



# LEGATO

## LEGumes for the Agriculture of TOMorrow

**Collaborative project**  
**Grant agreement no: 613551**  
**SEVENTH FRAMEWORK PROGRAMME**

**THEME [KBBE.2013.1.2-02]**  
**[Legume breeding and management for sustainable**  
**agriculture as well as protein supply for food and feed]**

### **Deliverable D7.1**

### ***Project public website***

**Due date:** 31 March 2014

**Actual submission date:** M3

**Project start date:** 1<sup>st</sup> January 2014    **Duration:** 48 months

**Workpackage concerned:** WP7

**Concerned workpackage leader:** Dunixi Gabiña. IAMZ-CIHEAM

**Dissemination level:** PU (public)

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## **I. Objectives**

The LEGATO Website <http://www.legato-fp7.eu/> is **the most important dissemination tool**, including all relevant information of the project and its activities and results. The web is aimed at external and internal users. Results and progress of the project are also published on the web as a tool to communicate with the stakeholders involved.

## **II. Deliverable procedure**

The present sections (they may evolve with the project) are:

- Homepage-Summary
- Project Overview
- Consortium (**logos and links** to each institution)
- Management Structure
- Scientific Methodology and Work Packages
- Events & Meetings
- Media centre
- Glossary
- Intranet. This section is managed by INRA Transfert through their Collaborative Platform

The deliverable has been produced by IAMZ-CIHEAM with its own personnel, in agreement with the LEGATO Coordinator (Dr. Richard Thompson; INRA Dijon) and following the suggestions from the WP8 (Management) leader (Caroline Sautot, INRA Transfert). The design of the LEGATO logo and banner has been produced by a graphical design company.

## **III. Conclusion**

The LEGATO website is operational since the beginning of the project and will be an important tool for dissemination and for internal communication via the Intranet.

## Annex 1: Graphical material

See below some of the LEGATO Web sections

### Home page

www.legato-fp7.eu

Comenzar a usar Firef... Últimas noticias FORESTERRA

**LEGATO**  
LEGumes for the  
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**LEGATO**

The **LEGATO** Project "LEGumes for the Agriculture of TOMorrow", project number 613551, is funded by the European Union under the FP7 Programme. The project has started in January 2014 and will finish in December 2017, and has a European contribution of 4,999,000 Euros.

LEGATO has 29 partners from eleven countries: France, UK, Czech Republic, Spain, Italy, Germany, Serbia, Portugal, Poland, Austria and Sweden and includes including 9 SMEs, as well as one international institution, the International Centre for Advanced Mediterranean Agronomic Studies (IAMZ-CIHEAM).

The project has been conceived to promote the culture of grain legumes in Europe by identifying priority issues currently limiting grain legume cultivation and devising solutions in term of novel varietal development, culture practices, and food uses. LEGATO will develop tools and resources to enable state of the art breeding methodology and to exploit fully the breadth of genetic resources available.

The overall aim of LEGATO is to contribute to the increased sustainable reintroduction of grain legumes in European cropping systems. Working on the major European grain legumes, pea, faba bean, and with specific objectives on white lupin and grass pea, the project will focus on the identification and testing of novel legume breeding lines possessing valuable characters such as disease and pest resistance and quality for human consumption.

**LEGATO KICK-OFF MEETING**  
Dijon, France, 4-5 March  
PRESS RELEASE  
IN DIFFERENT LANGUAGES

**News**

- Message of interest in collaborations. H2020 Calls. 30 January 2014
- Starting legato web. 1 January 2014

**Events & Meetings**


















- LEGATO kick-off meeting Dijon, France. 4-5 March 2014
- Starting legato web. 1 January 2014

All events »

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no 613551

The views expressed in this website are the sole responsibility of the author and do not necessarily reflect the views of the European Commission.

## Consortium

<ul style="list-style-type: none"> <li>› Homepage</li> <li>› Project Overview</li> <li>› <b>Consortium</b></li> <li>› Management Structure</li> <li>› Scientific Methodology and Work Packages</li> <li>› Deliverables and Publications</li> <li>› Events &amp; Meetings</li> <li>› Media centre</li> <li>› Glossary</li> <li>› Intranet</li> </ul>	<h3>Consortium</h3>  <p>INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE - INRA France</p>  <p>ABERYSTWYTH UNIVERSITY - AU United Kingdom</p>  <p>AGRITEC, vyzkum, slechteni a sluzby s.r.o. - AGRITEC Czech Republic</p>  <p>Agrovegetal S.A. Agrovegetal Spain</p>  <p>CONSIGLIO PER LA RICERCA E LA SPERIMENTAZIONE IN AGRICOLTURA - CRA Italy</p>  <p>AGENCIA ESTATAL CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS - CSIC Spain</p>  <p>FORSCHUNGSZENTRUM JUELICH GMBH JUELICH Germany</p>  <p>GENXPRO GMBH - GXP Germany</p>  <p>INSTITUTO ANDALUZ DE INVESTIGACION Y FORMACION AGRARIA PESQUERA ALIMENTARIA Y DE LA PRODUCCION ECOLOGICA - IFAPA Spain</p>  <p>INSTITUT ZA RATARSTVO I POVRTARSTVO - IFVNS Serbia</p>  <p>INSTITUTO NACIONAL DE INVESTIGACAO AGRARIA E VETERINARIA - INIAV Portugal</p>  <p>INRA TRANSFERT S.A. - IT France</p>  <p>INSTITUTO DE TECNOLOGIA QUIMICA E BIOLOGICA - UNIVERSIDADE NOVA DE LISBOA - ITQB Portugal</p>  <p>INSTYTUT GENETYKI ROSLIN POLSKIEJ AKADEMI NAUK IPG Poland</p>  <p>JOHN INNES CENTRE - JIC United Kingdom</p>  <p>MEDITERRANEAN AGRONOMIC INSTITUTE OF ZARAGOZA / INTERNATIONAL CENTRE FOR ADVANCED MEDITERRANEAN AGRONOMIC STUDIES - IAMZ-CIHEAM Spain</p>  <p>MOULIN DECOLLOGNE SAS - Decollogne France</p>
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....more institutions and companies

## Management structure



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### Management Structure



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    IPUC[Intellectual Property Use & Dissemination Committee] --- GA[General Assembly]
    IPUC --- EC[Executive Committee]
    GA --- AB[Advisory Board]
    GA --- CO[Coordinator]
    EC --- CO
    CO --- EUC[European Commission]
    CO --- AT[Administrative team]
    AT --- WP1[WP1]
    AT --- WP2[WP2]
    AT --- WP3[WP3]
    AT --- WP4[WP4]
    AT --- WP5[WP5]
    AT --- WP6[WP6]
    AT --- WP7[WP7]
    AT --- WP8[WP8]
    
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The **General Assembly** is the decision-making body of the project. Chaired by the project coordinator, it is composed of one representative from each partner organisation, each having one vote for decision making purposes. The General Assembly will be responsible for the strategic and political direction of the Project: the overall direction of all activities – research, training and management – and re-orientation whenever necessary, budget revision, incorporation of new contractors, and dealing with defaulting partners.

The **Executive Committee** is the decision-implementing body of the project. It is made up of the leaders of each workpackage and chaired by the coordinator Dr. Richard Thompson. The Executive Committee will be in charge of the operational management of all the activities of LEGATO. It will also prepare the decisions to be taken by the General Assembly and ensure that these decisions are properly implemented, integrating recommendations, and surveying ethical and gender issues. The Executive Committee will also be in charge of resource management of workpackages. The Executive Committee will be supported by the work of the Administrative Team including quality control and preparing meetings with the EC, the preparation and transmission of deliverables.

The **Intellectual Property Use and Dissemination Committee** will advise on the management of knowledge and of intellectual property and of other innovation-related activities arising in the project. The IPUDC will also monitor the implementation of the principles governing intellectual property rights which will partially be covered by the Consortium Agreement dispositions.

The objective of the **Advisory Board** is on the one hand to provide external points of view on the research conducted: (choice of genotypes x cropping systems x locations to be evaluated, adaptation to specific zones or markets) so it brings maximum outcomes to the agricultural/breeding sector and, on the other hand to serve as a key dissemination channel for project outcomes to facilitate project exploitation and impact. Membership will be open throughout the project.

Daily administrative management work and handling of the project logistics will be handled by the Administrative Team. The **Administrative Team** will be made up of an experienced project manager assisted by a project administrator.



Scientific Methodology and Work Packages



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### Scientific Methodology and Work Packages

**Overall strategy and general description**

As a baseline, we plan to develop tools and resources to enable the application of state of the art breeding methodology to the principal EU grain legume crops. The breeding tools will benefit from new data sources including our interaction with the Pea genome sequencing project (WP1). This will provide a much higher marker density than that hitherto available, and greatly accelerate plant breeding by speeding up introgression of favourable alleles of genes of interest. Due to the phylogenetic proximity of *Pisum sativum*, *Vicia faba*, and *Lathyrus* species, the data obtained for pea will be readily transferable to the other species under study. In parallel, and interacting synergistically with improved marker availability, wide genetic resources for these species will be tapped in the project (WP1). These will include: recombinant inbred line mapping populations, wide crosses between *Pisum sativum* and wild relatives (*P. fulvum*, *P. elatius*), white lupin (*Lupinus albus*) genetic resource collection, faba bean landraces, and wide crosses in grass pea (*L. sativa* x *L. cicera*).

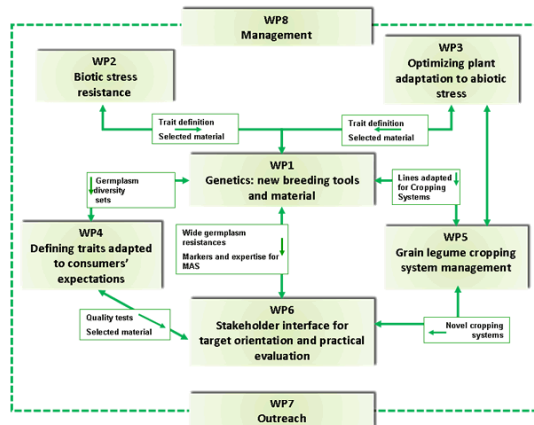
By exploiting these genetic resources, we should get access to new sources of resistance to different pests and pathogens: (WP2), and robustness and symbiotic efficiency (WP3). The project will necessarily focus on a limited number of pathogens and pests (WP2), in order to make a significant impact, and to complement other ongoing studies. Our targets chosen represent major constraints in different climatic zones of Europe. In addition to major pests and pathogens (weevils, *Ascochyta*, *Potyvirus*) of worldwide distribution, we have chosen pathogens of regional importance, such as *Aphanomyces* in central Europe and *Orobanche* in the Mediterranean basin, for which available control methods are ineffective, and levels of resistance insufficient. Sitona weevils have also been relatively little studied in the past, necessitating the standardisation of pest damage protocols.

These studies will also be carried out under drought-stressed conditions, to select genetic material best able to cope with this stress (WP3). We will identify the loci controlling auto-fertility in faba bean, to guide the introduction of this character into more robust varieties that can set seed even in the absence of the insect pollinator (WP1). Whereas European pea and faba bean breeding has been mainly concentrated on developing varieties for livestock feed, LEGATO includes an exploratory work package devoted to traits needed to increase human consumption (WP4). We will evaluate consumer's preferences, including their perception of the sustainability of legumes. We will identify accessions possessing favourable nutritional, organoleptic and/or processing quality traits for breeding programs, and devise rapid screening methods to accelerate the introduction of these traits. Although the development of new legume varieties is a priority, their successful exploitation will also depend on the adoption of new culture practices. We plan to use a novel modelling approach to devise and propose legume-based cropping systems adapted to each pedo-climatic zone, based on local consultation (MASC@). These cropping systems will then be tested in situ and evaluated for several properties (WP5).

Grain legumes fix atmospheric nitrogen in symbiosis with soil bacteria (Rhizobiaceae). The symbiotic interaction is bacterial strain-specific for a given host legume, and will not occur if the rhizobial strain concerned is not present in the soil. The rhizobial complement of the soil, and the effect of inoculation, will be studied for a network of different pedo-climatic zones within our project (WP5).

Promising pre-breeding material identified in WP1 through 5 will be transferred for testing in a network of pan-European trial sites to be further evaluated within cropping systems adapted to local conditions (WP6). Upcoming prebreeding material and new varieties, with the corresponding expertise, will be provided to and evaluated by, a network of plant breeders. The programme will also include tests with four plant breeders of marker-assisted selection on their material, using markers to emerge from the project.

LEGATO Work Breakdown Structure



WP1: Genetics and new breeding tools and material (Lead: CRA)


**WP1: Genetics and new breeding tools and material (Lead: CRA)**

The effort in this work package will be divided between generic marker generation, in the framework of the pea genome sequencing programme, and the development of genetic material for analysis of developmental traits. This workpackage involves the identification, distribution and deployment of allelic variation. Allelic variation with respect to aspects of fertility will be examined - the duration of the flowering period in pea and the ability to self-pollinate without insect tripping of flowers in faba bean (autofertility). WP1 will develop genetic markers for traits studied in other WPs and specific antinutritional metabolites in two of our target species. The real gain achievable from marker assisted selection will be assessed. Of our target crop species pea, despite having the most advanced genetics, lacks some important resources which we will develop. We will relate genetic maps to sequence data and deploy novel variation from wild pea species in discrete segments using chromosome substitution lines. Finally we will characterize the allele distribution in the main species of lupin cultivated in Europe. The SME participants will provide locus specific assays (SFH) and multi locus assays (GXP). The Pea genome Sequencing project is an international consortium devoted to applying nextgeneration sequencing technology (NGS) to elucidate the large (ca. 4.5 Gb) *P. sativum* genomic sequence. LEGATO will provide highly dense bin mapping SNPs, using RAD markers (Baird et al.), obtained by re-sequencing a set of F2 individuals from a cross between the variety Caméor and a distantly related wild pea accession.



**WP2: Biotic stress resistance (Lead: CSIC)**

Crop germplasm screens (pea, faba bean, grass pea) will be used to identify novel sources of resistance against weevils (both Sitona and Bruchus) and aphids, and to *Ascochyta* blights using several locations. To complement existing fungal resistance genes, additional sources of resistance will be searched for, playing particular attention to pre-penetration stages, such as papilla-based resistance, and their association with gene candidates known to confer this type of resistance in other crops will be tested. The availability of NGS sequence data will be exploited to refine markers for resistances against *Mycosphaerella pinodes*, *Aphanomyces euteiches* and insect pests. Knowledge on potyvirus resistance available for pea will be extended and applied to other related *Eschscholzia* spp. for example. 18Base resistance is mapped on a QTL candidate gene mapping within the QTL interval

## Events & Meetings



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### Events & Meetings

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**Intranet**

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