of ERA-PG. The academic Sub Call (A) was open for applications from researchers from nine countries; Belgium, Denmark, Finland, Italy, Netherlands, Norway, Portugal, UK and Germany. Additional research partners from other countries, including industrial partners, were welcome provided that they would bring their own funds and demonstrating true added value to the partnership. The public-private Sub Call (B) built upon positive experiences of the partners of the trilateral initiative between France, Germany and Spain and funds of BMBF, MEC and ANR are exclusively devoted to Sub Call B. Three other partners, BBSRC, FCT and AKA, were keen to support research teams from their country participating in Sub Call B projects. Thus, researchers from six countries (France, Germany, Spain, UK, Portugal and Finland) could apply for grants within Sub Call B. This Sub Call was also open to additional research partners bringing their own funds and demonstrating true added value to the partnership.

Table 1. ERA-PG members and their participation to the first call.

Country	Organisation	Sub Call A	Sub Call B
Belgium (BE):	Flemish Government, Dept. of Economy, Science and Innovation (EWI)	x	
Denmark (DK):	Danish Agency for Science, Technology and Innovation (DASTI)	x	
Finland (FI):	Academy of Finland (AKA)	x	x
France (FR):	National Research Agency (ANR)		x
Germany (DE):	Federal Ministry of Education and Research (BMBF)		x
Germany (DE):	German Research Foundation (DFG)	x	
Italy (IT):	Ministry of University and Research (MUR)	x	
The Netherlands (NL):	Netherlands Genomics Initiative, Netherlands Organisation for Scientific Research (NGI/NWO)	x	
Norway (NO):	The Research Council of Norway (RCN)	x	
Portugal (PT):	Foundation for Science and Technology (FCT)	x	x
Spain (ES):	Ministry of Education and Science (MEC)		x
United Kingdom (UK):	Biotechnology and Biological Sciences Research Council (BBSRC)	x	x
Austria (AT)	Federal Ministry of Education, Science and Culture (BMBWK)	These ERA-PG partners did not participate to the first call for proposals	
Israel (IL)	Ministry of Agriculture and Rural Development (MOARD)		
Sweden (SE)	Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning (FORMAS)		
Switzerland (CH)	Swiss National Science Foundation (SNF)		

The total preliminary allocated budget was about 31.5 million euros; the total budget finally granted is summing up to 38.5 million euros, 20 percent higher than the preliminary allocations. In addition, the contribution from companies in the form of own budget is estimated at about 4 million euros, making the total programme an investment in European plant genomics of more than 40 million euros.

A total of 29 projects were granted, 15 within Sub Call A and 14 within Sub Call B (Table 2). Even though some national budgets were raised, the ERA-PG members could not fund all the projects that the Programme Board had recommended. Only the very best were granted. Most of the applications which qualified as sub-top were rejected, along with the (small) number of projects which the Programme Board did not recommend for funding.

Table 2. ERA-PG members and their participation to the first call.

Country	Organisation	Preliminary allocated budget [€]	Final granted budget [M€]	Granted projects	
				Sub Call A	Sub Call B
BE	EWI	300.000	300.000	2	
DK	DASTI	2.000.000	1.940.800	4	
FI	AKA	1.000.000	1.210.380	5	
FR	ANR	2.500.000	3.181.305		14
DE	BMBF	6.000.000	8.042.153		12
DE	DFG	4.000.000	4.667.070	14	
IT	MUR	3.000.000	2.336.340	6	
NL	NGI/NOW	2.000.000	2.053.660	8	
NO	RCN	375.000	336.000	2	
PT	FCT	300.000	876.872	2	3
ES	MEC	3.000.000	4.241.000		14
UK	BBSRC	7.000.000	9.366.662	13	1
Total		**31.475.000**	**38.552.242**	**15**	**14**

5. Research Themes

The headline topics of the call were broad and inclusive, addressing common issues. Scientific approaches had to be genomic and/or post-genomic in nature and not primarily address the elucidation of function of single genes. A combination of various genomics and quantitative genetics tools should be employed. Within this framework the opportunity was given to emphasise specific activities in defined collaborations and in the context of two Sub Calls.

Research Themes for Sub Call A

- Genomic approaches to adaptation and acclimation to abiotic stresses
- Genomic approaches to adaptation and acclimation to biotic stresses
- Yield stability of plants
- Intrinsic genetic potential of plants including natural variation and biodiversity
- Crop breeding
- Development of crop and forage plants for low input systems including protein crops for Europe and crops for animal feed
- Quality traits including traits associated with food storage and processability, quality modification for foods and feeds, specialised uses of crops

- Genomic research into non-food uses for crops including; trees for fuel and fibre production; other plant sources of fuel, fibre and biodegradable packaging materials; bioproduction of therapeutics and other nutraceuticals
- Joint development of genomic tools (technologies and resources), where this addresses and supports the overall scientific objectives of ERA-PG
- Other topics are also suitable that contribute to the development of the European Research Area in plant genomics.

Plants under investigation can be reference/model plants as well as crops including ornamentals, trees and forage plants. The consortia were asked to indicate which themes were addressed by their application.

Research Themes for Sub Call B

- Improved quality in food and feed
- Sustainable agriculture with improved productivity and yield stability under low input production systems and under biotic and abiotic stress
- Plants for innovative uses such as energy crops or plants as factories
- Plants to improve and stabilize our environments

The research themes for Sub Call B were defined in a consultation between BMBF, MEC and ANR and address application oriented research under the headline 'Genomics approaches for the investigation of genetic diversity in crop plants and its use for innovation'. Corresponding research projects should be based on a combination of genomics and quantitative genetics tools, tackle global or regional challenges, and should be oriented at crop species with high agronomic as well as economic relevance for the partners of the *Trilateral Initiative*.

6. Organisation

The call procedures are developed and managed by a joint team of national Call Coordinators supported by a central Call Secretariat. There is one common Programme Board of independent experts in charge of the evaluation of the proposals of both Sub Calls and one peer-review process of full proposals. The Sub Call specific Moderating Panels addressed budgetary issues (for Sub Call A) or budgetary and strategic issues (for Sub Call B), after which the final funding decisions rested with the corresponding national authorities. The organizational structure is shown in Figure 1.

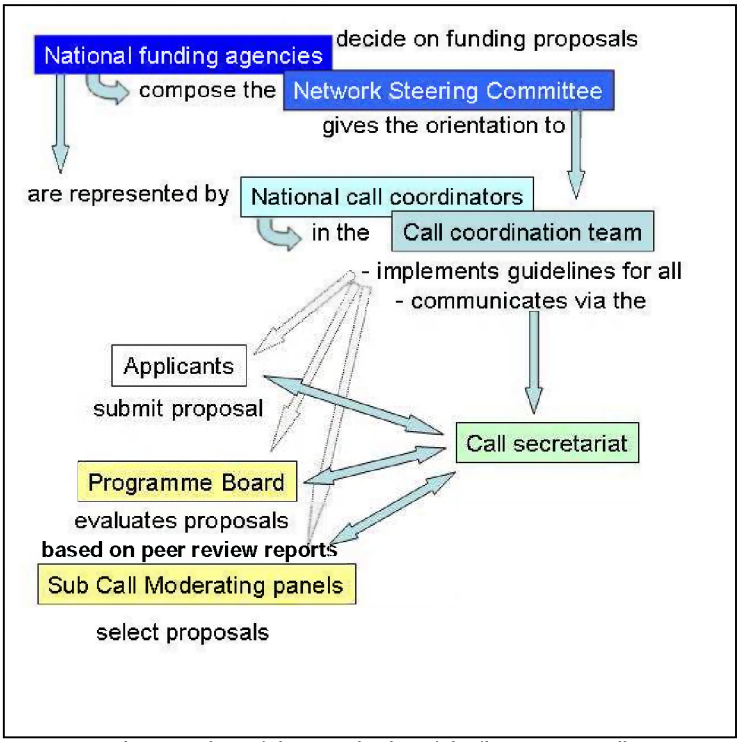


Figure 1. Chart of the organisation of the first ERA-PG call

7. Procedures

A two-stage application and selection procedure was used as for effectiveness and efficiency. The split-up in two stages is schematically drawn in Figure 2. The procedure includes pre-proposals assessed by a scientific advisory panel followed by full proposals of invited consortia, with peer-review by international experts, the opportunity for consortia to provide a rebuttal on the evaluation reports, and assessment by the Programme Board who rated and ranked the full proposals after which Moderating Panels made the funding recommendations to the national funding organisations.

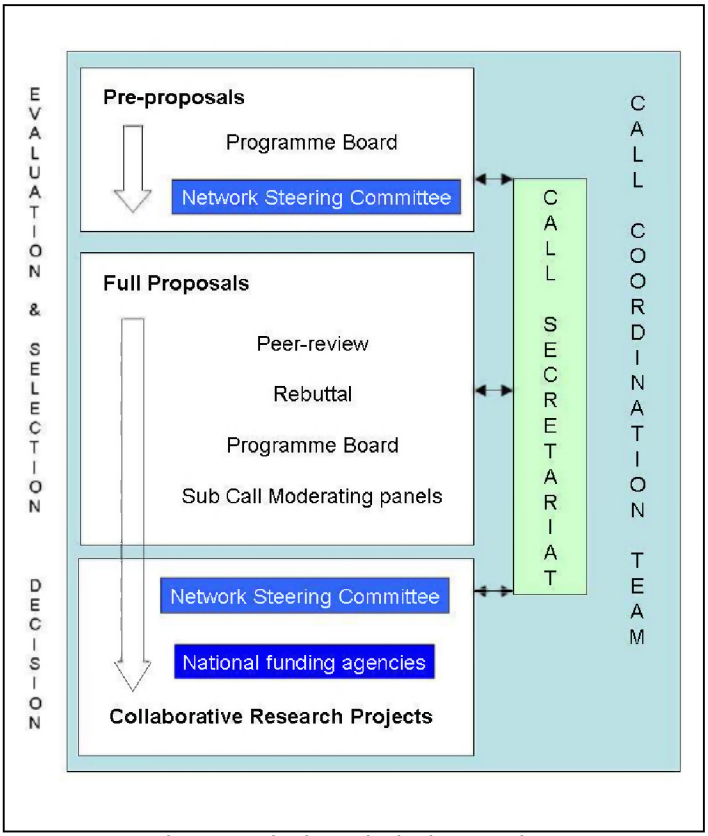


Figure 2. Evaluation and selection procedure

The application had to be submitted by the main applicant of the collaborative research consortium to the central call secretariat in electronic form, and follow the Guidelines for Application. A pre-proposal had to contain a short description of the joint project (maximum 4 pages), an estimate of costs and CV's and publication lists of the main applicant and all co-applicants. The pre-proposals were assessed by the Programme Board. A two-day meeting was held for the Board to group the pre-proposals and to reach a consolidated decision about their recommendations.

Within Sub Call A the joint funding bodies invited 44 of the 70 pre-proposals to submit a full proposal. These selected applications qualified 'Excellent' or 'Very Good' and represented a total requested budget of three times the budget allocated. Within Sub Call B 33 applications that met the formal criteria were invited. These requested more than twice as much budget

as allocated. Four pre-proposal applications, which were insufficiently matching the eligibility or selection criteria, were left out at this stage.

The full proposals had to contain a detailed project description (maximum 12 pages) including background, milestones, deliverables, coordination and plan for use and dissemination of knowledge. Furthermore, the full proposals had to contain a breakdown of costs per partner including requested and own contribution, with explanations, and for some funding agencies also specifications according to national funding rules.

The full proposals were evaluated by external reviewers coming from within as well as outside Europe. With inputs from the programme board members and the call coordinators a database of approximately 500 experts from 35 countries was composed for this purpose. Each proposal was evaluated by three to five external reviewers. After receiving the evaluation reports from the reviewers, the Call Secretariat sent them, anonymously, to the main applicant who could, on behalf of the consortium, give comments.

The Programme Board performed the assessment of full proposals based on the evaluation reports of the external reviewers, taking into account the rebuttals where appropriate, and with the benefit of their individual expertise. In October 2006 the second meeting of the Programme Board took place, to consider the assessments of the full proposals and bring the members to a consolidated decision about their recommendation. As the first Board meeting, it was organised and managed by a team consisting of the ERA-PG coordinators, the Call Secretariat and three of the Call Coordinators. The recommendations of the Programme Board were presented to the Sub Call Moderating Panels, who took into account budgetary considerations (for Sub Call A), and budgetary and strategic considerations (for Sub Call B). The funding recommendations reached by the Panels were communicated to the national funding bodies who take the national funding decisions. After all decisions for a specific project were taken, the main applicant was informed by the Call Secretariat. Finally, all applicants received a grant award announcement from their national organisation.

8. Evaluation Criteria

The proposals were evaluated according to the following criteria:

- Novel, innovative research within the scientific scope of the call and innovative potential of the expected results for industrial application where appropriate
- Scientific merit and feasibility of project
- Transnational added value and complementarity of expertise

- Scientific track record of applicants
- Evidence of true cooperation within the collaboration
- Economic, societal and environmental relevance
- Adequateness of used resources and financial requirements.

9. Time Schedule

The call was pre-announced 15th December 2005 to give interested scientists extra time to form international consortia and start preparing their collaborative research project. As shown in the time schedule (Table 3), the procedure from call announcement (1st February 2006) till funding recommendation to the national funding organisations (10th October 2006) took less than nine months. The majority of consortia could be informed about the final national funding decision in February 2007. The last national decisions were taken in May 2007. All projects started within the calendar year 2007.

Table 3. Time schedule of the first call

Step	Due date
Call announcement:	1st February 2006
Due-date pre-proposals:	16th March 2006, 12.00 CET
First meeting of Programme Board	19th – 20th April 2006
Communication of evaluation results:	5th May 2006
Due-date full proposals:	29th June 2006, 12.00 CET
Second meeting of Programme Board	8th – 9th October 2006
Communication of evaluation results:	November 2006
Start of selected projects:	March – November 2007

10. Success Rate

The plant genomics scientific community responded to the call with a total of 107 pre-proposal applications. One was not eligible, leaving 106 eligible applications to be considered. All major institutes and universities that conduct plant genomics research are represented, often multiple times and by different research groups.

The pre-proposals grant applications oversubscribed the allocated budget for all participating funding bodies. The lowest subscriptions were for BMBF (Germany) and MUR (Italy) where the ratio of requested and allocated was about 3. The highest was for FCT (Portugal) where 16 applicants applied for

nine times more budget than allocated. In absolute number the UK applicants oversubscribed the most to BBSRC oversubscribed the most by requesting 31 million euros by 82 participants in 55 projects. Overall the 106 applications requested five times as much budget as preliminary allocated (Figure 3).

Within Sub Call A the success rates in terms of applications rewarded as well as applicants rewarded were about two out of ten (Figure 4). Within Sub Call B this rates were about four out of ten (Figure 5).

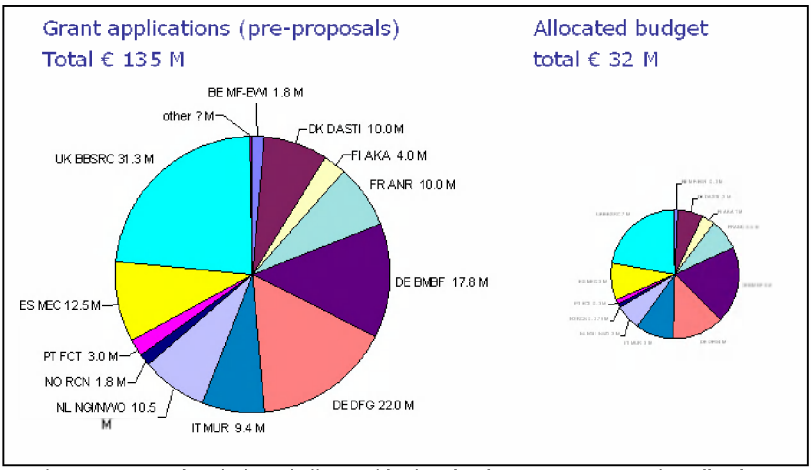


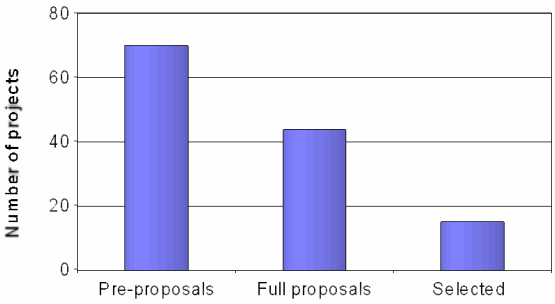
Figure 3. Oversubscription of allocated budget by the 106 pre-proposal applications

11. Applicants

Looking to all 106 applications at the pre-proposal phase, a research consortium consists on average of 5.2 partners, requesting on average 260,000 euros per partner. There were in total 517 researchers involved, of which 467, participated in one consortium and 50 individuals in more than one applications, making the total number of project applicants 589 (Table 4).

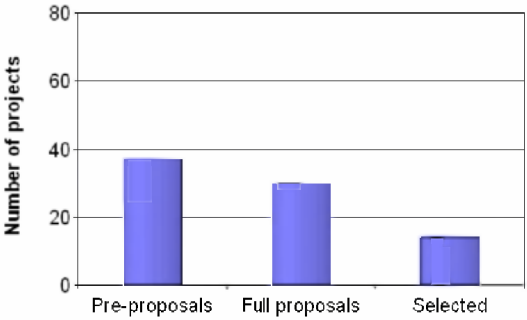
Sub Call A attracted in total 343 applicants from 20 countries, applying within 70 collaborative projects. Most consortia (60 %) consist of three or four partners (Table 5). The largest consortium consists of 11 partners from 11 different countries. The largest populations of applicants in the academic Sub Call A come from UK and Germany, then from The Netherlands, Italy and Denmark, followed by the other countries of funding

bodies contributing to this Sub Call. About 7 % of the applicants come from other countries (Table 6).



number of projects	**70**	**44**	**15**	**(21 %)**
number of applicants	343	219	79 (76)	**(22 %)**
number of institutions	130	89	44	
number of countries	20	18	10	

Figure 4. Success rate for Sub Call A applications



number of projects	**37**	**30**	**14**	**(38 %)**
number of applicants	242	212	111	**(46 %)**
number of institutions	136	124	72	
number of countries	11	11	8	

Figure 5. Success rate for Sub Call B applications

To the public-private sub call 242 applicants from 11 countries in 36 consortia responded. The consortia applying to the public-private sub call are generally a bit larger (average 6.1) than the ones applying to the academic sub call (average 4.7). In the PP Sub Call only 30 % of the consortia consist of three or four partners and there are four projects with more than ten partners, the largest being a project with 14 partners (Table 7). Obviously, most partners (92 %) in Sub Call B applications come from France, Germany and Spain. Notably, the numbers of applicants to funding organisations from these three countries are almost the same, while the budget allocated by BMBF is twice that of MEC and of ANR. About eight percent of the partners within the Sub Call B pre-proposals come from other countries (Table 8).

Table 4. Numbers of researchers in one or more applications

Nº of proposals/ researcher	Nº researchers
1	467
2	35
3	9
4	5
5	1
total	517

Table 5. Sub Call A consortium sizes.

Consortium size (nº of partners/ consortium)	Number of consortia
3	21
4	20
5	10
6	9
7	3
8	4
9	2
10	0
11	1
Total	70

Table 7. Sub Call B consortium sizes.

Consortium size (nº of partners/ consortium)	Number of consortia
3	6
4	5
5	7
6	4
7	7
8	1
9	1
10	1
11	3
14	1
total	36

Table 6. Number of applicants per country in Sub Call A applications.

Country	Nº of applicants	Applicants%
Belgium	12	3.5%
Denmark	31	9.0%
Finland	20	5.8%
Germany	82	23.9%
Italy	32	9.3%
Norway	8	2.3%
Portugal	11	3.2%
The Netherlands	43	12.5%
UK	81	23.6%
Austria	1	0.3%
France	6	1.7%
Ireland	1	0.3%
Hungary	1	0.3%
Israel	1	0.3%
Japan	1	0.3%
Russian Federation	1	0.3%
Spain	2	0.6%
Sweden	3	0.9%
Switzerland	4	1.2%
Chech Republic	1	0.3%
USA	1	0.3%
Total	*343*	*100.0%*

Table 8. Number of applicants per country in Sub Call B applications.

Country	Nº of applicants	Applicants%
Belgium	1	0.4%
Denmark	1	0.4%
France	67	27.7%
Germany	74	30.6%
Italy	3	1.2%
Portugal	8	3.3%
Spain	82	33.9%
Switzerland	1	0.4%
The Netherlands	2	0.8%
UK	2	0.8%
Vietnam	1	0.4%
Total	*242*	*100.0%*

12. Granted Projects Sub Call A

The Programme Board ranked all 44 submitted full proposals. The ERA-PG consortium granted the 15 highest ranked proposals with a total budget of nearly 21 million euros. Five of the granted projects are headed by a German coordinator, also five by a UK coordinator, three by a Dutch, one by a Danish and one by a coordinator from Finland. The consortia consist of research teams from 3 to 8 organisations, with an average of 4.8 organisations per project (Figure 6). The selected projects are listed with abbreviation, title, main applicant, consortium size and total granted budget in Table 9.

Table 9. List of granted projects of Sub Call A (abbreviation, title, PI, number of consortium partners, granted budget)

Abbreviation	Project title	Main applicant	Size	granted budget (€)
ACT	Genome wide analysis of auxin-cytokinin cross-talk	Prof. Y. Helariutta	3	976,494
ARelatives	Leveraging the genome sequences of two Arabidopsis relatives for evolutionary and ecological genomics	Prof. D. Weigel	8	2,263,398
BARCODE	Genomics-assisted dissection of barley morphology and development	Dr. R. Waugh	3	1,532,940
CISCODE	Conservation and diversity in transcriptional regulation of developmental processes in crop and model plant species	prof. G.C. Angenent	7	2,210,517
Effectoromics	Understanding host plant susceptibility and resistance by indexing and deploying obligate pathogen effectors.	prof. J.L. Beynon	4	1,295,221
EXBARDIV	Genomics-asisted analysis and exploitation of barley diversity	Prof. A.J. Flavell	7	2,020,953
MultiStress	Multiple stress responses and adaptations	Prof. J. Mundy	7	1,788,397
PLANT STEM CELL NETWORK (PSCN)	Integrated analysis of stem cell function in plant growth and development	Prof. J.A.M. Murray	5	1,950,060
PRECIAR	Proteomics analysis of endosomal compartments in *Arabidopsis*	Prof. G. Jürgens	6	939,059
RLPRLKs	RLP- and RLK-mediated innate immune responses in *Arabidopsis* and tomato triggered by pathogen-associated molecular patterns (PAMPs) and avirulence factors (AVRs)	Prof. P.J.G.M de Wit	8	1,919,664
Seeds for growth	Seeds for growth - Identification of transcriptional programs controlling seed growth and development from *Arabidopsis* to rice	Dr. A. Schnittger	3	717,450

STRESSNET	Regulation of the plant metabolic network during stress	Dr. A.R. Fernie	3	1,444,045
STRESSsRNA	Genome-wide analysis of short RNAs as modulators in dehydration stress tolerance using tolerant and genetic model systems	Prof. D. Bartels	3	895,638
TRANSLEG	Using translational genomics to underpin germplasm improvement for complex traits in crop legumes	Dr. L. Skøt	4	975,970
TRITOP	Thrips resistance in tomato plants	Prof. P.G.L. Klinkhamer	3	639,396

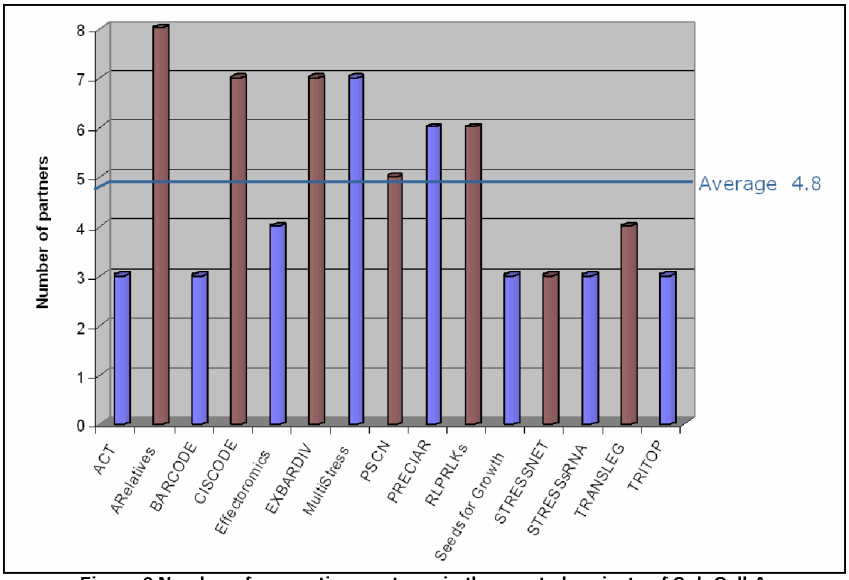


Figure 6 Number of consortium partners in the granted projects of Sub Call A

The themes of Sub Call A are listed in Table 10. The bars indicate the number of projects addressing each of the themes. Table 11 shows the themes for each individual projects in the order as indicated by the applicants. Many projects target biological questions on adaptation and acclimatisation of plants to stress conditions. Either specific abiotic or biotic factors imposing stress or multiple stresses are investigated. Also the study of intrinsic genetic potential of plants is a theme frequently addressed. The joint development of genomic tools is also an aim of many of the projects.

Table 10. Headline themes of Sub Call A and their frequency in the granted projects, including only the themes selected as number 1, 2 or 3 in the list on the full proposal application form.

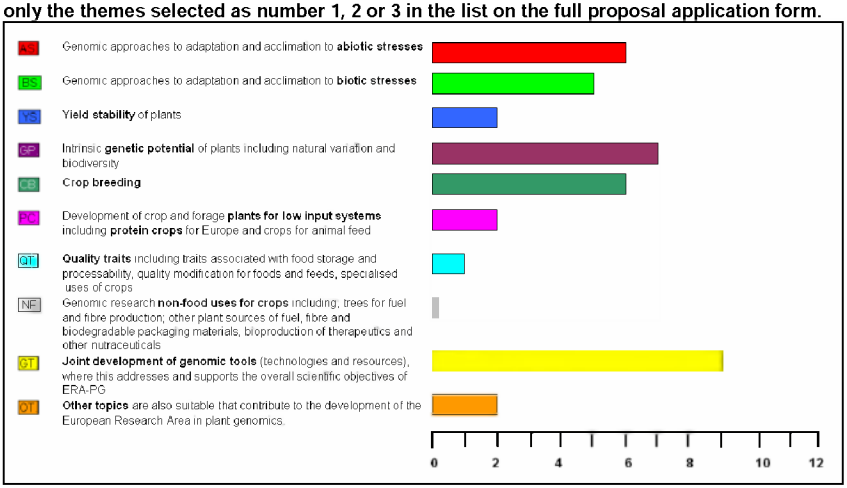


Table 11. Themes of the granted research project of Sub Call A

Project	Themes addressed
ACT	YS, GP, CB, NF, GT, OT
ARelatives	GT, GP
BARCODE	BS, GP, CB, GT
CISCODE	CB, GP, GT
Effectoromics	BS, GP, GT
EXBARDIV	GP, CB, GT, AS, BS
MultiStress	AS,BS, GT, GP
Plant Stem Cell Network	OT, AS
PRECIAR	OT
RLPRLKs	BS, AS, GT
Seeds for Growth	YS, CB, QT
STRESSNET	AS, BS, GT
STRESSsRNA	AS, GT, PC
TRANSLEG	PC, AS, GT
TRITOP	CB, BS, GP

Figure 7 shows the links between the projects and the countries where the participating institutions are located. The sizes of the circles representing the countries are proportional to the total granted budgets from the respective funding bodies. This is except for the Spanish researchers in PRECIAR and

RLPRLKs, since MEC is not taking part in Sub Call A; these consortia have used the option that teams of other countries were welcome to join a project on own costs and if this brought added value to the consortium. There are eight collaborations between three countries: Seeds for growth, ACT, STRESSNET, BARCODE, TRITOP, TRANSLEG, Effectoromics and STRESSRNA. Three of these three-partner collaborations are between UK, Germany and The Netherlands. PRECIAR unites groups from four countries.

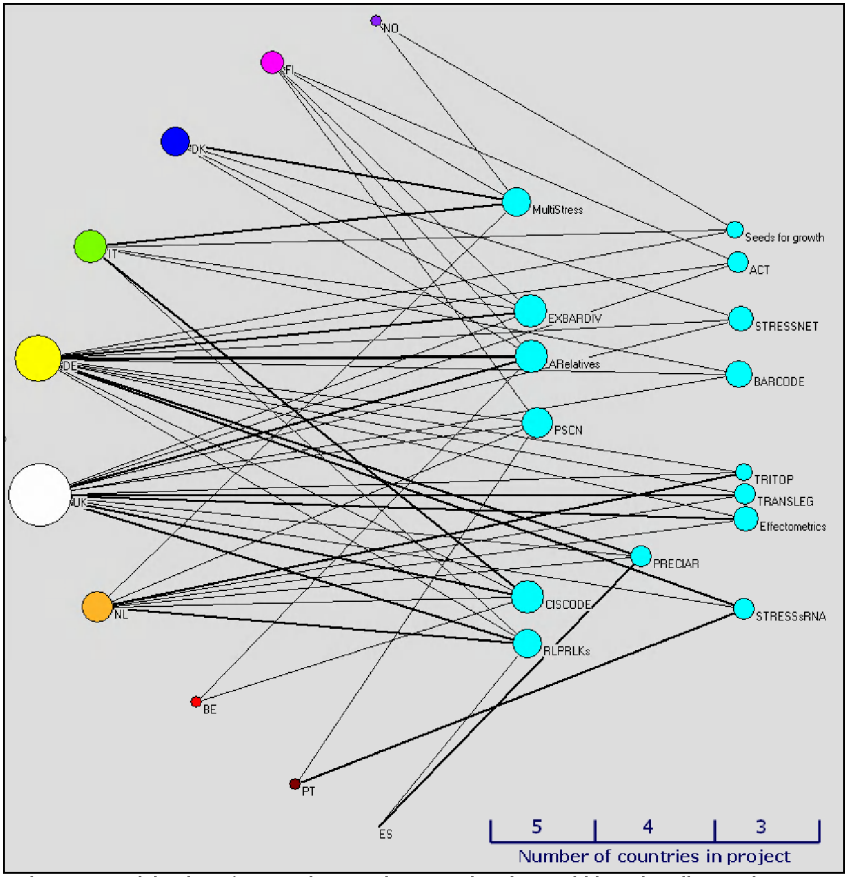


Figure 7. Participation of research teams in granted projects within Sub Call A. Projects are represented by aqua circles, with the size proportional to the total project budget. Countries of which the funding organisation is contributing to Sub Call B are represented by circles with size representing the total granted budget. Countries where project partners are located but no Sub Call A funding organisation are represented by dots. Lines connect the projects with the countries where the institutions are located. Thicknesses of lines represent number of partners from respective country.

The remaining six; MultiStress, EXBARDIV, ARelatives, PSCN, CISCODE, RLPRLKs, are collaborations between researchers from five different countries. In 10 projects some partners are from the same country, thus the number of countries is lower than the number of partners.

The total project budgets range from 0.6 million euros for project TRITOP to 2.3 million euros for ARelatives. The average total granted budget for a Sub Call A project is 1.47 million euros. Figure 8 shows the total budgets for each project, and the grants from the funding organisations involved for the researchers of the respective countries. Relative to the total budget BBSRC contributes almost 40 %, DFG over 20 %, DASTI, MUR and NWO about 10 % each and AKA 6 %. Contributions of FCT, RCN and EWI are about 1.5 %. It should be noted that the budgets are not directly proportional to the participation in person months due to differences between the countries in personnel costs and coverage of overhead costs by grants. Furthermore, most project partners give also an own contribution to the projects, such as time of project leader supervision the PhD student or postdoc, technical support and use of equipment. The average budget per grant holder is 330,000 euros.

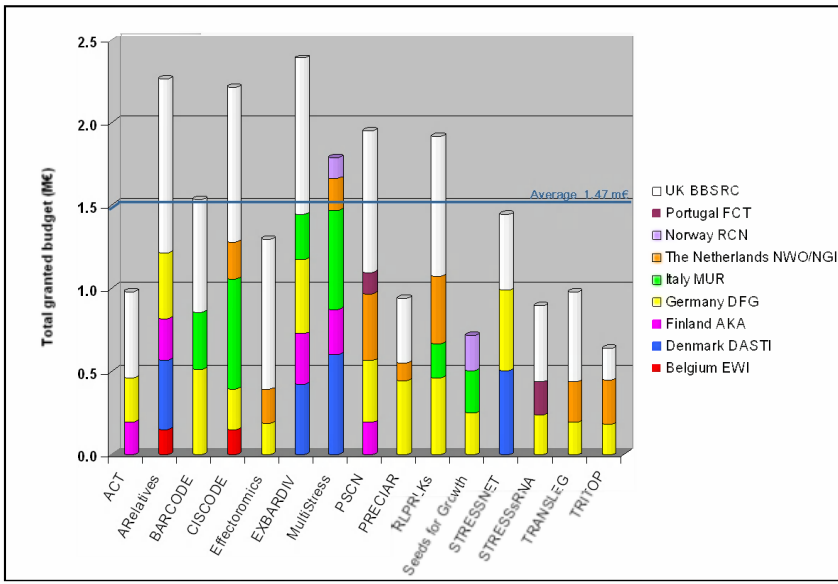


Figure 8. Budgets (M€) granted to the selected projects within Sub Call A.

13. Granted Projects Sub Call B

The Programme Board rated all 30 submitted full proposals, after which a moderating panel made a final funding recommendation. The ERA-PG consortium granted 14 proposals of which 13 public-private partnerships with a total budget of 16.6 M€. Six of the granted projects are headed by a German coordinator, five by a Spanish, two by a French, and one by a coordinator from the UK. The consortium sizes range from 3 to 16 partners, with an average of 7.9 organisations per project (Figure 9). Industry participation in the 13 PPPs ranges from 1 to 4 companies involved. The selected projects are listed with abbreviation, title, main applicant, consortium size and total granted budget in Table 12.

Table 12. List of granted projects of Sub Call B (abbreviation, title, PI, number of consortium partners, granted budget).

Abbreviation	Project title	Main applicant	Size	Granted budget (€)
ARABRAS	Identifying relevant candidate genes for improving plant growth under abiotic stress conditions in Brassica crops	Prof. M. Koornneef	7	897.677
BIOREGULATORS	Identification of molecular markers for the detection of bioregulators that enhance plant productivity and quality	P. Eckes	6	2.179.822
CEREHEALTH	Securing a sustainable production of food and feed ? a functional genomic-guided strategy for improving biotic stress tolerance in cereals.	Dr. G. Strittmatter	11	2.446.286
COGS	Comparative genomics of shoot branching	Prof. O. Leyser	6	1.073.006
EUCANET	Sustainable Fiber: Eucalypt genomics research for improved wood properties and adaptation to drought.	Dr. J. Grima-Pettenati	8	620.290
FIELD RESISTANCE IN RICE TO BLAST (FRRB)	Deciphering the genetic basis of field resistance to blast in European rice varieties to improve breeding for durable resistance	Dr. L. Marqués Falcó	7	433.222
FROSTY	New investigations of the CBF cold response pathway using natural variation, genetics, genomics and metabolomics	Dr. H.I. McKhann	5	827.519
GRASP GRAPE WINE	Genomic Research-Assisted breeding for Sustainable Production of quality GRAPEs and WINE - GRASP GRAPE WINE	Dr. E. Zyprian	16	1.546.496
LEGRESIST	LEGRESIST: Exploiting Genetic Variability of Resistance Genes in major European Food Legumes to Improve Varieties for Sustainable Agriculture	Dr. P.J. Winter	14	1.587.381
MELRIP	Understanding the climacteric vs non-climacteric fruit ripening mechanisms in melon using transcriptomic, metabolomic and reverse genetic approaches	Dr. J. Garcia-Mas	7	922.522

MUEXPRESS	Isolation of key genes for kernel development through the identification, in a collection of 300 mutant lines, of Mutator insertions in genes expressed in the maize seed	Dr. G. Hueros	4	703.556
PROTEIN STORAGE	An integrated genomic and proteomic characterization of induced seed storage organelles for the optimal production of biopharmaceuticals in plants and plant cells (Acronym: ProteinStorage)	Prof. P. Christou	7	808.107
RCA GENOMICS	International reference center for the genomics and diagnosis of viruses with small circular DNA	Prof. H. Jeske	4	1.031.039
TRIESTER	TRIESTER: Trilateral Initiative for enhancing salt tolerance in rice	Prof. B. San Segundo	9	1.485.317

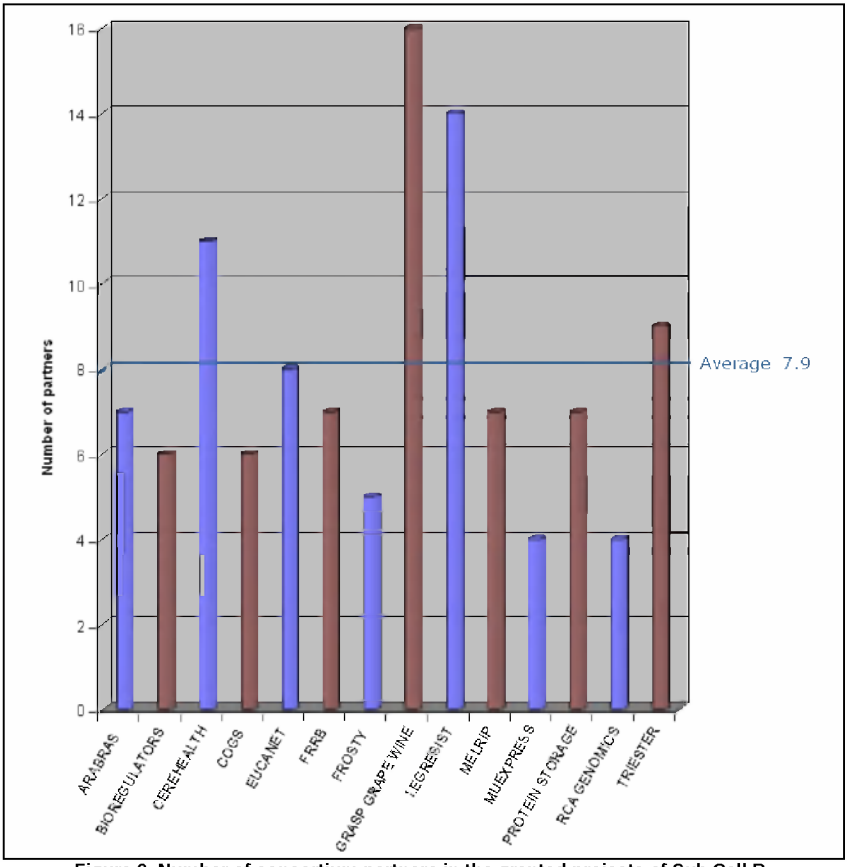


Figure 9. Number of consortium partners in the granted projects of Sub Call B.

The themes of Sub Call B are listed in Table 13. In Table 14 the ticked themes, up to three in the full proposal form, are listed per project. All but two projects target a subject under the broad headline 'Sustainable agriculture with improved productivity and yield stability under low production systems and biotic and abiotic stresses'. The other headline topics, improved quality, innovate use of plants, and plant improving our environment, are indicated less often. The projects focus on a number of different crops, such as rice (FRRB, TRIESTER), maize (CEREHEALTH, MUEXPRESS), grapevine (GRASP GRAPE WINE), melon (MELRIP), legumes (LEGREST), rapeseed (ARABAS), and Eucalyptus (EUCANET, FROSTY). The projects BIOREGULATORS, COGS and PROTEIN STORAGE apply a number of species studying metabolism, plant development. RCA Genomics works on diagnosing viruses. At least five projects employ the model species *Arabidopsis* within their projects.

Table 13. Headline themes of Sub Call B and their frequency in the granted projects, including only the themes selected as number 1, 2 or 3 in the list on the full proposal application form.

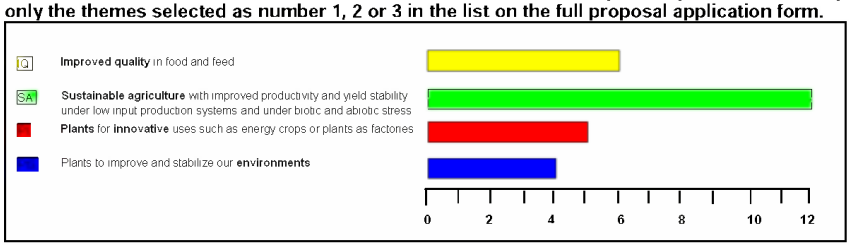


Table 14. Themes of the granted research projects of Sub Call B.

Project	Themes addressed
ARABAS	SA. PI.
BIOREGULATORS	IQ. SA. PI.
CEREHEALTH	IQ. SA.
COGS	SA. PI.
EUCANET	SA.
FRRB	SA.
FROSTY	SA.
GRASP GRAPE WINE	SA. IQ.
LEGRESIST	SA. IQ.
MELRIP	IQ.
MUEXPRESS	IQ. SA.
PROTEIN STORAGE	PI.
RCA GENOMICS	SA.
TRIESTER	SA.

Figure 10 shows the links between the projects and the countries where the participating institutions are located. The sizes of the circles representing the countries are proportional to the total granted budgets from the respective funding bodies. This is except for The Netherlands, Italy and Switzerland. Researchers from these countries participate in Sub Call B projects without an ERA-PG grant. The number of partners from one country within projects range from 1 (thinnest lines) to 7 (thickest line).

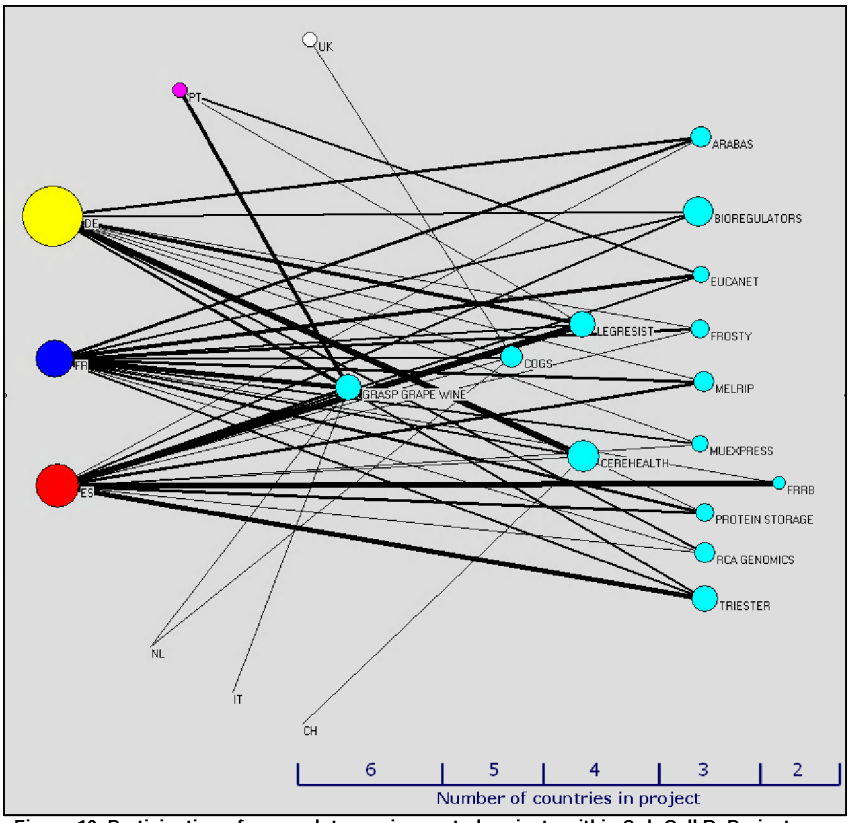


Figure 10. Participation of research teams in granted projects within Sub Call B. Projects are represented by aqua circles, with the size proportional to the total project budget. Countries of which the funding organisation is contributing to Sub Call B are represented by circles with size representing the total granted budget. Countries where project partners are located but no Sub Call B funding organisation are represented by dots. Lines connect the projects with the countries where the institutions are located. Thicknesses of lines represent number of partners from respective country.

FIELD RESISTANCE OF RICE TO BLAST (most right blue circle) has seven partners, but only from two countries: Spain and France. GRASP GRAPE WINE has partners from six different countries, of which two on own budget, COGS from five, and LEGRESIST and CEREHEALTH from four. The rest of the projects, nine in total, all have partners from only the trilateral countries; Germany, France and Spain.

The total granted budgets for the projects range from 0.4 million euros for FRRB (7 partners) to 2.4 million euros for CEREHEALTH (13 partners). The two very large consortia, GRASP GRAPE WINE with 16 partners and LEGREST with 14 partners receive total grants of about 1.6 million euros. The average total project budget is 1.18 million euros. Budgets are not directly proportional to the participation in person months due to differences in grant systems and own contributions from academic as well as industrial partners. BMBF is the largest contributor to the projects, providing nearly half of the total granted budget. Then, 25 % comes from MEC, 20 % from ANR and both 3 % from UK (1 grantholder), and from Portugal (7 grantholders in three projects of which 2 companies). Grants to industrial partners, 31 in total, are between 5.000 and 770.000 euros with an average of 122.000 euros, grants to academic partners are on average 162.000 euros.

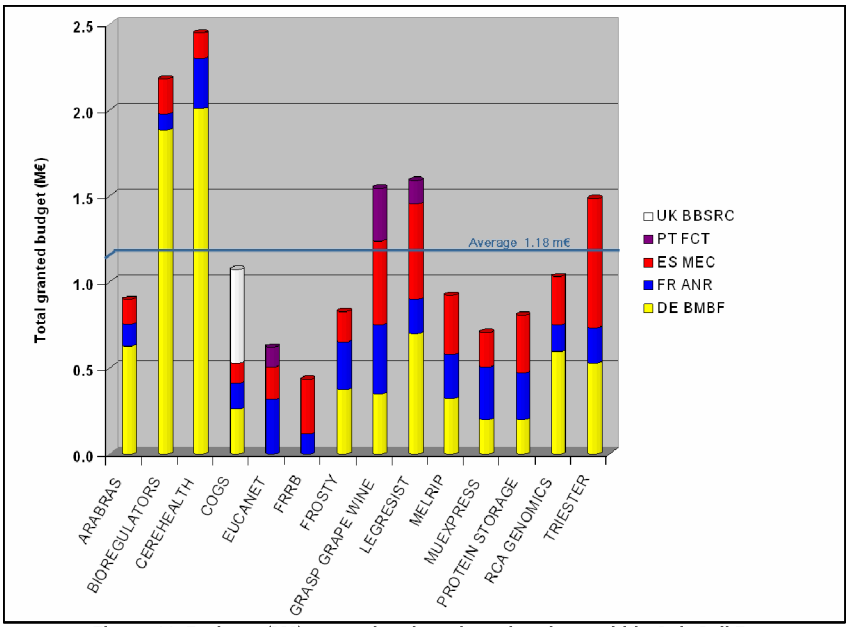


Figure 11. Budgets (M€) granted to the selected projects within Sub Call B.

14. Programme Management

For networking the researchers involved in the programme, as well as to create a forum for researchers, industry, and funding organisations grantholders meetings are organised. The first meeting is held at the 2nd of October 2007, at PlantGEMs, at Tenerife. At this time projects have just started. The second grantholders meeting is preliminary scheduled for September 2008, and the third grantholders meeting for the projects of the first call is foreseen for 2010, when the projects end.

The joint funding organisations will request two progress reports during the duration of the project; at mid-term (18 months after the start of the project) and at end-term. The reports should follow the reporting form and be submitted to the central Call Secretariat. Besides the central reporting, each funding body may request additional progress reports.

Financial reporting is handled on the national level. Each grantholder should provide financial reports according to the rules of their funding organisation.

An international evaluation commission will be installed in due time for monitoring of the programme.

Genome wide analysis of auxin-cytokinin cross-talk (ACT).

Y. Helariutta (University of Helsinki, Finland), O. Leyser (University of York, UK), J. Friml (University of Tübingen, Germany).

Plant hormones have a major role in regulating virtually all aspects of plant physiology. Alterations in hormone distributions and responses have also been responsible for several important agricultural advances, such as the breeding of semi dwarf varieties and increased grain production. In recent years it has become apparent that, in comparison to animal hormones, plant hormones rarely act alone, but rather their signalling pathways are interlocked in complex networks. A prime example is in the interactions between auxin and cytokinins, which are classes of plant hormones that play a particularly important role in regulating plant development. Both hormones act as signals for cell division, cell elongation and cell differentiation in various developmental contexts and often regulate the same developmental process in an antagonistic manner. Despite the obvious importance of the interactions between hormonal pathways, relatively little progress has been achieved in identifying the mechanisms or molecular components that mediate their cross-talk. We feel that with recent advances of our knowledge on the molecular mechanisms of plant hormone action and with genome-wide tools in Arabidopsis, it is now possible to address this issue successfully. In this proposal we plan to elucidate the molecular mechanisms underlying auxin and cytokinin interaction in different developmental contexts.
We bring together European world-class research expertise in auxin and/or cytokinin research focused on three developmental contexts: (1) shoot branching, (2) root branching and (3) vascular morphogenesis. From our work so far on different developmental process we have generated number of tools and materials, which will be shared and systematically tested in all studied processes; our groups have highly complementary specialist expertise in the core genomic and post-genomic technologies needed for the project: (1) cell sorting-coupled microarrays, (2) bioinformatics, (3) cell biology, which will be shared and further developed to achieve our objectives. As the complexity of our studied problem is far too high to allow intuitive interpretations, we plan to generate a mathematical model(s), which will serve as platform to describe the interactions of other signalling pathways. From the analysis of auxin and cytokinin interactions at the molecular level in three parallel systems we aspire to build a conceptual framework and genomic resources for further analyses of the role of the hormonal control of plant development and productivity. As the crosstalk between auxin and cytokinin is a central determinant of plant development and architecture, these aims are of direct

relevance to multiple research themes of the current call related plant productivity. Furthermore, especially through our cell biological approach we will develop new tools for genome wide analysis in plants cultivars. This will allow us to determine the efficiencies of identification and extraction of useful alleles in barley breeding programs based upon wide crosses. Our third major project objective is to use the huge DNA and marker data set obtained in the project to determine important population genetic parameters for barley.

Leveraging the genome sequences of two Arabidopsis relatives for evolutionary and ecological genomics (ARelatives).

D. Weigel (MPI for Developmental Biology, Germany), D. Charlesworth (Univ. of Edinburgh, UK), M. Lenhard (Univ. of Freiburg), B. Mable (Univ. of Glasgow, UK), B.Neuffer (Univ. of Osnabrück, Germany), O. Savolainen (Univ. of Oulu, Finland), M. Schierup (Univ. of Aarhus, Denmark), Y. van de Peer (Ghent Univ., Belgium).

The overall strategic objective of ERA-PG is to build links between leading research teams and to boost the overall competitiveness of plant genomics in Europe. This proposal brings together some of the very best European scientists in the areas of evolutionary and ecological genomics, including junior and senior groups. Understanding the forces driving plant evolution is an essential prerequisite if we want to comprehend the mechanisms underlying plant adaptation. This, in turn, will enable the more efficient breeding of crops that are better adapted to the environment. Thus, the present proposal will make fundamental contributions to achieving the various specific objectives of the ERA-PG.
The ARelatives Consortium will exploit the impending completion of two new plant genome sequences, those of Arabidopsis lyrata and Capsella rubella, currently under way at the Joint Genome Institute of the US Department of Energy (http://www.jgi.doe.gov/CSP/). Although this multi-million dollar project is funded entirely by the US government, members of this ERA-PG team have played key roles in developing this project, with the main ERA-PG applicant having previously taken the lead in preparing the DOE-JGI proposal. We now propose to use ERA-PG resources to leverage the information generated by DOE-JGI, both through bioinformatic analyses that address questions of selection and adaptation on a genome-wide scale, and through functional genomic, genetic and ecological avenues that will provide experimental evidence for specific adaptation events. Together, these approaches will set the stage for applying similar strategies in crop species. We are currently experiencing a drastic decline in whole-genome sequencing costs, which will provide unprecedented opportunities in all crop plants. This proposal will help us to exploit these new opportunities. Our specific aims are: "Detect genomic regions responsible for species-specific adaptation", “Identify genetic variation affecting a model adaptive trait in Arabidopsis and Capsella” and " Compare evolution of self-incompatibility in Arabidopsis and Capsella”.

Genomics-assisted dissection of barley morphology and development (BARCODE).

R. Waugh (Scottisch Crop Research Institute, UK), N. Stein (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany), M. Morgante (University of Udine, Italy).

We will use Illumina Oligo Pool Assay (OPA) technology to genotype 480 Bowman backcross derived nearly isogenic mutant lines at 3072 mapped genetic loci (6144 alleles). We will use simple pair-wise comparison with Bowman, their recurrent parent, to define the boundaries of the segments containing mutated alleles and compile a detailed comparative putative gene content map for each locus based on the barley, rice and emerging Brachypodium and maize genome sequences. While OPA genotyping will narrow the location of each mutant locus to a small genetic interval, identifying the mutated gene from all potential candidates will likely still require a forward genetics approach. To facilitate this, and all similar studies in the future, we propose to contribute to an established international strategy for the staged development of a genetically anchored physical map of the barley genome by end sequencing BACs that are currently undergoing High Information Content Fingerprint analysis and Overgo hybridisation to >12,000 unigenes. This will provide up to 400 Mbp of barley genomic DNA sequence information and will assist in anchoring the physical map to the barley gene map (~5-6000 mapped genes) and rice genome sequence. To demonstrate the utility of the developed information, resources and approach, each partner lab will identify a minimum BAC tiling path spanning a morphological /developmental mutant locus, identify candidate genes and initiate their functional characterisation by a combination of comparative allele sequencing (WT vs. Mutant) and the use of functional genomics tools available to the group (TILLING, transgenics, VIGS). All information will be made publicly available to the community for broader exploitation through existing web-based informatics resources.

Conservation and diversity in transcriptional regulation of developmental processes in crop and model plant species (CISCODE).

G. Angenent (Radboud University Nijmegen, The Netherlands), L. Colombo (University of Milan, Italy) R. Sablowski (John Innes Centre, UK), B. Davies (University of Leeds, UK), Y. van de Peer (Ghent University, Belgium), J. Lohrmann (Max Planck Institute for Developmental Biology, Germany), G. Morelli (National Research Institute for Food and Nutrition, Italy).

This project will use genomics technologies in a comparative context to harness the information present in the diversity of species to fill in the gaps in our understanding of model and crop plants. We will focus on a fundamental, economically important and experimentally tractable biological system, plant reproduction, and use genomic and post-genomic tools to model and manipulate the regulatory network at the centre of the reproductive process. Using a comparative approach, we aim to understand how evolutionary variation in non-coding DNA regions has led to variation in reproductive processes in (crop) species. To derive maximum benefit from a broad comparative analysis, we will focus on a key set of genetic interactions characterised in depth in the reference species, Arabidopsis. Our final aim of this project is to achieve an understanding of the cis-regulatory elements controlling reproduction in plants, to understand the evolutionary variation in this network and to benefit from this information to predictably manipulate the system.

Understanding host plant susceptibility and resistance by indexing and deploying obligate pathogen effectors (Effectoromics).

J. Beynon (University of Warwick, UK), J. Jones (John Innes Centre, UK), G. van den Ackerveken (Utrecht University, The Netherlands), J. Parker (Max Planck Institute for Plant Breeding Research, Germany).

Plants have evolved multiple layers of defence to prevent the invasion of micro-organisms but the processes underlying them are still poorly understood. To overcome such defence systems pathogens have evolved a battery of proteins (effectors) that suppress host resistance at several levels. A new class of pathogen effector proteins has recently been identified in the oomycetes, a taxonomic group of pathogens causing serious yield losses in many crops. Recent work on oomycete effectors has revealed conserved motifs, proposed to be target effectors into the host cell, which enable their identification through bioinformatics. In this proposal we will deploy the effector complement of the obligate biotrophic oomycete Hyaloperonospora parsitica (Hpat) that causes downy mildew disease of Arabidopsis. Four major EU labs with complementary expertise on the Arabidopsis-Hpat system will identify effectors from the recently released Hpat genome sequence, study their variation in 5 races of Hpat, and use them to understand their role in host plant resistance and susceptibility. We will adopt a range of delivery systems and assays to reveal the roles of different effectors in triggering or suppressing host defence mechanisms, exploiting natural variation in host and pathogen, and identify the host proteins with which they interact. Thus, we aim to use the Hpat genome to probe the Arabidopsis genome for defence and susceptibility determinants. Knowledge obtained will be important in understanding fundamental processes of plant disease resistance and should generate novel approaches to producing disease resistant crops.

Genomics-Assisted Analysis and Exploitation of Barley Diversity (EXBARDIV).

A. Flavell (University of Dundee, UK), K. Pillen (University of Bonn, Germany), Germany), A. Schulman (University of Helsinki, Finland), A. Graner (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), L. Cattivelli (Experimental Institute for Cereal Research, Italy), S. Rasmussen (Royal Veterinary and Agricultural University, Denmark), J. Russell (Scottisch Crop Research Institute, UK). A total of 2021 k€ has been awarded by BBSRC, DFG, AKA, MUR, DASTI and the Scottish Funding Council.

Crop plants have evolved from their wild ancestors through domestication and selective breeding over approximately the last 10 000 years. This process has captured many useful gene alleles for breeders but, unfortunately, many other potentially useful alleles have also been lost during this process. There is therefore a need to identify and recruit new alleles from the wild, including niche adaptation, stress tolerance and morphology development for sustainable, environmentally benign crop production in the face of climate change. The association genetics approach potentially offers a powerful way to achieve this, by building upon extensive genomics information and detailed phenotypic analysis. Unfortunately, whole genome association mapping in wild samples requires hundreds of thousands of gene-linked markers, owing to the low levels of linkage disequilibrium in these populations. We propose an experimental strategy to overcome this problem, which exploits the fact that linkage disequilibrium decays at dramatically different rates in different populations. Our approach will use barley as a paradigm for investigating the effectiveness of association mapping in identifying useful gene alleles from the wild. Our second objective is to recruit these new useful gene alleles, into advanced back-cross breeding programs derived from wide crosses between wild barley (H. spontaneum) germplasm and elite cultivars. This will allow us to determine the efficiencies of identification and extraction of useful alleles in barley breeding programs based upon wide crosses. Our third major project objective is to use the huge DNA and marker data set obtained in the project to determine important population genetic parameters for barley.

Multiple Stress Responses and Adaptations (MultiStress).

J. Mundy (University of Copenhagen, Denmark), S. Brunak (Danish Technical University, Denmark), P. Costantino, I. Ruberti (University of Rome La Sapienza, Italy), T. Palva (University of Helsinki, Italy), D. Vreugdenhil (Wageningen University, The Netherlands), A. Bones (Norwegian Universtiy of Science and Technology, Norway). A total of 1788 k€ has been awarded by DASTI, MUR, AKA, NWO/NGI, and RCN.

The general objectives are to analyze responses and adaptations of plants to multiple stresses and to identify the level and functions of stress regulatory networks and crosstalk. Both biotic (pathogens & insects) and abiotic (unfavourable environmental conditions) stresses will be taken into account. Genomic approaches in the model Arabidopsis will be used to provide knowledge and tools for breeding crops with enhanced tolerance to stress conditions in the field.

Integrated analysis of stem cell function in plant growth and development (Plant Stem Cell Network).

J. Murray (University of Cambridge, UK), B. Scheres (Utrecht University, The Netherlands), T. Laux (University of Freiburg, Germany), Y. Helariutta (University of Helsinki, Finland), A. Campilho (University of Porto, Portugal).

Stem cells are essential to the growth and development of plants and provide the ultimate origin of all agriculture and forestry. Although some key genes required for the establishment and maintenance of stem cells are identified, we lack information on the networks governing cell differentiation and cell cycle of different stem cell populations, on how these mechanisms determine common and specific behaviours of the different stem cell groups and how they integrate stem cell activity with changing environmental conditions.

This proposal integrates the work of world-leading labs that perform key research on stem cell populations of the shoot, root and vascular meristems, cell cycle control, growth modelling and image analysis. Europe has a global lead in plant stem cell research and cell division control, and this proposal will integrate the research of the different labs involved, creating new synergies and substantial added value. New tools and strategies combining genomics, reverse genetics, smart genetic screens, and novel cell biology will be exploited to address the key issue of how specification of stem cell regions by transcription factors translates to cellular mechanisms for division and differentiation and identify common and distinct regulatory networks in different stem cell populations.

Proteomics analysis of endosomal compartments in Arabidopsis (PRECIAR).

G. Jürgens (University of Tübingen, Germany), K. Lilley (University of Cambridge, UK), S. de Vries (Wageningen University, The Netherlands), D. Robinson (University of Heidelberg, Germany), F. Anciento (University of Valencia, Spain), E. de la Viesca (National Institute of Agricultural and Environmental Research and Technology INIA, Spain).

This proposal addresses "other topics that contribute to the development of the European Research Area in plant genomics" (Sub Call A). Plant performance including yield stability largely depends on the interaction with the biotic and abiotic environment as well as on cell-cell communication within the plant itself. Nutrient uptake and signaling are mediated by plasma membrane-localised proteins such as transporters and receptors whose activity is determined by interaction with downstream effectors as well as their availability through endosomal trafficking and sorting. Endosomal sorting results either in protein degradation via targeting to the vacuole or in protein recycling to the plasma membrane. To provide a necessary foundation for functional studies of plant performance as specified in other topics of Sub Call A, this project aims to analyse endosomal compartments of Arabidopsis by proteomics. Specifically, resident and cargo proteins of immuno-isolated, ultrastructurally defined endosomal compartments will be identified by MS and subsequently analysed for endosomal localisation in transgenic plants expressing Myc-tagged or GFP-fusion versions of newly-identified proteins. The anticipated results will establish the role of endosomal compartments in plasma-membrane protein trafficking and enable distinction of early/sorting from recycling endosomes.

RLP- and RLK-mediated innate immune responses in Arabidopsis and tomato triggered by pathogen-associated molecular patterns (PAMPs) and a virulence factors (Avrs) (RLPRLKs).

P. de Wit, B. Thomma (Wageninen University, The Netherlands), J. Jones (John Innes Centre, UK), M. Tör (University of Warwick, UK), G. Felix , T. Nürnberger (University of Tübingen, Germany), G. de Lorenzo (University of Rome La Sapienza, Italy), A. Molina (Technical University of Madrid, Spain).

Crop plants are continuously threatened by devastating diseases caused by microbial pathogens. Plants possess an innate immune system that is activated after recognition of microbes through general pathogen-associated molecular patterns or specific pathogen-derived avirulence factors. Two types of extracellular plant plasma membrane receptors (receptor-like proteins (RLPs) and receptor-like kinases (RLKs)) perceive PAMPs and Avrs in the intercellular space and initiate an immune response. Both types contain extracellular leucine-rich repeats (eLRR) that monitor the presence of specific pathogen molecules. For RLPs, these eLRRs are anchored in the plasma membrane and carry only a short cytoplasmic domain that lacks obvious signalling motifs. In contrast, RLKs contain a cytoplasmic kinase domain for downstream signalling. Arabidopsis and tomato are well-characterized model plants. The genome sequence of Arabidopsis is available whereas that of tomato will become available within 2-3 years. In tomato, Avr-perceiving RLPs encompass the well-characterized Cladosporium fulvum and the Verticillium dahliae resistance proteins. Tomato RLPs involved in PAMP perception include LeEix proteins that recognize Trichoderma viride. RLKs involved in Avr and PAMP recognition are rice Xa21, recognizing Xanthomonas oryzae, Arabidopsis FLS2 and EFR, recognizing the PAMPs flagellin and EF-Tu, and Arabidopsis BAK1 and ERECTA that are required for resistance against various pathogens. In this proposal we aim to investigate the role of RLPs and RLKs in the perception of microbial pathogens through extracellular PAMPs and Avrs in the plant species tomato and Arabidopsis. Furthermore we want to dissect downstream defense signalling pathways in the two plant species activated upon pathogen perception. The various project partners will study these mechanisms using genetic, proteomics and transcriptomics approaches.

Seeds for growth - Identification of transcriptional programs controlling seed growth and development from Arabidopsis to rice (Seeds for Growth).

A. Schnittger (Max Planck Institute for Plant Breeding Research, Germany), P. Grini (University of Oslo, Norway), M. Kater (University of Milan, Itlay).

Plant seeds are the largest food source for humankind. In particular, the seeds of cereal species such as rice, wheat, barley, rye, oat, corn, sorghum, and others are of tremendous agronomical importance, for instance for rice more than 600 million megatons are produced every year from an acreage of more than 150 million hectares. In this proposal we create an European collaborative effort incorporating Norwegian, German and Italian national genomics research programs. We will exploit the unique properties of a recently identified mutant in the Arabidopsis cdc2a homolog CDKA;1 to genomically dissect seed development. First, we will dissect regulatory circuits and expression programmes controlling seed growth and development in Arabidopsis; in particular we will focus on the regulatory network controlled by MADS-box transcription factors. Complementarily, we will follow two high-through-put and genome wide genetic screens to identify new seed growth regulators. This newfound knowledge will then be compared with and transferred to an agronomical important model species, i.e. rice. This work aims at an increased yield and higher quality of seeds. Importantly, the work on the cdka;1 mutant has revealed a new signalling pathway that can lead to seed development in the absence of fertilization. Here we will decipher this pathway and study how seeds can develop in the absence of fertilization. Aspiring to new avenues of plant breeding and plant reproduction, a long term goal of this research is the generation of apomictic crops.

Regulation of the plant metabolic network during stress (STRESSNET).

A. Fernie (Max Planck Institute for Molecular Plant Physiology, Germany), L. Sweetlove (University of Oxford, UK), B. Moller (Royal Veterinary and Agricultural University, Denmark).

An understanding of the way in which plants respond and adapt to stress conditions is of fundamental importance for the generation of new varieties of staple crop species to allow agricultural yield to be maintained in the face changing land use and impending global climate changes. A central consequence of a variety of stress conditions is oxidative damage due to increased production of reactive oxygen species and other free radicals.Much progress has been made in understanding the response of plants to oxidative stress and particular attention has focused on identifying and characterizing the antioxidant machinery and specific protective proteins and metabolites. What is often overlooked, is that cellular metabolism must also be reconfigured to support increased demands for reductant, for metabolites with antioxidant activity and to provide precursors for the synthesis of protective metabolites. This metabolic change can be profound and is a central element of the array of molecular events that lead to stress tolerance. However, the exact nature of the metabolic change has not been quantified and a precise understanding of how the competing demands on central and secondary metabolism are met is not known. Metabolic regulation is a multi-faceted process being mediated at transcriptional, post transcriptional, post translational, structural (protein- protein) and allosteric levels. Therefore understanding metabolic regulation requires analysis of the hierarchical importance of each of these levels under each given biological condition. For this reason in the project proposed here particular attention will be paid to dissecting the level at which metabolic change is effected in different parts of the network(change in enzyme abundance versus regulation of enzyme activation state / efficiency) and the reconfiguration of metabolism in response to oxidative stress.

Genome-wide analysis of short RNAs as modulators in dehydration stress tolerance using tolerant and genetic model systems (STRESSsRNA).

D. Bartels (University of Bonn, Germany), J. Philips (University of Bonn, Germany), T. Dalmay (University of East Anglia, UK), M. Fevereiro, M. Pais (University of Lisbon, Portugal).

The lack of understanding of drought tolerance mechanisms has impeded efforts to improve drought tolerance of crop plants. Production of the next generation of dehydration tolerant crops requires a better understanding of the molecular and genetic basis of dehydration tolerance. Our objective is to combine the expertise developed in German, Portuguese and UK laboratories to explore the roles of regulatory small 21-25nt RNAs (sRNAs) in dehydration tolerance using dehydration tolerant and genetic model systems. New families of stress associated sRNAs will be identified using innovative bioinformatics and high throughput genomics tools. The potential of these sRNAs will be characterised in transgenic plants. Our results will have important implications for gene regulation under dehydration stress, engineering stress tolerance and also contribute significantly to the long-term goal of having a comprehensive profile of sRNAs in different plant species.

Using translational genomics to underpin germplasm improvement for complex traits in crop legumes (TRANSLEG).

L. Skot, M. Abberton, I. Donnison (Institute of Grassland and Environmental Research, UK), G. Oldroyd (John Innes Centre, UK), R. Geurts (Wageningen University), K. Mayer (GSF-National Research Center for Environment and Health, Germany).

The objective is to create a robust physical map of diploid clover (Trifolium pratense) that will be anchored to the genome sequence of the legume reference species Medicago truncatula, and aligned to the clover genetic map. The anchored physical map will facilitate dissection of biological traits, future genetic improvement and marker assisted breeding in this important legume crop. The proposal will allow comparative analysis across legume species and create a model for translational genomics in crop legumes. Fingerprinting and end-sequencing of BAC clones from an existing red clover library will be used to obtain 2000 BAC contigs and anchor them to the M. truncatula genome using the closest homologue. Cytogenetics will assess the level of coverage of the clover physical map and resolve issues with misaligned contigs. Approximately 70 gene specific molecular markers previously tested in clover will permit an approximate positioning in the M. truncatula genome to be determined. A web accessible clover information resource with the alignment to M. truncatula, and integrated with the alfalfa resource developed in the US will be established. Integration with other databases will allow us to derive conserved orthologous sequence markers from the clover end-sequence tags that can be integrated with their counterparts in M. truncatula and Lotus japonicus.

Thrips resistance in tomato plants (TRITOP).

P. Klinkhamer, R. Verpoorte (University of Leiden, The Netherlands), C. Martin (John Innes Centre, UK), A. Fernie (Max Planck Institute for Molecular Plant Physiology, Germany).

Despite the general belief that a successful applied genomics project requires a combination of molecular, genetic, metabolomic and ecological approaches our programme is one of the first to integrate this range of expertise. We intend to study a phenolic compound, chlorogenic acid (CGA), which acts as an antioxidant in plants and is expected to protect against degenerative, age related diseases. While most studies on CGA have focussed on human health aspects, our programme will study the importance of CGA for plant resistance against herbivorous insects. Specifically we want: 1) to develop tomato lines resistant to western flower thrips (Frankliniella occidentalis) by increasing natural CGA levels, 2) to explore the natural variation in CGA levels in tomatoes, 3) to identify the genetics behind CGA production levels, 4) to understand the relationship of CGA biosynthesis to other primary and secondary metabolite pathways, 5) to increase our understanding of the role of CGA in thrips resistance, in particular to identify possible synergy of CGA with other (phenolic) compounds and to determine the activity of various other cinnamic acid esters against thrips. The excessive use of pesticides has led to resistance of WFT to various insecticides and to residue problems on marketable crops. Host-plant resistance to thrips will, therefore, be an important contribution towards economic, environmental and health benefits.

Identifying relevant candidate genes for improving plant growth under abiotic stress conditions in *Brassica* crops (ARABAS).

M. Koornneef (Max Planck Institute for Plant Breeding Research, Germany), D. Weigel (Max Planck Institute for Developmental Biology, Germany), O. Loudet (INRA Versailles, France), C. Granier (INRA Agro Montpellier, France), C. Alonso-Blanco (CSIC National Centre of Biotechnology CNB, Spain), *G. Leckband (Norddeutsche Pflanzenzucht Hans-Georg Lembke KG NPZ, Germany), J. Weyen (Saaten Union Resistenzlabor GmbH SURL, Germany).*

Mapping populations derived from crosses between natural accessions of the model plant Arabidopsis thaliana will be tested under conditions of abiotic stress, allowing the genetic analysis of genetic variation underlying abiotic stress tolerance. This genetic information together with the genomic information and resources available in Arabidopsis will be used to identify the genes responsible for variation in these traits. In parallel the performance of two Brassica napus (rapeseed) mapping populations will be analysed, allowing the detection of stress related QTL in this crop plant. Based on synteny between the two species the genetic and genomic information of Arabidopsis can be related to the genetic locations identified in B napus and used to develop molecular markers allowing the application of marker assisted selection for his complicated traits in this crop species.

Identification of molecular markers for the detection of bio-regulators that enhance plant productivity and quality (Bioregulators).

P. Eckes (Bayer CropScience GmbH, Germany), S. Schillberg (Frauenhofer Institute for Molecular Biology and Applied Ecology, Germany), *J. Waples (BIOTEK Agriculture, France)*, *G. Guerreiro (ARVALIS - Institute du végétal, France)*, P. Christou (Lleida University, Spain), J. Guardiola (Technical University of Valencia, Spain).

We have identified a number of biologically active chemicals that influence plant growth and development by activating or inhibiting metabolism. The objective of this project is to exploit the potential of these bioregulators by identifying genes, proteins and metabolites that are up or down regulated when the chemicals are applied under stress or non-stress conditions and positively influence plant growth and productivity. Since comprehensive genomic resources are available for Arabidopsis thaliana and rice, gene expression in response to ten different active molecules will be analyzed using the Arabidopsis whole genome microarray and equivalent rice resources. Similar analysis of proteome and metabolome profiles will be carried out. Profiles will be compared to the biochemical and morphological effects of bioregulator application, resulting in the identification of genes, proteins and metabolites that indicate improved plant growth. These studies will include cell-based in vitro assays and greenhouse tests.
The suitability of these markers will be verified in important crop species. Orthologs will be identified in maize, wheat, rapeseed and vegetables using molecular biology techniques and in silico analysis. The crops will then be treated with the appropriate chemicals and assessed for expression profiles as well as biochemical, physiological and morphological characteristics as described above. In addition, chemicals will also be tested under field conditions using maize, wheat, rapeseed and vegetables.
Universal markers identified in these experiments will be used to establish a cell-based high-throughput assay. Promoters driving the marker genes will be fused to a fluorescent protein gene and plant expression cassettes will be introduced into Arabidopsis and rice plant suspension cells. The cell-based fluorescence assay will be verified using the already identified bioregulators and will allow the identification of novel or superior compounds that enhance crop yield and quality, which will be of significant benefit for the crop production markets. Moreover, markers for improved plant growth could also be used to select new plant lines with sustainable yield stability under biotic

and abiotic stress. The successful implementation of this project will reflect the increasing impact of plant genomics on applied plant biotechnology.

Securing a sustainable production of food and feed - a functional genomic-guided strategy for improving biotic stress tolerance in cereals (CEREHEALTH).

A. Murigneux (BIOGEMMA, Aubiere, France), M. Trottet (INRA-Agrocampus Rennes, France), T. Miedaner (University of Hohenheim, Germany), *G. Strittmatter (KWS Saat AG, Einbeck, Germany)*, P. Karlovsky (University of Göttingen, Germany), L. Hartl (Bav. State Res.Cen. (LfL), Freising, Germany), *E. Ebmeyer (Lochow-Petkus GmbH, Bergen, Germany)*, P.Schweizer (IPK Gatersleben, Germany), D. J. Stahl (PLANTA GmbH, Germany), S. G. Atienza (Consejo Superior de Investigadoro Siencia, Spain), B. Keller (University of Zurich, Switzerland).

The aim of this project is to develop innovative resistance breeding strategies for wheat and maize. Quantitative genetic approaches, genomics and bioinformatics will be employed to exploit and extend natural plant resistance against Fusarium and Septoria. 4 workpackages will be pursued: (i) analysis of genetic diversity of crops and pathogens; (ii) identification and characterisiation of functional genomic regions; (iii) candidate gene selection and genetic engineering. The deliverables will be used in workpackage 4 for a meta analysis across pathosystems. The meta analysis will be used in molecular breeding approaches for improved varieties with durable disease resistance by the industrial partners.

Comparative genomics of shoot branching (COGS).

O. Leyser (University of York, UK), P. Cubas (CSIC National Centre of Biotechnology CNB, Spain), K. Theres (Max Planck Institute for Plant Breeding Research, Germany), C. Rameau (INRA Versailles, France), A. Bendahmane (INRA - Plant Genomics Research Unit URGV, France), *J. Heldens (Enza Zaden BV, The Netherlands).*

Our project has two objectives:
1. To integrate European expertise on shoot branching control, building a holistic understanding
2. To provide tools to expedite exploitation of the knowledge generated, strengthening European competitiveness in plant breeding for improved shoot system architectures

Shoot branching is a key agronomic trait and changes in branching habit have been central in the domestication of wild species for agricultural use. Continued breeding for improvement in shoot branching characteristics can make important contributions to yield stability. Furthermore, rational approaches for architectural optimisation are essential for ongoing initiatives to increase the diversity of agricultural products through the domestication of additional species, for example to develop bioenergy crops.
The groups collaborating in this proposal encompass expertise in the key gene systems known to regulate branching. It is already clear that these systems have wide relevance across higher plants. However, it is equally clear that there are important differences in the way the systems operate in different species. We therefore propose a systematic comparative study of these gene systems and their interactions in a range of species. This will allow the development of a tool kit for marker assisted breeding for optimised branching habit, and for genetic modification of branching, when it becomes publicly acceptable.

Eucalyptus genomics research network for improved wood properties and adaptation to drought (EUCANET).

J. Grima-Pettenati (CNRS and University Paul Sabatier Mixed Unit of Research UMR , France), C. Plomion (INRA and University of Bordeaux Mixed Unit of Research UMR Biodiversity Genes & Community BioGeCo, France), P. Vigneron (French Agricultural Research Centre for International Development CIRAD, France), *L. Harvengt (AFOCEL, France)*, *J. Majada (SERIDA, Spain)*, B. Fernández-Muñiz (University of Oviedo, Spain), *C. Marques (Forestry and Paper Research Institute, RAIZ, Portugal)*, AM. Pires (Technical University of Lisbon, Portugal).

Eucalypt plantations in the EU represent an important economic activity. They are the main source of short fibre pulpwood for European pulp and paper industry and are important alternative sources of income for rural communities. Improvements in forest productivity have been achieved through breeding and silviculture but they remain lower in the EU than in the tropics, due to climatic limitations. However, wood properties (in particular for pulp manufacture) of EU eucalypt plantations are superior. It is important for EU forestry and pulp and paper sector to pursue further improvements in eucalypt wood quality in order to remain competitive in the world market
The projects research focus is on genomics of wood properties but this cannot be separated from the broader issue of drought tolerance of eucalypt plantations. While the former aspect is obvious for the wood end-use quality point of view, the latter is becoming an increasing ecological and economic concern.
The goal of this project is to identify a restricted number of Candidate Genes (CG) that are likely to impact wood traits and productivity under drought conditions in Eucalyptus, a major forest species in Southern Europe. Moreover, this project addresses key fundamental issues in genomics, namely (i) the extent to which major genes determine trait differences within and between species, (ii) the contribution of structural and/or regulatory genes in trait expression. EUCANET is a network of industry-based eucalypt breeding organizations and research groups working in forestry genomics, physiology and statistics By combining efforts and materials from the 3 different countries we will be able to construct a multispecies consensus map, produce and exchange data on QTL location, identify CG of interest by means of transcriptomics and proteomics, pre-validate CG through co-localisation with QTL and genetic transformation..
The results will constitute a solid foundation for future association studies for specific wood genes and traits of importance for productivity and drought

tolerance. The long-term goal of this project is to apply these advances to the molecular selection of genotypes. This should increase the selection efficiency of elite trees for improved and sustainable variety deployment.

Genetic basis of field resistance to blast in European rice varieties to improve breeding (FIELD RESISTANCE IN RICE TO BLAST).

D. Tharreau (CIRAD, France), R.M. Carreres (IVIA, Spain), *L. Marqués (COPSEMAR, Spain)*, G. Peñas (IRTA, Spain), J. M. Osca (UPV, Spain), M. Aguilar (CIFA-IFAPA, Spain), *C. Baixauli (Fundación RURALCAJA, Spain).*

Rice blast (caused by Magnaporthe grisea) is the most damaging fungal disease of rice (Oryza sativa L.), and it is the only pathogen of rice treated with pesticides in Europe, where most of the rice growing areas are river deltas and damps, with special environmental protection. The use of resistant rice varieties is a cost effective method to control the disease and can be incorporated as component of an integrated pest management (IPM) strategy, avoiding fungicide applications in such fragile areas. Determining the genetic and molecular basis of resistance in European varieties and including this knowledge in breeding programs is of primary importance to develop rice varieties durably resistant to blast. This project aims at using the appropriate genomic tools to identify the important genes for durable blast resistance and to start creating resistant varieties adapted for European growing conditions, through the combined efforts of different teams and using different methods: evaluation of resistance to blast in the field and in controlled conditions, study of expression patterns of genes involved in defense mechanisms, characterization of allelic variability, and QTL analysis.

Cold tolerance for the future: the CBF genes and beyond (FROSTY).

H. McKhann (INRA Study of Polymorphisms in Plant Genomes EPGV, France), E. Teoule (INRA Genetic and Plant Breeding Station SGAP, France), C. Teulieres (University of Toulouse, France), D. Hincha (Max Planck Institute for Plant Molecular Physiology, Germany), J. Salinas ((National Institute of Agricultural and Environmental Research and Technology INIA, Spain).

Much of the work on freezing tolerance in the last several years has focused on the CBF pathway. Despite many studies on these genes, it still remains to be determined how their expression is regulated and what the precise contribution of each individual gene to freezing tolerance and cold acclimation is. The general objective of this proposal is twofold: 1) to better understand the regulation of CBF gene expression and the involvement of the CBF cold response pathway in freezing tolerance and 2) to examine other pathways involved in freezing tolerance. We will use Arabidopsis and a commercially important tree species, Eucalyptus. For the first objective, we propose to use three complementary approaches: i) the study of natural variation, ii) the use of reporter-genes as well as RNAi and over-expressing (OE) lines, and iii) the study of mutants affected in CBF regulation. In Arabidopsis, we will identify more efficient natural variants of CBF genes (coding sequences and promoters), as well as new regulators of CBF expression. In Eucalyptus, the project aims to characterize CBF gene expression, to identify the CBF regulon(s), and to obtain molecular markers for EguCBF genes. In a second part, we will use recombinant inbred lines (RILs) of Arabidopsis that are available at the SGAP for phenotyping with respect to freezing tolerance in order to begin to examine non-CBF pathways. The results we expect to obtain from this project will constitute an important step for better applying our knowledge of the CBF genes, and perhaps others, to improve the freezing tolerance of many crop plants.

Genomic research-assisted breeding for sustainable production of quality grapes and wine (GRASP GRAPE WINE).

S. Delrot (CNRS, Bordeaux, France), F. Artiguenave (INRA, Evry, France), D. Merdinoglu (UMR 1131 INRA-University of Strasbourg, Colmar France), C. Romieu (UMR 1083 INRA-ENSAM-University of. Montpellier, France), *O. Zebic (SFERIS - SIANEO, La Boissiere, France)*, E. Zyprian (BAZ-Institute for Grapevine Breeding, GWH Germany), J. Kopka (Max Planck Insitute for Molecular Plant Physiology, Golm, Germany), M.M. Zapater (CNB - CSIC, Madrid, Spain), J. Carreno (IMIDA, La Alberca, Spain), *F. Carillo (I.T.U.M., Blanca, Spain)*, M.P. Fevereiro (ITQB/Universidade Nova de Lisboa, Portugal), S.S. Pais (ICAT, Portugal), S.B.Q. Amancio (Institutio Superior de Agronomia, Portugal), *H.-J. Böhm (PLANSEL Lda (JBP), Portugal)*, R. Verpoorte (Leiden University, The Netherlands), S. Grando (IASMA, Trento, Italy).

Grapes are currently grown on 3.6 Million ha in Europe (EU 25) and amount to a total yearly production of app.185 Million hl wine production (2004) in the European Union (OIV 2004). Europe is also an important producer of table grapes with Italy, Spain and Greece producing close to 2 Million tons of the total 12 Million tons world production in 2004 (USDA 2004). The concerns of consumers for improved food quality produced with environmentally safe and sustainable agriculture demands the development of cultivars of table- and wine grapes improved in natural pathogen resistance and fruit quality to reduce the extensive use of fungicides and ensure high-quality production. Demand of viticulturists for quality varieties adapted to changing environmental conditions must be anticipated in the context of global climatic changes.
Breeding of grapevines is a long-lasting task and urgently requests novel tools to achieve these aims efficiently. The fundamental goal of this proposal is to identify the gene sequences and mutations responsible for phenotypic variation of resistance and berry quality traits in grapevine through the combination of genomic, functional genomic, metabolomic and quantitative genetical methods. It will link the Europan research activities in this area and construct a common platform for compilation and exploitation of Vitis phenotypic, metabolomic, transcriptomic and genetic/genomic data.

Exploiting genetic variability of resistance genes in major European food legumes to improve varieties for sustainable agriculture (LEGREST).

L. Gentzbittel (EA 3013 INP-ENSAT, Castenet-Tolsa, France), A. Baranger (INRA-Agrocampus, Rennes, France), *P.J. Winter (GENXPro GmbH, Frankfurt, Germany)*, G. Kahl (JWG Univ. of Frankfurt, Germany), *F. Eickmeyer (Saatzucht Steinach GmbH, Steinach, Germany)*, *J. Geistlinger (Array-on GmbH, Gatersleben, Germany)*, M. Perez (Univ. of Leon, Spain), A. Ramos (Univ. of Valladolid, Spain), C. Caminero (ITACyL, Valladolid, Spain), A.M. Torres (IFAPA-CICE, Cordoba, Spain), D. Rubiales (CSIC, Spain), T. Millan (Univ. of Cordoba, Spain), *I. Solis (Agrovegetal S.A., Sevilla, Spain)*, M.C. Vaz Patto (Univ. of Lisbon, Portugal).

LEGRESIST is a consortium of 12 leading European centers for legume breeding and molecular biology, and 2 leading technology providers. In Europe, agronomical, economical and ecological benefits of legumes for the entire agro-system are notoriously under-exploited due to their unstable yield caused by the plants susceptibility to a wide range of pathogens. Despite considerable investment and progress in use of molecular tools for resistance breeding, application of Marker-Assisted Selection and Marker-Assisted Pyramiding of resistance genes to obtain durable resistance is still hampered by non-sufficient knowledge of allelic diversity in resistance genes and the lack of insight into plant-pathogen interactions responsible for the hard-to-handle quantitative nature of resistance. Moreover, affordable, modern tools for advanced resistance breeding are missing. Therefore, LEGRESIST aims at i) exploiting genetic diversity of resistance genes on the level of Single Nucleotide Polymorphisms (SNPs) for genetic mapping of all expressed resistance genes in major crop legumes, ii) understanding quantitative resistance through characterization of the interacting transcriptomes of plants and their pathogens by SuperSAGE analysis and iii) mapping of expression(e)QTL underlying quantitative resistance. The project delivers polydimensional SNP-Arrays for rapid and cost efficient mapping of resistance genes and the Legume-Biotic-Stress-Array for eQTL mapping. Applying these modern tools, LEGRESIST will produce the most advanced expression maps for all major crop legumes. Further, exploiting synteny between the crops and the model legume Medicago truncatula, the project will result in the first comparative biotic stress map of the legumes. Such innovative tools will enable breeders to provide durable resistant, non-GMO legumes for the Multibillion Euro market for vegetable protein currently

served by soybean imports. That way, novel plant biotechnology will prove its benefits likewise for European economy and ecology.

Understanding the climacteric vs non-climacteric fruit ripening mechanisms in melon using transcriptomic, metabolomic and reverse genetic approaches (MELRIP).

J. Garcia-Mas (CSIC, Spain), A. Bendahmane (INRA - Plant Genomics Research Unit URGV, France), M. Pitrat (INRA - Research Unit for Genetic Improvement of Fruit and Vegetables GAFL, France), M. Stitt (Max Planck Institute for Molecular Plant Physiology, Germany), F. Nuez (Center for the Conservation and Breeding of the Agricultural Biodiversity COMAV, Spain), *D. Hosemans (Vilmorin Clause & Cie, France), T. Jahrmann (Semillas Fitó S.A., Spain).*

Melon is an attractive model species that may help to understand the molecular differences between non-climacteric and climacteric fruit ripening because it contains both types of genotypes. This proposal involves the simultaneous use of transcriptome and metabolome analysis in climacteric and non-climacteric melon lines in order to understand the molecular differences between both types of fruit ripening. A search and analysis of melon mutants in key genes in fruit ripening will also be performed. The TILLING and EcoTILLING technologies will enable the identification of mutants that do not have a distinctive visible phenotype. The discovery of such novel variants could directly lead to the creation of new melon hybrid cultivars with commercial interest, a task that will be undertaken by the two private partners that participate in this proposal.

Isolation of key genes for kernel development through the identification, in a collection of 300 mutant lines, of *Mutator* insertions in genes expressed in the maize seed (MuExpress)

G. Hueros (University of Alcalà de Henares, Spain), P. Rogowsky (University of Lyon, France), U. Wienand (University of Hamburg, Germany), *P. Perez (Biogemma, France).*

Maize is essential for world nutrition and widely cultivated in France, Spain and Germany. The size and shape of the two seed compartments (embryo and endosperm) is determined during seed development, a process involving an estimated 1000 genes. Less than 10% are known today and the identification and characterisation of genes involved in seed development presents a major scientific and agronomic challenge.
The project aims at the identification and functional analysis of genes involved in maize seed development via the large scale molecular characterisation of transposon induced maize seed mutants. It is based on a collection of 300 mutants selected from a much larger initial collection based on a clean 3:1 segregation of the mutant phenotype and a stable phenotype over at least 3 generations. These mutants have been selected as being particularly defective in endosperm rather than embryo formation, thus enriching for mutations in genes preferentially involved in endosperm formation. After a minimum of 2 backcrosses the material is genetically quite homogenous and genomic DNA of wildtype and mutant pools is available. In a sister group of 300 mutants the bottleneck has been the identification of the transposon copy responsible for the phenotype among the roughly 100 copies present in the genome. To circumvent the very low efficiency of the AIMS technique on genomic DNA encountered in previous experiences, we propose here to decomplexify the system and to apply the technique to seed cDNA. All FSTs will be systematically sequenced opening not only the way for the subsequent co-segregation studies that will link the phenotype to a single FST but also creating a valuable inventory of Mutator insertions in coding sequences present in the material. A strong bioanalysis of the candidate sequences using all available tools in maize as well as the synteny to rice and other cereals will provide insight into the potential molecular function of the candidate genes. Among others the expression profiles of the candidates will be extracted from existing micro-array data and the in silico map position in the maize genome compared with the positions of seed QTLs.

An integrated genomic and proteomic characterization of induced seed storage organelles for the optimal production of biopharmaceuticals in plants and plant cells (ProteinStorage).

M. Rossignol (INRA URP), Montpellier, France), *P. Soularue (PartnerChip, Evry, France)*, *D. Courtois (Nestle R&D, Tours, France)*, E. Stoger (University of Aachen, Germany), P. Christou (University of Lleida, Spain), *M. Bastida (ERA Biotech, Barcelona, Spain)*, D. Ludevid (CSIC-IRTA, Barcelona, Spain).

The scientific objectives of the Project aim towards developing a comprehensive understanding of the genome and proteome of rice and Arabidopsis, in the first tier but also tobacco, a species that has unique attributes for specific applications in the field of molecular farming. The project's key objectives are: (1) Understand qualitative and quantitative changes in protein composition a plant undergoes during the formation of endogenous and induced storage protein bodies (PBs) at the genomic and proteomic levels; (2) characterize the final protein composition (proteome) of induced storage bodies in order to understand the mechanism of PB formation, specifically focusing on their use as production tools and delivery vehicles for molecular farming applications; (3) establish a knowledge basis, founded on proteomic and genomic characterisation, that will allow identification of genes and proteins that might influence either positively or negatively the accumulation of exogenous proteins in plants and plant cells; (4) use the above knowledge to propose more refined strategies for maximizing productivity of valuable recombinant proteins for molecular farming applications and test these using a commercially relevant protein (EGF, Epidermal Growth Factor).

International reference centre for the genomics and diagnosis of viruses with small circular DNA (RCA Genomics).

H. Jeske (University of Stuttgart, Germany), *S. Ullmann (Qiagen GmbH, Germany)*, B. Gronenborg (CNRS Plant Science Institute ISV, France), E. Bejarano (University of Malaga, Spain).

A collaborative research project uniting participants of Universität Stuttgart, CNRS Gif, Universidad Malaga and Qiagen, Hilden is proposed to utilize the innovative power of rolling circle amplication (RCA) for diagnosis and genomics of viruses with small circular DNA, like geminiviruses and nanoviruses as well as satellite DNAs. Procedures and materials will be developed that allow the centralized analysis of infected plant samples from all over the world, with emphazisis on subtropical and tropical countries. A reference database will be established for plant protection measurements as open access. For functional genomics, RCA-based techniques will be developed to identify relevant genes in the interaction of viruses and hosts, with the primary goal to select or engineer virus resistance. The project is intended to provide added value to crop sustainablity of tomato, cotton, beet and cassava among others.

Trilateral initiative for enhancing salt tolerance in rice (TRIESTER).

B. San Segundo (CSIC Plant Molecular Genetics Laboratory, Spain), F. Quintero (CSIC Institute of Natural Resources and Agrobiology, Seville (IRNAS), Spain), A. Rodriguez-Navarro (Technical University of Madrid, Spain), M. Talón (Valencian Institute for Agricultural Research IVIA, Spain), H. Sentenac (INRA Agro Montpellier, France), E. Guiderdoni (French Agricultural Research Centre for International Development CIRAD, France), B. Müller-Roeber (MPI for Molecular Plant Physiology, Germany), *T. Maes (Oryzon Genomics, Spain), A. Krotzky (Metanomics GmbH, Germany).*

Soil salinity accounts for large yield losses in crops worldwide. Understanding how plants cope with high salinity in the environment is thus an issue of great agricultural importance. The proposed project exploits the full potential of the rice genome information to identify and characterize major determinants of salt tolerance in rice by i) surveying and functionally characterizing natural or induced allelic variation in genes involved in salt tolerance, and by ii) analysing particular components, signalling pathways and network integration in the plant response to salt stress. To discover new salt determinants, forward and reverse genetic technologies, and expression profiling in mutant rice collections will be used. The natural allelic variation of salt-associated genes will be approached by using EcoTILLING and comparative whole genome hybridization (CGH). The project also aims at the functional characterization of selected gene families involved in signal transduction, transcriptional control and ion homeostasis. For this, knockout and overexpressor rice lines will be generated and used for global expression analyses. The functional characterization of salt-associated genes (natural variant and mutagenized alleles) in heterologous systems (yeast, Xenopus) will be also approached. The project integrates genomic approaches with rice physiology and agronomical behaviour (electrophysiology, water content and osmotic adjustment, metabolite profiling in vegetative and grain tissues, growth and productivity under saline conditions in containment greenhouse conditions). The project also develops technologies and tools based on oligo-DNA microarrays (CGH), HTP gene validation and metabolite profiling. The knowledge generated in this project is required to integrate post-genomic research into suitable breeding programmes for the development of new salt-tolerant rice cultivars. Progresses in understanding tolerance to salinity in rice plants will benefit other cereal research programs.

Programme Board & Moderating Panel

The Programme Board is an advisory panel consisting of 15 international experts in charge of the evaluation of the pre-proposals and full proposals that were submitted the ERA-PG call for proposals.

Members of the Programme Board

Prof. Thomas Boller (chair)
University of Basel, Institute of Botany, Basel, Switzerland

Prof. Jan K. Schjørring
Royal Veterinary and Agricultural University (KVL), Plant Nutrition Laboratory, Copenhagen, Denmark

Dr. Dominique Job
CNRS / Bayer CropScience Joint laboratory (UMR2847), Lyon cedex, France

Prof. Dierk Scheel
Leibniz Institute of Plant Biochemistry, Halle (Saale), Germany

Prof. Francesco Salamini
University of Milan, Department of Plant Breeding and Physiology, Milan, Italy

Prof. Willem Stiekema
Plant Research International/Centre for BioSystems Genomics, Wageningen, The Netherlands

Dr. Anders Lønneborg
DiaGenic ASA, Oslo, Norway

Prof. José Feijó
Instituto Gulbenkian de Ciência (IGC), Oeiras, Portugal

Prof. Pablo Vera
IBMCP, Instituto de Biología Molecular y Celular de Plantas (CSIC-UPV) / Technical University of Valencia, Spain

Prof. Michael Gale
John Innes Centre, Norwich, UK

Prof. Marc Zabeau
European Plant Science Organisation (EPSO), Ghent, Belgium

Prof. Leena Vestala
Ministry of Agriculture and Forestry, Department of Agriculture, Helsinki, Finland

Dr. Julia Lafferty
Saatzucht Donau GesmbH & CoKG, Probstdorf, Austria

Dr. Amnon Lers
Agricultural Research Organization, Dept. of Postharvest Science of Fresh Produce, The Volcani Center, Bet Dagan, Israel

Prof. Per Kjellbom
Lund University, Department of Biochemistry, Sweden

After the evaluation, moderating panels have made the final recommendations for funding to the national agencies. The final selection rested with the national funding bodies.

Members of the Moderating Panel for Sub Call A

Prof. Thomas Boller (chair)
University of Basel, Institute of Botany, Basel, Switzerland

Dr. Kathleen D'Hondt
Flemish government, Department Economy, Science and Innovation, Belgium

Dr. Katrin Hahlen
Deutsche Forschungsgemeinschaft (DFG), Germany

Assoc. Prof. Karen Skriver
Danish Research Council for Technology and Production, Danish Agency for Science, Technology and Innovation, Denmark

Dr. Sirpa Huuskonen and Dr. Leila Häkkinen
Suomen Akatemia (AKA), Finland

Mr. Mauro Massulli
Ministero dell'Università e della Ricerca (MUR), Italy

Dr. Frans Martens
Netherlands Organisation for Scientific Research (NWO), The Netherlands

Dr. Päivi A. Teivainen-Lædre
Norges forskningsråd (RCN), Norway

Prof. Cândido Pinto Ricardo
Fundação para a Ciência e a Tecnologia (FCT), Portugal

Dr. Sophie Laurie and Dr. Alf Game
Biotechnology and Biological Sciences Research Council (BBSRC), UK

Members of the Moderating Panel for Sub Call B

Prof. Thomas Boller
(chair)

Prof. Dieter Berg
(Bayer CropScience AG, Germany)

Dr. Martin Ganal
(TraitGenetics GmbH, Germany)

Prof. Dierk Scheel
(Leibniz-Institut für Pflanzenbiochemie, Germany; Programme Board member)

Dr. Rainer Büschges
(advisor from PTO-FZJ/BMBF, Germany)

Prof. Frank Laplace
(observer from BMBF, Germay)

Prof. Ignacio Romagosa
(Universidad de Lleida Centro UdL-IRTA, Spain)

Dr. Antonio Leyva
(Centro Nacional de Biotecnologa -CSIC, Spain)

Prof. Pablo Vera
(Instituto de Biologa Molecular y Celular de Plantas (CSIC-UPV), Spain; Programme Board member)

Dr. Julio Barbas
(advisor from MEC, Spain)

Dr. José M. Pardo
(advisor from MEC, Spain)

Dr. Rosa R. Bernabé
(observer from MEC, Spain)

Dr. Georges Pelletier
(INRA, France)

Dr. Georges Freyssinnet
(LIMAGRAIN, France)

Dr. Dominique Job
(CNRS/Bayer CropScience Joint Laboratory, France; Programme Board member)

Dr. Francis Quétier
(advisor from ANR, France)

Prof. Manuel Carrondo
(Universidade de Lisboa, Portugal)

Dr. Luisa Henriques
(advisor from FCT, Portugal)

Dr. Catarina Resende
(advisor from FCT, Portugal)

Prof. Cândido P. Pinto Ricardo
(observer on behalf of FCT, Portugal)

Dr. Alf Game
(advisor from BBSRC, UK)

Dr. Sophie Laurie
(advisor from BBSRC, UK

Meeting Support Team for the Moderating Panel Meetings

Dr. Okker van Batenburg
(NGI/NWO; ERA-PG executive coordinator)

Mr. Paul Beckers
(NGI/NWO; ERA-PG Call Secretariat)

Dr. Christine Bunthof
(NGI/NWO; ERA-PG executive coordinator)

Dr. Stephan Micha
(PTO-FZJ, German ERA-PG coordinator)

Dr. Sophie Laurie
(BBSRC, UK ERA-PG coordinator)

Mr. Bernard Strée
(Génoplante, French ERA-PG coordinator)

Observers

Dr. Machi Dilworth
(NSF, USA)

Dr. Jason Grant
(SNSF, Switzerland)

Dr. Aysim Yilmaz
(SNSF, Switzerland)

Contact Details: Teams in the Consortia

Belgium

Prof. dr. Y. van de Peer
Universiteit Gent
Department of Plant Systems
Biology Flanders Institute for
Biotechnology (VIB)
Technologiepark 927
9052 Gent
yvpee@psb.ugent.be

Denmark

Prof. dr. S. Brunak
Technical University of Denmark
BioCentrum-DTU
Builing 208
DK-2800 Lyngby
brunak@cbs.dtu.dk

Prof. B.L. Møller
Royal Veterinary and Agricultural
University
Center of Molecular Plant
Physiology and Plant
Biochemistry
40, Thorvaldsensvej
D-1871 Copenhagen
blm@kvl.dk

Prof. dr. J.W. Mundy
Institute of Molecular Biology
Dept. of Plant Physiology
Oester Farimagsgade 2A
DK-1353 Copenhagen K
mundy@my.molbio.ku.dk

Dr. S.K. Rasmussen
Royal Veterinary and Agricultural
University
Thorvaldsensvej 40
DK-1871 Copenhagen
skr@kvl.dk

Prof. dr. M.H. Schierup
University of Aarhus
Bioinformatics Research Center
Deparment of Biology
Hoegh Guldbergs Gade 10
8000 C Aarhus
mheide@birc.au.dk

Contact Details: Teams in the Consortia

Finland

Prof. Y. Helariutta
University of Helsinki
Institute of Biotechnology,
Biocenter 1 Developmental
Biology Programme
PO Box 56
FIN-00014 Helsinki
yrjo.helariutta@helsinki.fi

Prof. T. Palva
University of Helsinki
Department of Biosciences-
Genetics
P.O. Box 56
00014 Helsinki
tpalva@ladybird.helsinki.fi

Dr. O. Savolainen
University of Oulu
Department of Genetics
Linnanmaa A5
SF90570 Oulu 57
outi.savolainen@oulu.fi

Dr. A.H. Schulman
University of Helsinki
Institute of Biotechnology Plant
Genomics Laboratory
P.O.Box 56
FIN-00014 Helsinki
alan.schulman@helsinki.fi

France

Dr. F. Artiguenave
INRA URGI Group :
Bioinformatics
Tour Evry 2- 1er etage 523 Place
des Terasses
91000 Evry
francois.artiguenave@versailles.in
ra.fr

Dr. A. Baranger
Institut National de la recherche
agronomique
Agrocampus Rennes Plant
Genetics and Biotechnologies Lab
BP 35327
35653 Le Rheu Cedex
alain.baranger@rennes.inra.fr

Dr. A. Bendahmane
Institut National de la Recherche
Agronomique
Etude de Polymorphisme des
Génomes Végétaux
Rue Gaston Gremieux 2
91057 Evry
bendahm@evry.inra.fr

Dr. D. Courtois
Nestlé R&D centre
101 avenue G. Eiffel
BP 49716 37097
didier.courtois@rdto.nestle.com

Prof. S. Delrot
CNRS
Universite de Poitiers
Avenue du Recteur Pineau 40
86022 Poitiers
serge.delrot@univ-poitirs.fr

Contact Details: Teams in the Consortia

Dr. C. Granier
INRA-Agro Montpellier
2 Place Viala
34060 Montpellier Cedex 1
granier@ensam.inra.fr

Dr. J. Grima-Pettenati
Univerite Paul Sabatier
Pole de Biotechnologie Vegetales
BP 42617 Castanet Tolosan
grima@scsv.ups-tlse.fr

Dr. B. Gronenborn
Centre National de la Recherche
Scientifique en France
Institut des Sciences Végétales
Avenue de la Terrasse
91198 Gif sur Yvette Cedex

Mr. L. Guerreiro
Arvalis
Institut du Végétal
Paris

Dr. L. Harvengt
AFOCEL
Laboratory of Biotechnology
Domaine de l'Etancon
F-77370 Nangis
luc.harvengt@afocel.fr

Dr. D. Hosemans
Vilmorin Clause & Cie
Biotechnology laboratory Clause
Tezier
avenue de Bois l'Abbé
49070 Beaucouzé
daniele.hosemans@clausetezier.com

Dr. F. Legeai
INRA URGI
523 place des Terrasses de
l'Agora
91034 Evry cedex
fabrice.legeai@versailles.inra.fr

Dr. Loudet
Institut National de la recherche
agronomique
Station de Génétique et
d'Amelioration des Plantes
Route de Saint-Cyr
78026 Versailles cedex

Dr. H.I. McKhann
Institut National de la Recherche
Agronomique
Etude de Polymorphisme des
Génomes Végétaux
Rue Gaston Gremieux 2
91057 Evry
mckhann@cng.fr

Dr. D. Merdinoglu
UMR SVQV, INRA-ULP Labo.
de Génétique et d´Amélioration de
la Vigne
28 rue de Herrlisheim
BP20507 F-68021 Colmar Cedex

Dr. A. Murigneux
Biogemma
Wheat & Maize Genomics Team
24, Avenue des Landais
F-63170 Aubière
alain.murigneux@biogemma.com

Contact Details: Teams in the Consortia

Dr. N. Ollat
INRA
UREFV , BP 81
33883 Villenave D'Ornon
ollat@bordeaux.inra.fr

Dr. P. Perez
Biogemma
Wheat & Maize Genomics Team
24, Avenue des Landais
F-63170 Aubière
pascual.perez@biogemma.com

Dr. M. Pitrat
Institut National de la recherche agronomique
Génétique et Amélioration des Fruits et Légumes
Domaine Saint Maurice BP94
84143 Montfavet
Michel.Pitrat@avignon.inra.fr

Dr. C. Plomion
Institut National de la Recherche Agronomique
UMR Biodiversity Genes & Community
69 route d'Arcachon
33612 Cestas Cedex

Dr. C. Rameau
Institut National de la recherche agronomique
Station de Génétique et d'Amelioration des Plantes
Route de Saint-Cyr
78026 Versailles cedex
rameau@versailles.inra.fr

Dr. P. Rogowsky
Ecole Normale Superieure de Lyon
Plant Reproduction and Development
46 allée d'Italie
F-69364 Lyon Cedex 07
peter.rogowsky@ens-lyon.fr

Dr. C. Romieu
INRA-Agro Montpellier
2 Place Viala
34060 Montpellier Cedex
romieu@ensam.inra.fr

Dr. M. Rossignol
Agro Montpellier INRA
Laboratoire Biochimie et Physique Moleculaire des Plantes
2, place Viala
34060 Montpellier Cedex 1
rossignol@ensam.inra.fr

Dr. P. Soularue
PartnerChip
Bat G2 PC-EVRY
2 rue Gaston CREMIEUX
91000 Evry
pascal.soularue@cea.fr

Mrs. D. Steinbach-Samson
INRA URGI
523 place des Terrasses de l'Agora
91034 Evry cedex
delphine.samson@versailles.inra.fr

Contact Details: Teams in the Consortia

Dr. E. Téoulé
Institut National de la recherche agronomique
Station de Génétique et d'Amelioration des Plantes
Route de Saint-Cyr
78026 Versailles cedex
teoule@versailles.inra.fr

Prof. C. Teulières
Universite Paul Sabatier
Equipe de Recherche Technologique Surfaces Cellulaires et Signalisation chez les Végétaux
Chemin de Borde Rouge 24
31326 Castanet-Tolosan
teulieres@scsv.ups-tlse.fr

Dr. D. Tharreau
Campus international de Baillarguet
CIRAD-CA
Cedex 5
34398 Montpellier
tharreau@cirad.fr

Dr. P. This
Institut National de la Recherche Agronomique
Diversité et Génomes des Plantes Cultivées
this@ensam.inra.fr

Dr. L. Torregrosa
Agro Montpellier INRA
Laboratoire Biochimie et Physique Moleculaire des Plantes
laurent.torregrosa@ensam.inra.fr

Dr. M. Trottet
Institut National de la Recherche Agronomique
UMR Plant Breeding and Plant Biotechnology
BP 35327 35653 Le Rheu
maxime.trotter@rennes.inra.fr

Dr. P. Vigneron
CIRAD
Research unit: Genetic
Flhor TA50/PS4 Boulevard de la Lironde
34398 Montpellier Cedex 5
philippe.vigneron@cirad.fr

Dr. J.G. Waples
BIOTEK Agriculture
Route de Viélaines
10120 Saint Pouange
jwaples@euroag.com

Dr. O. Zebic
Sferis
2 place Viala
34060 Montpellier
olivier.zebic@sferis.com

Contact Details: Teams in the Consortia

Germany

Prof. dr. E.F.P. Bartels
Universität Bonn
Institut für Zellulaere und
Molekulare Botanik Zellbiologie
der Pflanzen
Kirschallee 1, D-53115 Bonn
dbartels@uni-bonn.de

Dr. E. Ebmeyer
Lochow-Petkus GmbH
Plant Breeding
1197 1
D-29296 Bergen
ebmeyer@lochow-petkus.de

Dr. P. Eckes
Bayer CropScience GmbH
Research Discovery
Frankfurt am Main
peter.eckes@bayercropscience.co
m

Dr. F. Eickmeyer
Saatzucht Steinach GmbH
Wittelsbacher Str. 15
D-94377 Steinach
eickmeyer.fred@saatzucht.de

Prof. dr. G. Felix
Universität Tübingen
Lehrstuhl Mikrobiologie I
Auf der Morgenstell 28
D-72076 Tübingen
geor.felix@zmbp.uni-
tuebingen.de

Dr. A.R. Fernie
Max-Planck-Institut für
Molekulare Pflanzenphysiologie
Wissenschaftspark Golm
D-14424 Potsdam
fernie@mpimp-golm.mpg.de

Prof. I. Feußner
Georg-August-Universität
Göttingen
Department of Plant Biochemistry
Faculty of Biology
Justus von Liebig Weg 33
D-37077 Göttingen
ifeussn@gwdg.de

Dr. J. Friml
Universität Tübingen
Zentrum fur Molekularbiologie
der Pflanzen
Auf der Morgenstelle 3
D-72076 Tübingen
jiri.friml@zmbp.uni-tuebingen.de

Dr. J. Geistlinger
Array-on GmbH
Am Schwabeplan 1 B
06466 Gatersleben
geistlinger@array-on.com

Prof. dr. A. Graner
Leibniz Institute
Institute for Plant Genetics and
Crop Plant Research (IPK)
Corrensstrasse 3
D 06466 Gatersleben
graner@ipk-gatersleben.de

Contact Details: Teams in the Consortia

Dr. l. Hartl
Bayerische Landesanstalt für Landwirtschaft
Bavarian State Research Center for Agriculture Institut für Pflanzenbau & Pflanzenzüchtung
Am Gereuth 8
D-85354 Freising
lorenz.hartl@lfl.bayern.de

Dr. D.K. Hincha
Max-Planck-Institut für Molekulare Pflanzenphysiologie
Wissenschaftspark Golm
D-14424 Potsdam
hincha@mpimp-golm.mpg.de

Dr. B. Holtschulte
KWS SAAT AG
Grimsehlstrasse 31
D-37574 Einbeck
b.holtschulte@kws.com

Prof. dr. H. Jeske
Universität Stuttgart
Biologisches Institut Lehrstuhl fur Molekularbiologie und Virologie der Pflanzen
Pfaffenwaldring 25
70550 Stuttgart
holger.jeske@bio.uni-stuttgart.de

Prof. dr. G. Jürgens
Universität Tübingen
Abteilung VI (Molecular biology)
Spemannstrasse 37-39
D-72076 Tübingen
gerd.juergens@zmbp.uni-tuebingen.de

Prof. dr. G. Kahl
Johann Wolfgang Goethe Universität
Institute of Biochemistry, Biocenter
Marie-Curie-Strasse 9
D-60439 Frankfurt a. Main
kahl@em.uni-frankfurt.de

Prof. dr. P. Karlovsky
University of Goettingen
Department of Crop Sciences
Grisebachstrasse 6
D-37077 Goettingen
pkarlov@gwdg.de

Prof. dr. ir. M. Koornneef
Max-Planck-Institut für Züchtungsforschung
Carl-von-Linné-Weg 10
D-50829 Köln
koornnee@mpiz-koeln.mpg.de

Dr. J. Kopka
Max-Planck-Institut für Molekulare Pflanzenphysiologie
Wissenschaftspark Golm
D-14424 Potsdam
kopka@mpimp-golm.mpg.de

Prof. T. Laux
Universität Freiburg
Department of Biology III
Schaenzlestrasse 1
D-79104 Freiburg
laux@biologie.uni-freiburg.de

Contact Details: Teams in the Consortia

Dr. G. Leckband
Norddeutsche Pflanzenzucht
Hans-Georg Lembke KG (NPZ)
Hohenlieth
D-24363 Holtsee
G.Leckband@npz.de

Dr. M. Lenhard
Universität Freiburg
Department of Biology III
Schaenzlestrasse 1
D-79104 Freiburg
lenhard@biologie.uni-freiburg.de

Dr. J.U. Lohmann
Max-Planck-Institut für
Entwicklungbiologie
Abteilung Evolutionsbiologie
Spemannstraße 37
D-72076 Tübingen
jlohmann@tuebingen.mpg.de

Dr. K. Mayer
GSF-National Research Center for
Environment and Health
Institute of Epidemiology
1 Ingolstaedter Landstr
85764 Neuherberg
Kmayer@gsf.de

Dr. T. Miedaner
University of Hohenheim
Institute of State Plant Breeding
Fruwirthstrasse 11
D-70593 Stuttgart
miedaner@uni-hohenheim.de

Prof. B. Neuffer
Universität Osnabrück
Department of Systematic Botany
Barbarastrasse 11
D-49076 Osnabrück
Barbara.Neuffer@biologie.uni-
osnabrueck.de

Prof. dr. T. Nürnberger
Universität Tübingen
Zentrum fur Molekularbiologie
der Pflanzen
Auf der Morgenstelle 3
D-72076 Tübingen
nuernberger@zmbp.uni-
tuebingen.de

Dr. M. Ouzunova
KWS SAAT AG
Grimsehlstrasse 31
D-37574 Einbeck
m.ouzunova@kws.com

Dr. J. Parker
Max-Planck-Institut für
Züchtungsforschung
Abteilung Molekulare
Phytopathologie
Carl-von-Linné-Weg 10
D-50829 Köln
parker@mpiz-koeln.mpg.de

Dr. J.R. Philips
Universität Bonn
Institut für Zellulaere und
Molekulare Botanik Zellbiologie
der Pflanzen
Kirschallee 1
D-53115 Bonn
phillips@uni-bonn.de

Contact Details: Teams in the Consortia

Dr. K. Pillen
Universität Bonn
Algemeine Pflanzenbau
Katzenburgweg 5
D-53115 Bonn
k.pillen@uni-bonn.de

Prof. dr. D.G. Robinson
Universitat Heidelberg
Plant Sciences
Im Neuenheimer Feld 230
69120 Heidelberg

Dr. P. Schweizer
Leibniz Institute
Institute for Plant Genetics and
Crop Plant Research (IPK)
Corrensstrasse 3
D 06466 Gatersleben
schweiz@ipk-gatersleben.de

Dr. D.J. Stahl
PLANTA GmbH
Grimsehlstrasse 31
D-37555 Einbeck
d.stahl@kws.com

Dr. N. Stein
Leibniz-Institut
Institut für Pflanzengenetik und
Kulturepflanzenforshcung (IPK)
stein@ipk-gatersleben.de

Prof. dr. M. Stitt
Max-Planck-Institut für
Molekulare Pflanzenphysiologie
Department of Developmental
Physiology & Genomics
Am Mühlenberg 1
D-14476 Potsdam-Golm
mstitt@mpimp-golm.mpg.de

Dr. E. Stoger
Rheinisch-Westfälische
Technische Hochschule
Institut für Biologie IV
Microbiologie
Worringerweg 1
D-52074 Aachen
stoger@molbiotech.rwth-
aachen.de

Dr. G. Strittmatter
KWS SAAT AG
Grimsehlstrasse 31
D-37574 Einbeck
h.harling@kws.com

Prof. dr. K. Theres
Max-Planck-Institut für
Züchtungsforschung
Planzenzüchtung und Genetic
Carl-von-Linne-Weg 10
50829 Köln
theres@mpiz-koeln.mpg.de

Prof. dr. R. Töpfer
Federal Centre for Breeding
Research on Cultivated Plants
Institute for Grapevine Breeding
Geilweilerhof
76833 Siebeldinge
r.toepfer@bafz.de

Dr. S. Ullman
QIAGEN GmbH
Nucleic Acid Preparartion
Research
Qiagen Str. 1
40724 Hilden

Contact Details: Teams in the Consortia

Prof. dr. D. Weigel
Max-Planck-Institut für
Entwicklungbiologie
Abteilung Molekulare Biologie
Spemannstraße 35/IV
D-72076 Tübingen
weigel@weigelworld.org

Dr. J. Weyen
Saaten-Union Resistenzlabor
GmbH
Research Tissue Culture
Hovedisser Str. 92
D-33818 Leopoldshoehe
weyen@saaten-union-labor.de

Dr. U. Wienand
Universität Hamburg
Applied Plant Molecular Biology
Ohnhorststrasse 18
D-22609 Hamburg
udo.wienand@uni-hamburg.de

Dr. P.J. Winter
GenXPro-GmbH
Frankfurt Innovation Centre
Biotechnology
Altenhöferallee 3
D-60438 Frankfurt
p.winter@em.uni-frankfurt.de

Dr. E. Zyprian
BAZ Institut für Rebenzüchtung
Geilweilerhof
Genetics Molecular Genetics
Geilweilerhof
D-76833 Siebeldingen
e.zyprian@bafz.de

Italy

Dr. L. Cattivelli
CRA - Experimental Institute for
Cereal Research
Section of Fiorenzuola d'Arda
Via S. Protaso, 302
I-29017 Fiorenzuola d'Arda PC
luigi.cattivelli@entecra.it

Dr. L. Colombo
Università degli studi di Milano
Dipartimento di Biologia
Via Celoria 26
I-20133 Milano
lucia.colombo@unimi.it

Prof. P. Costantino
Universita Roma La Scapienza
Dipartemento Genetica e Biologia
Molecolare
Piazzale Aldo Moro 5
I-00185 Roma
Paolo.Costantino@uniroma1.it

Dr. S. Grando
Istituto Agrario di San Michele
all'Adige IASMA
Centro Sperimentale
Via Mach 1
38010 Trento
stella.grando@iasma.it

Prof. dr. M. Kater
Università degli studi di Milano
Department of Biomolecular
Sciences and Biotechnology
Via Celoria 26
20133 Milano
martin.kater@unimi.it

Contact Details: Teams in the Consortia

Prof. dr. G. de Lorenzo
Università di Roma La Sapienza
Dipartemento Biologia Vegetale
Piazzale Aido Moro.5
00185 Rome
delorenzo@axrma.uniroma1.it

Dr. G. Morelli
Institutio nazionale della nutrizione
Unità di Nutrizione Sperimentale
Via Ardcatina 546
I-00178 Roma

Dr. M. Morgante
Università di Udine
Dipartimento di Scienze Agrarie ed Ambientali
michele.morgante@uniud.it

Prof. I. Ruberti
Università di Roma
Dipartimento di Genetica e Biologia Molecolare
P.Le Aldo Moro, 5
ida.ruberti@uniroma1.it

Dr. R. Velasco
Instituto Agrario San Michele all'Adige- Biology Department
Via Mach 1
38010 San Michele a/A
riccardo.velasco@iasma.it

Norway

Prof. dr. A.M. Bones
Norwegian University of Science and Technology
Department of Biology
Hogskoleringen 5
DU1-114 Trondheim
Atle.Bones@bio.ntnu.no

Dr. P.E. Grini
University of Oslo
Department of Molecular Biosciences
P.O.Box 1041
0316 Oslo
p.e.grini@imbv.uio.no

Portugal

Dr. S.B.Q. Amâncio
Instituto Superior de Agronomia
DBEB/CBAA
1349-017 Lisbon

Dr. H.J. Boehm
PLANSEL Lda (JBP)
Montemor o Novo
hans.boehm@hp.com

Prof. A.J.C. Campilho
Faculdade de Engenharia da
Universidade do Porto
Instituto de Engenharia Biomédica
Rua Dr. Roberto Frias
4200-465 Porto,

Dr. J.E.J. Dias
Estação Vitivinicola Nacional
Viticulture
Quinta d' Almoinha
2565-191 Runa
evn.eiras.dias@mail.net4b.pt

Prof. M.P.S. Fevereiro
Universidade of Lisboa
Instituto de Tecnologia Quimica e
Biologica
Aparatado 127
2781-901 Oeiras
psalema@itqb.unl.pt

Mrs. A.M. Fortes
Instituto de Ciencia Aplicada e
Tecnologia ICAT
Molecular Biology & Plant
Biotechnology
Ed. ICAT, Campo Grande
1749-016 Lissabon

Dr. C.M.P. Marques
RAIZ - Forestry and Pulp Institute
Av. da Republica, apt. 127
2781-901 Oeiras

Prof. M.S.S. Pais
Institute of Applied Science and
Technology Science Faculty
Campo Grande
1749-016 Lisboa
maria.pais@icat.fc.ul.pt

Dr. A.M.N.V.N. Pires
Instituto Superior Tecnico
Departement of Mathematics
Avenida Rovisco Pais
1049-001 Lisboa
apires@math.ist.utl.pt

Dr. M.C. Vaz Pato
Universidade of Lisboa
Instituto de Tecnologia Quimica e
Biologica
Aparatado 127
2781-901 Oeiras
cpatto@itqb.unl.pt

Contact Details: Teams in the Consortia

Spain

Dr. M. Aguilar Portero
Instituto de Investigación y Formación Agroalimentaria y Pesquera.
Unidad de Mejora y Agronomía.
Departamento de Mejora y Agronomía de
Apartado Oficial
41200 Alcala del Rio (Sevilla)
manuel.aguilar.portero@juntadeandalucia.es

Dr. C. Alonso-Blanco
Centro Nacional de Biotecnologia
Department of Genetics Molecular and Plants
C/ Darwin 3, Campus de Cantoblanco
28049 Madrid

Prof. dr. F. Aniento
Universidad de Valencia
Department of Biochemistry and Molecular Biology
Ave. Doctor Moliner 50
E-46100 Burjassot Valencia

Dr. S.G. Atienza Penas
Consejo Superior de Investigaciones Cientificas
Instituto de Agricultura Sostenible
Agronomía y Mejora Vegetal
Finca Alameda del Obispo s/n
14004 Cordoba
es2atpes@uco.es

Dr. C. Baixauli Soria
Fundación Ruralcaja Valencia
Apartado 194
46200 Paiporta, Valencia
carlosbaixauli.ruralcaja@cajarural.com

Dr. M. Bastida Virgili
ERA Biotech
Parc Científic de Barcelona
C/Josep Samitier, 1-5
08028 Barcelona
mbastida@erabiotech.com

Prof. dr. E.R. Bejarano
University of Malaga
Department of Philosophy
Campus de Teatinos
E 29071 Malaga

Dr. C.C. Caminero-Saldaña
Instituto Tecnologico Agrario de Castilla y Leon
Departamento de Produccion Vegetal y Agronomia
Ctra. Burgos km 119
47071 Valladolid
camsalco@itacyl.es

Dr. J. Carreno Espin
Instituto Murciano de Investigacion y Desarrollo agrario y alimentario
Department Table Crapes
Mayor s/n. La Alberca
30150 Murcia
juan.carreno@carm.es

Contact Details: Teams in the Consortia

Prof. R.M. Carreres
Instituto Valenciano
Investigaciones Agrarias
Departamento del Arroz
Moncada- Naquera, km 4.5
46113 Valencia
rcarreres@ivia.es

Prof. P. Christou
Universitat de Lleida
Department de Produccio Vegetal
i Ciencia Forestal
Av. Alcada Rovira Roure 191
E-25198 Lleida
paul.christou@icrea.es

Drs. P. Cubas
Centro Nacional de Biotecnologia
Department of Genetics Molecular
and Plants
C/ Darwin 3, Campus de
Cantoblanco
28049 Madrid
pcubas@cnb.uam.es

Dr. B. Fernández-Muñiz
Universidad de Oviedo
Plant Physiology Group
CATEDRÁTICO RODRIGO
URÍA s/n
33071 Oviedo

Dr. J. Garcia-Mas
Laboratori de Genetica Molecular
Vegetal
Departament de Gentica Vegetal
Carretera de Cabrils s/n
08348 Barcelona
jordi.garcia@irta.es

Prof. dr. Genzbittel
AGROALIMED
Fundación de la Comunidad
Valenciana para la Investigación
Moncada-Náquera km 4,5
46113 Moncada (Valencia)
gentz@ensat.fr

Prof. dr. J.L. Guardiola
Universidad Politecnica de
Valencia
Departamento de Biologia Vegetal
Grupo de Fisiologia Vegetal
46071 Valencia
jlguardiola@bvg.upv.es

Dr. G. Hueros
University of Alcalà de Henares
Department of Cell Biology and
Genetics
28871 Alcalà de Henares
Madrid
gregorio.hueros@uah.es

Dr. T. Jahrmann
Semillas Fitó
Molecular Markers Department
S.A., Selva de Mar 111
08019 Barcelona
torben@fito.es

Mrs. D. Ludevid
Instituto de Biologia Molecular de
Barcelona
Department Molecular & Cell.
Biology - IBMB-CSIC
Jordi Girona 18-26
Barcelona
dlmgmd@ibmb.csic.es

Contact Details: Teams in the Consortia

Dr. J.P. Majada Gruijo
Servicio Regional de
Investigación y Desarrollo
Agrario (SERIDA)
Sección Forestal
Finca Experimental "La Mata"
33825 Grado. Asturias
jmajada@serida.org

Dr. L. Marqués Falcó
Cooperativa de Productores de
Semillas de Arroz
Cooperativa de Productores de
Semillas de Arroz
Avda del Mar, 1
46410 Sueca (Valencia)
copsemar@copsemar.com

Dr. J.M. Martinez-Zapater
Centro Nacional de Biotecnologia
Department of Genetics Molecular
and Plants
C/ Darwin 3, Campus de
Cantoblanco
28049 Madrid
zapater@cnb.uam.es

Prof. dr. T. Millan
Universidad de Cordoba
Departamento Genetica
Campus Rabanales Edif. C-5
14071 Cordoba
ge1mivat@uco.es

Prof. dr. A. Molina
Centro de Biotecnología y
Genómica de Plantas
Dep. Biotecnología E.T.S.
Ingenieros Agrónomos
Avda. Complutense
E-28040 Madrid
antonio.molina@upm.es

Dr. A.R. Monreal
Universidad de Valladolid
Campus La Yutera
Avenida de Madrid 57
34004 Palencia
rammonal@jcyl.es

Prof. F. Nuez
Universidad de Valencia
Center for the Conservation and
Breeding of the Agricultural
Biodiversity
Camino de Vera, s/n,
46021 Valencia
fnuez@btc.upv.es

Dr. J.M. Osca Lluch
Universidad Politécnica de
Valencia
Escuela Técnica Superior del
Medio Rural y Enología Dpt.
Vegetal Production
Avda Blasco Ibáñez, 21
46021 Valencia
josca@prv.upv.es

Contact Details: Teams in the Consortia

Dr. G. Peñas
IRTA Investigator of the Àrea de Conreus Extensius
Estació Experimental Agrícola Mas Badia
Carretera de la Tallada s/n
17130 La Tallada d'Empordà

Prof. dr. M. Pérez de la Vega
Universidad de Leon
Area de Genetica
Campus de Vegazana
240714 Leon
degmpv@unileon.es

Prof. dr. D. Rubiales
Universidad de Cordoba
Institute for Sustainable Agriculture
Alameda del Obispo s/n, Apdo. Correos 4084
E-14080 Cordoba
ge2ruozd@uco.es

Dr. J. Salinas
Instituto Nacional de Investigacion y Technologia Agraria y Alimentaria
Departemento de Biotecnologia
Ctra. de La Coruña km 7
28040 Madrid
salinas@inia.es

Dr. I. Solis
AGROVEGETAL S.A.
Demetrio de los Rios 15
41003 Sevilla
isolis@faeca.es

Dr. A.M. Torres
IFAPA-CICE, Junta de Andalucía
CIFA "Alameda del Obispo" Area de Mejora y Biotecnología
Apdo. 3092
14080 Córdoba
anam.torres.romero@juntadeandalucia.es

Dr. E.R. Viesca de la
Instituto Nacional de Investigacion y Technologia Agraria y Alimentaria
Departemento de Biotecnologia
Ctra. de La Coruña km 7
28040 Madrid

Contact Details: Teams in the Consortia

Switzerland

Prof. dr. B. Keller
Universität Zürich
Institut für Plant Biology
Zollikerstrasse 107
CH-8008 Zürich
bkeller@botinst.unizh.ch

The Netherlands

Dr. G. van den Ackerveken
Universiteit Utrecht
Departement Biologie Moleculaire
& Cellulaire Biologie
Postbus 80056
3508 TB Utrecht
g.vandenackerveken@bio.uu.nl

Prof. dr. G.C. Angenent
Radboud Universiteit Nijmegen
Fac. Natuurwetenschappen,
Wiskunde en Informatica
Experimental Botany
Toernooiveld 1
6525 ED Nijmegen
G.Angenent@science.ru.nl

Dr. R. Geurts
Wageningen Universiteit
Plantenwetenschappen
Lab. voor Moleculaire Biologie
Postbus 8128
6700 ET Wageningen
rene.geurts@wur.nl

Mr. J. Heldens
Enza Zaden Research and
Development B.V.
Postbus 7
1600 AA Enkhuizen
j.heldens@enzazaden.nl

Contact Details: Teams in the Consortia

Dr. P.G.L. Klinkhamer
Universiteit Leiden
Faculteit der Wiskunde en
Natuurwetenschappen
Biologie
Postbus 9505
2300 RA Leiden
P.G.L.Klinkhamer@biology.leide
nuniv.nl

Prof. dr. B.J.G. Scheres
Universiteit Utrecht
Departement Biologie
Moleculaire & Cellulaire Biologie
Postbus 80056
3508 TB Utrecht
b.scheres@bio.uu.nl

Dr. B.P.H.J. Thomma
Wageningen Universiteit
Plantenwetenschappen
Laboratorium voor Fytopathologie
Postbus 8025
6700 EE Wageningen
bart.thomma@wur.nl

Prof. dr. R. Verpoorte
Universiteit Leiden
Faculteit der Wiskunde en
Natuurwetenschappen Biologie
Postbus 9505
2300 RA Leiden
verpoort@chem.leidenuniv.nl

Dr. D. Vreugdenhil
Wageningen Universiteit
Plantenwetenschappen
Laboratorium voor
Plantenfysiologie
Arboretumlaan 4
6703 BD Wageningen
dick.vreugdenhil@wur.nl

Prof. dr. S.C. de Vries
Wageningen Universiteit
Agrotechnologie en
Voedingswetenschappen
Postbus 8128
6700 ET Wageningen
sacco.devries@wur.nl

Prof. dr. ir. P.J.G.M. de Wit
Wageningen Universiteit
Plantenwetenschappen
Laboratorium voor Fytopathologie
Postbus 8025
6700 EE Wageningen
pierre.dewit@wur.nl

Contact Details: Teams in the Consortia

United Kingdom

Dr. M.T. Abberton
Institute of Grassland and
Environmental Research
Plant Genetics and Breeding
Plas Gogerddan
SY23 3EB Aberystwyth
michael.abberton@bbsrc.ac.uk

Prof. J.L. Beynon
University of Warwick
Horticulture Research
International
Wellesbourne
CV35 9EF Warwick
jim.beynon@warwick.ac.uk

Prof. D. Charlesworth
University of Edinburgh
Institute of Cell, Animal and
Population Biology
West Mains Road
Edinburgh
Deborah.Charlesworth@ed.ac.uk

Dr. T. Dalmay
University of East Anglia
Norwich
t.dalmay@uea.ac.uk

Dr. B.H. Davies
University of Leeds
Center for Plant Sciences Faculty
of Biological Sciences
LS2 9JT Leeds
b.h.davies@leeds.ac.uk

Dr. I.S. Donnison
Institute of Grassland and
Environmental Research
Plant Genetics and Breeding
Plas Gogerddan
SY23 3EB Aberystwyth
iain.donnison@bbsrc.ac.uk

Dr. A.J. Flavel
University of Dundee
School of Life Sciences Plant
Research Group
Invergowrie
DD2 5DA Dundee
a.j.flavell@dundee.ac.uk

Prof. dr. J.D.G. Jones
John Innes Centre
Sainsbury Laboratory Norwich
Research Park
Colney Lane
Norwich NR4 7UH
jonathan.jones@sainsbury-
laboratory.ac.uk

Prof. dr. O. Leyser
University of York
Department of Biology
POBox 373
YO10 5YW York
hmol1@york.ac.uk

Dr. K.S. Lilley
University of Cambridge
Department of Chemistry
Lensfield Road
CB2 1EW Cambridge

Contact Details: Teams in the Consortia

Prof. B.K. Mable
University of Glasgow
Development of Environmental
and Evolutionary Biology Biology
Graham Kerr Building IBLS
G12 8QQ Glasgow
b.mable@bio.gla.ac.uk

Prof. C.R. Martin
John Innes Centre
Department of Genetics Norwich
Research Park
Colney Lane
Norwich NR4 7UH
cathie.martin@bbsrc.ac.uk

Prof. J.A.H. Murray
University of Cambridge
Institute of Biotechnology
Tennis Court Road
CB2 1QT Cambridge
j.murray@biotech.cam.ac.uk

Dr. G.E.D. Oldroyd
John Innes Centre
Dicease ans Stress Biology
Norwich Research Park 1
NR4 7UH Norwich
giles.oldroyd@bbsrc.ac.uk

Dr. J.R. Russell
Scottish Crop Research Institute
Department of Biodiversity
Genetics
Invergowrie
Dundee, DD2 5DA
joanne.russell@scri.ac.uk

Dr. R. Sablowski
John Innes Centre
Department of Cellular and
Developmental Biology
Colney Lane
Norwich NR4 7UH
robert.sablowski@bbsrc.ac.uk

Dr. L. Skot
Institute of Grassland and
Environmental Research
Plas Gogerddan
SY23 3EB Aberystwyth
leif.skot@bbsrc.ac.uk

Dr. L.J. Sweetlove
University of Oxford
Department of Plant Sciences
South Parks Road
Oxford OX1 3RB
lee.sweetlove@plants.ox.ac.uk

Dr. M. Tör
University of Warwick
Coventry, CV4 7AL

Dr. R. Waugh
The Scottish Research Institute
Genetics Division Unit of Applied
Genetics
Invergowrie
DD2 5DA Dundee
Robbie.Waugh@scri.ac.uk

Contact Details: National Call Coordinators and ERA-PG Managing Office

National Call Coordinators

Appointed from 20 September 2005 unless otherwise mentioned

Belgium

Until 1-9-2006
Dr. Monika Sormann
Flemish Government, Dept. of Economy, Science and Innovation
Boudewijnlaan 30, 1000 Brussels
Tel: +32 2 553 58 64
monika.sorrman@wim.vlaanderen.be

From 1-9-2006
Dr. Kathleen D'Hondt
Flemish government
Departement Economy, Science and Innovation Koning Albert II-laan 35, B-1030 Brussels
Tel: +32 2 553 57 71
kathleen.dhondt@ewi.vlaanderen.be

Denmark

Mr. Per Kolbeck Nielsen
The Secretariat of the Danish Research Council for Technology and Production, Danish Agency for Science, Technology and Innovation
Bredgade 40, DK-1260
Copenhagen
Tel: +45 3544 6345
pkn@fist.dk

Finland

Dr. Sirpa Huuskonen
Suomen Akatemia (AKA)
PO Box 99, (Vilhonvuorenkatu 6)
FI-00501 Helsinki
Tel: +358 (0)9 7748 8370
sirpa.huuskonen@aka.fi

Until 15-5-2006 also
Dr. Reetta Kettunen
ESGEMO coordination office
Dept. Applied Biology
PO Box 27, FI-00014 University of Helsinki
Tel: +358 (0)9 191 59666
reetta.kettunen@helsinki.fi

France

Dr. Francis Quétier
Agence Nationale de la Recherche (ANR)
22 rue Monge, F-75005 Paris
Tel: +33 (0) 6 80 99 16 83
francis.quetier@gip-anr.fr

Contact Details: National Call Coordinators and ERA-PG Managing Office

Germany - DFG

Until 1-6-2006 and from 1-7-2007
Dr. Catherine Kistner
Deutsche Forschungsgemeinschaft (DFG)
Kennedyallee 40, D-53175 Bonn
Tel: +49 228 885 28 03
catherine.kistner@dfg.de

From 1-6-2006 until 1-7-2007
Dr. Katrin Hahlen
Deutsche Forschungsgemeinschaft (DFG)
Kennedyallee 40, D-53175 Bonn
Tel: +49 (0)228 885 28 03
Katrin.Hahlen@dfg.de

Germany – FZJ on behalf of BMBF

Dr. Rainer Büschges
Projektträger Jülich,
Forschungszentrum Jülich
Leo-Brandt-Strasse, D-52428 Jülich
Tel: +49 (0) 2461 61 87 82
r.bueschges@fz-juelich.de

Italy

Until 23-12-2005
Dr. Stefano Garofoli
c/o Dr. Riccardo Carelli
Ministero dell'Istruzione, dell'Università e della Ricerca (MIUR)
P. le Kennedy 20, 00144 Roma
Tel: +39-333-589-7755
stefano.garofoli@roma1.infn.it

From 10-1-2006 until 10-3-2006
Mrs. Gloria Livoli
Ministero dell'Istruzione, dell'Università e della Ricerca (MIUR)
D.G.S.S.I.R.S.T - Ufficio III
P.le Kennedy, 20
00144 Rome
Tel: + 39 06 58497961
gloria.livoli@miur.it

From 10-3-2006
Mr. Mauro Massulli
Ministero dell'Istruzione, dell'Università e della Ricerca (MIUR), D.G.S.S.I.R.S.T - Ufficio III
P.le Kennedy, 20, 00144 Rome
Tel: + 39 06 58497961
mauro.massulli@miur.it

Contact Details: National Call Coordinators and ERA-PG Managing Office

The Netherlands

Dr. Christine Bunthof
Netherlands Genomics Initiative (NGI)
PO Box 93035 (Laan van Nieuw Oost Indië 300),
NL - 2509 AA Den Haag
Tel: +31 (0) 317 477189
bunthof@genomics.nl

Norway

Until 15-10-2006
Dr. Päivi Teivainen-Lædre
Norges forskningsråd (RCN)
PO Box 2700, (St. Hanshaugen),
N-0131 Oslo
Tel: +47 22 03 72 06
patl@rcn.no

From 15-10-2006
Dr. Steinar Bergseth
Norges forskningsråd (RCN)
PO Box 2700, (St. Hanshaugen),
N-0131 Oslo
Tel: +47 22 03 73 23
stb@rcn.no

From 1-3-2007 until 1-7-2007
Dr. Jowita Sleboda
Norges forskningsråd (RCN)
PO Box 2700, (St. Hanshaugen),
N-0131 Oslo
Tel: +47 22 03 73 87
jsl@rcn.no

Portugal

Until 19-10-2006
Dr. Luisa Henriques
FCT- Fundação para a Ciência e a Tecnologia Av. D. Carlos I, 126 – 2, 1249-074 Lisboa
Tel: +351 21 392 44 54
lh@fct.mctes.pt

From 19-10-2006
Dr. Catarina Resende
FCT- Fundação para a Ciência e a Tecnologia Av. D. Carlos I, 126 – 2, 1249-074 Lisboa
Tel: +351 21 3924456
catarina.resende@fct.mctes.pt

Spain

Dr. Julio Barbas
Ministerio de Educación y Ciencia (MEC)
Paseo de la Castellana 160, 28071 Madrid
Tel: +34 91 34 94 586
julio.barbas@mec.es

United Kingdom

Dr. Sophie Laurie
Biotechnology and Biological Sciences Research Council (BBSRC)
Polaris House, North Star Avenue, SN2 1UH Swindon
Tel: +44 1793 41 33 40
sophie.laurie@bbsrc.ac.uk

ERA-PG Managing Office

Netherlands Genomics Initiative,
Netherlands Organisation for Scientific Research
(NGI/NWO)
P.O. Box 93035, 2509 AA The Hague

Dr. Wilma van Donselaar
Principle coordinator
Tel: +31 (0) 70 344 06 40
donselaar@genomics.nl

Dr. Okker van Batenburg
Executive coordinator
Tel: +31 (0) 70 324 40 43
batenburg@genomics.nl

Dr. Christine Bunthof
Executive coordinator
Tel: +31 (0)317 477 189
bunthof@genomics.nl

Mr. Paul Beckers
Contact Call Secretariat
Tel: +31 (0) 70 3440 517
beckers@genomics.nl

Mrs. Anja Langeveld
Secretary ALW office

Mrs. Jantien Kats
System administrator, ALW office

ERA-PG contract nº ERAC-CT-2003-510189