



Summary of PlantLink Seed Money Projects

2012–2015

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Table of Contents

PlantLink

Pg. 5	PlantLink — 18 seed money projects later
Pg. 6	Background
Pg. 6	Participating partners
Pg. 6	Scientific overview
Pg. 6	Financial outcome
Pg. 9-33	Summary of individual seed money projects
Pg. 34	Interview with seed money researcher
Pg. 36	Contact and more information

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PlantLink — 18 seed money projects later

When PlantLink was initiated in 2011 it was decided early on to devote a large part of its resources to seed money projects. The idea was clear – to stimulate novel, innovative pilot projects and kick-start new collaborations in plant science between Lund University and SLU Alnarp. Scientific excellence, a high degree of freedom and a low administrative burden were leading lines. During the first five years, roughly half of the PlantLink’s funds was spent on four rounds of in total 18 seed money projects.

Six years and 7.8 MSEK later leading to more than 15 scientific publication, we sum up the results in this report. And they are encouraging! To start with the seed money projects reflects the width and depth of plant science in Southern Sweden. With over 50 researchers participating they also show that plant science – even if it not always so clear from the outside – is spread over many different academic departments and private companies in the region. It continues to play an important role in Southern Sweden!

Secondly, as you can see in the individual summaries of the projects, many young researchers in the form of MSc, PhD students and post docs have benefitted from the funding. A strong support for young plant researchers is now a stated goal of PlantLink.

Finally, and of great importance, several major grants have sprung out of the seed money projects. In total more than 75 MSEK, ensuring that several of the projects are still very much alive. In addition, a new industrial research center, ScanOats, which will promote innovation and functional food based on oats, with several PlantLink-associated researchers at both universities and with involvement from local companies was granted no less than 100 MSEK this year!

So what could be more inspiring than to celebrate Lund University’s 350 years and SLU’s 40 years of existence than looking through and reflect back on the outcomes of these projects putting plant research first!

Alnarp, 25 September 2017

Editorial



Erik Alexandersson,
director of PlantLink.

Background of seed money projects

In 2011, the research network **PlantLink** was created as an alliance between Lund University and the Swedish University of Agricultural Sciences in Alnarp (SLU Alnarp), with financial support from the Skåne Regional Council (Region Skåne). The financial support from the Skåne Regional Council was primarily used to encourage and strengthen research interactions between academic groups and with commercial enterprises in Skåne. For this purpose, calls for PlantLink seed money projects were announced annually in 2012–2015. A total of 18 projects were granted, equalling 7.8 million SEK. The number of successful projects was 5 projects each in 2012, 2013, 2014 and 3 projects in 2015. The scientific and financial outcomes of the seed money projects are summarized in this report.

Participating partners

The participation from LU and SLU was relatively equal, and commercial enterprises were involved in several projects (Figure 1). In total, over 50 researchers from the Skåne region were involved in the seed money projects.

Scientific overview

The seed money projects span over a range of research topics that are in line with the PlantLink's aim to bridge the gap between basic and applied plant research, and to enable production of materials, medication and energy from plants in a sustainable way. The granted projects investigate plant stress, plant protection, plant-insect-microorganism interactions, biotech in new crops and new plant-based products, and pollination biology (Figure 2). These projects have led to over 15 publications and a number of manuscripts are still in preparations (see the individual project reports).

Financial outcome

In addition to sparking scientific collaborations in the Skåne region, the seed money projects have been a gateway to larger scientific collaborations. seed money was used for part of postdoc and PhD-financing, making it possible to involve young scientists in new projects. International contacts were established and further grants were applied from Crafoord, SIDA, the Ice-3 Strategic fund, Formas and VR. The Foundation for Strategic Research (SSF) granted 2 former seed money projects funding, equaling over 60 MSEK together.

One of these projects focuses on using plants as insect pheromone factories. The seed money projects have also resulted in funding to for example solutions for sustainable production of organic clover seeds. This additional national funding amounts to longterm investments ensuring that several of the PlantLink seed money projects are still ongoing.

In total, the invested 7.8 MSEK in seed money has resulted in scientific project funding in the region of over 75 MSEK and in addition PlantLink researchers are now collaborating in the ScanOats project. Earlier this year the new Research Centre Scanoats at Lund University received 100 MSEK for research on functional foods and oat genomics, where both LU and SLU Alnarp are partners.

Background

»In total, the invested 7.8 MSEK in seed money has resulted in scientific project funding in the region of over 75 MSEK.«

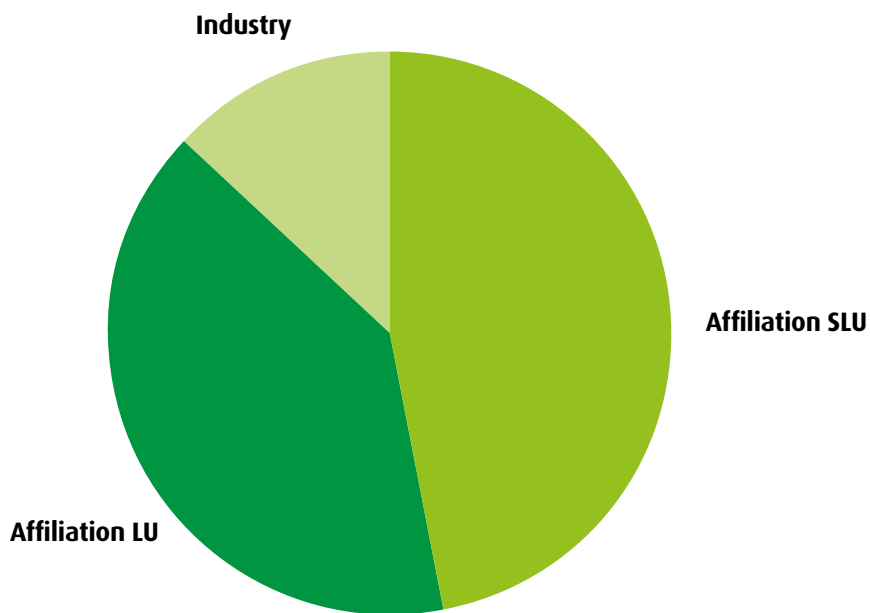


Figure 1. Overview of the participating researchers in the 18 PlantLink seed money projects granted between 2012-2015.

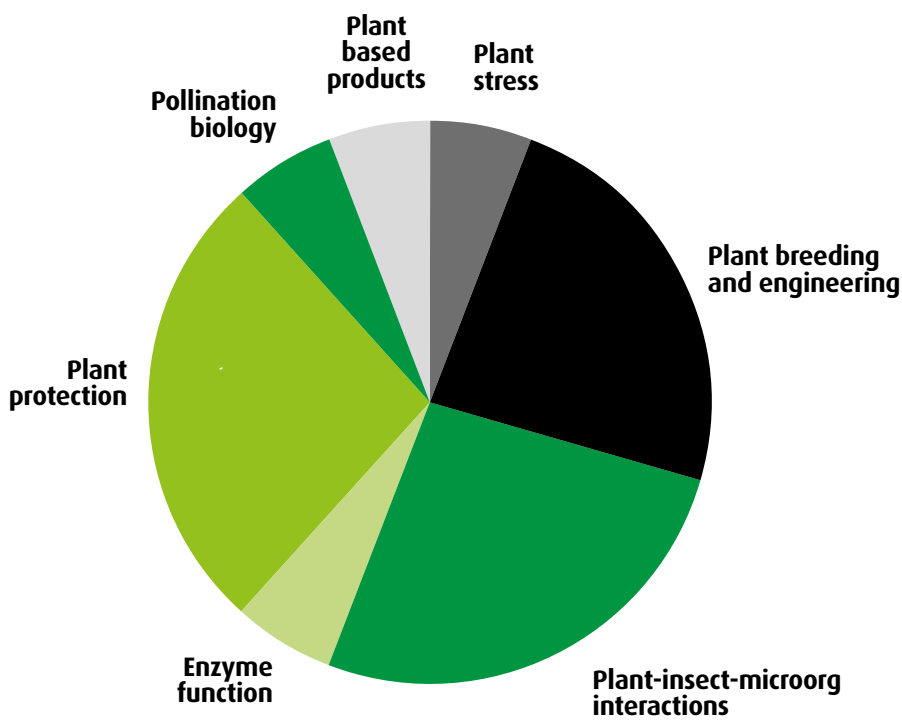


Figure 2. Topics represented in the granted seed money projects.



Scientific output of individual seed money projects

- Pg. 10 **Redox restrictions in plant biotic stress responses?**
- Pg. 11 **A plant factory for moth pheromone production - proof of principle**
- Pg. 12 **Influence of hemoglobin expression on oil seed qualities**
- Pg. 14 **Enzymatic fractionation of oils from new crops**
- Pg. 16 **Tripartite Plant-Yeast-Insect Interactions**
-

- Pg. 17 **Identification of glycerophosphocholine acyltransferase (GPCAT) genes in yeast and plants**
- Pg. 18 **Devising a morphodynamic computational model for hypersensitive reaction development**
- Pg. 19 **Biogas digestate promotes plant production but reduces mycorrhizal abundance**
- Pg. 20 **Towards the ecological meaning of Streptomyces-produced and induced volatiles in plant-insect-microbe interactions**
- Pg. 22 **Selection of plant defense against natural enemies: Induced defense and environmental effects within and between generations**
-

- Pg. 23 **Unravelling Fusarium-Oat interaction mechanisms by proteomics**
- Pg. 24 **Pollinators – How attractive is the colour, odour and shape of clover flowers?**
- Pg. 26 **Variability in sugar beet for impact of Trichoderma biocontrol**
- Pg. 27 **Novel mass spectrometrical analyses for the identification of potato pathogens on potato leaves and their targets in the leaf apoplast**
-

- Pg. 28 **Aboveground-effects of volatiles produced by Streptomyces soil bacteria on plants and insects**
- Pg. 30 **Evaluating a multi-scale structural-mechanistic modeling approach of plant protein based materials with interesting properties: tuning structure with functionality**
- Pg. 32 **Genetic variation and gene expression analysis of tolerance to infection by Phytophthora infestans in a wild Solanum species**
-

Index

2012

2013

2014

2015

Redox restrictions in plant biotic stress responses?

2012

Plants experience severe abiotic and biotic environmental variations, that strain the internal redox homeostasis. The world is facing increased needs for plant-derived products, while climatic changes are expected to increase agricultural plant stress. Plant stress already imposes the largest restriction on agriculture worldwide [1]. Biotechnological modifications have improved stress tolerance of agricultural plants, but a major hinder for further development has been a lack of understanding of metabolic systems and their perturbation by stress [2]. Especially, the central redox compound NADPH, and its oxidised form NADP⁺ is involved in supporting growth and photosynthesis, as well as powering biotic and abiotic stress signalling and ROS detoxification [3].

The aim of this investigation was to determine if plants genetically modified for mitochondrial NADPH oxidation capacity, and showing variations in cellular NADPH/NADP⁺-ratio [4] would display changes in the defence to the common pathogen *Phytophthora infestans*, e.g. indicating a broken resistance at lowered NADPH/NADP⁺. After infection, we observed dynamic changes in NADPH/NADP⁺ and NADPH-producing pathways. Mainly, short term treatment lowered and long term increased NADPH/NADP⁺ in all lines (the latter correlated to an upregulated glucose-6-phosphate pathway capacity), but accentuated in the transgenic lines. Visual phenotypic changes were not consistently observed in response to infection. Nevertheless, among pathogen defence markers, staining for H₂O₂ and callose production, which were strongly increased by infection, were surprisingly both negatively correlated to NADPH/NADP⁺-ratios. The mechanism for this is, however, not known. The results indicate dynamic interactions involving NADP(H) during the infection by *Phytophthora*, affecting the response outcome of the biotic interaction, but that more research is needed to clarify the mechanistic changes.

The project was part of a PhD student project.

Participants

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1. Chrispeels MJ, Sadava DE (2003) Plants, genes, and crop biotechnology. Sudbury, MA: Jones and Bartlett Publishers.

2. Vinocur B, Altman A (2005) Recent advances in engineering plant tolerance to abiotic stress: Achievements and limitations. *Current Opinion in Biotechnology* 16: 123-132.

3. Rasmusson AG, Wallström SV (2010) Involvement of mitochondria in the control of plant cell NAD(P)H reduction levels. *Biochem Soc Trans* 38: 661-666.

4. Liu YJ, Nunes-Nesi A, Wallström SV, Lager I, Michalecka AM, Norberg FE, et al. (2009) A redox-mediated modulation of stem bolting in transgenic *Nicotiana sylvestris* differentially expressing the external mitochondrial NADPH dehydrogenase. *Plant Physiology* 150: 1248-1259.

A plant factory for moth pheromone production — proof of principle

2012

Using *Nicotiana benthamiana* as a plant factory, we produced typical moth sex pheromone components (long chain fatty alcohols and acetates) by transient expression of up to four genes coding for consecutive biosynthetic steps. We specifically produced biologically active multi-component sex pheromones for two moth species. The fatty alcohol fractions from the genetically modified plants were acetylated synthetically and mixed to mimic the respective sex pheromones of the small ermine moths *Yponomeuta evonymella* and *Y. padella*. These mixtures were very efficient and specific for trapping of male moths, matching the activity of conventionally produced synthetic pheromones. Our long-term vision is to design tailor-made production of any moth pheromone component in genetically modified plants. Such semi-synthetic preparation of sex pheromones may be a novel and cost-effective way of producing moderate to large quantities of pheromones with high purity and a minimum of hazardous waste. The approach is just in its infancy, but the results are already promising. The manuscript was part of the PhD thesis of Baojian Ding that was defended on the 14th of February 2014, and is now published in Nature Communications [1].

Our long-term vision is to design tailor-made production of any moth pheromone component in stably transformed plants. Such sustainable preparation of sex pheromones from plants will be a novel and cost-effective way of producing moderate to large quantities of pheromones with high purity and a minimum of hazardous waste. Moving from transient expression to stable transformants will further improve the system. Genetically modified plants may eventually be used in inter-cropping as natural dispensers of insect pheromones and as part of a push-pull strategy, provided that they can be shown to have no negative environmental side effects. Our proposed strategy is innovative and environmentally friendly. Although it contains fundamental research challenges, it has the potential to become an economically sound part of many IPM programs

Additional remark from PlantLink: Present funding (2017) include grants from The Swedish Research Council FORMAS, The Carl Tryggers Foundation and the Crafoord Foundation. In 2014 PlantLink funding was prolonged with an additional grant in a special call.

Publications from this project:

1. Bao-Jian Ding, Per Hofvander, Hong-Lei Wang, Timothy P. Durrett, Sten Stymne, Christer Löfstedt (2014). A plant factory for moth pheromone production. Nature communications 5:3353.
2. Ding, B. J., Lager, I., Bansal, S., Durrett, T. P., Stymne, S., & Löfstedt, C. (2016). The yeast ATF1 acetyltransferase efficiently acetylates insect pheromone alcohols: implications for the biological production of moth pheromones. Lipids, 51(4), 469-475.

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Influence of hemoglobin expression on oil seed qualities

2012

The main aim of this project was to increase the seed oil content through overexpressing non-symbiotic hemoglobin (Hb) in *Lepidium campestre*. Stable transgenic *Lepidium* lines expressing Hb genes of *Arabidopsis* (**AtHb2**), sugar beet (**BvHb2**) and *Vitreoscilla* (**VHb**) were obtained. Both **AtHb2** and **BvHb2** heterozygous lines have showed increased seed oil content based on seed weight.

Lepidium campestre is a wild, winter hardy and biennial oil species. It could overwinter in Umeå and has high seed yield potential (5 ton/ha). It could be a very promising oilseed and catch crop for the cold climates. However, its low oil content (ca 20%) needs to be improved for commercial production.

It is well known that oxygen is mandatory for germination. Oxygen deprivation is in fact exploited in some mechanisms of coat-imposed dormancy where the tissues surrounding the embryo form a chemical barrier to oxygen, thus preventing or constraining efficient energy metabolism in the seed. In both developing and germinating seeds which display a very active metabolism, and hence oxygen consumption, the internal tissues are likely to face hypoxic conditions because of limitation in oxygen diffusion. An intriguing question is how respiratory oxygen consumption is regulated under the hypoxic conditions that prevail in developing seeds in the dark, or in germinating seeds, in which carbon metabolism is heterotrophic. In mammals, the gaseous radical nitric oxide (NO) is a major regulator of oxygen homeostasis through different mechanisms, and in recent years it has also emerged as an important signaling molecule in plants. The intracellular level of NO can be controlled and engineered in several different ways. Particularly, non-symbiotic plant hemoglobins (Hb) have been useful to modify and manipulate endogenous levels of NO in seeds. It has been shown that transgenic *Arabidopsis* plants overexpressing **AtHb2** can lead to a 40% increase in the lipid content of the seeds. However, there is no report on if overexpression of Hb genes could also increase the oil content in other oilseed crops and the mechanisms about the oil increase by Hbs are still poorly understood.

In total, over 30 transgenic lines were obtained for each of three genetic constructs. The oil analysis showed that both **AtHb2** and **BvHb2** genes could increase the oil content and this increase could be over 20% in some cases. Partial results of the oil analyses are presented in Fig.1 and are now published in [1]. It has been previously reported that **AtHb2** gene has been supposed to increase the level of unsaturated fatty acids in *Arabidopsis*. However, our preliminary results of oil composition analysis in the heterozygous lines of *Lepidium* did not show this change.

The seed money project has resulted in a 4-year SFF grant (RBP14-0055) for 31 MSEK, with partners from LU and SLU Alnarp.

Publication from this project

1. Ivarson, E., Leiva-Eriksson, N., Ahlman, A., Kanagarajan, S., Bulow, L., Zhu, L.H. (2017). Effects of Overexpression of WR11 and Hemoglobin Genes on the Seed Oil Content of *Lepidium campestre*. *Frontiers in Plant Science* 7:2032.

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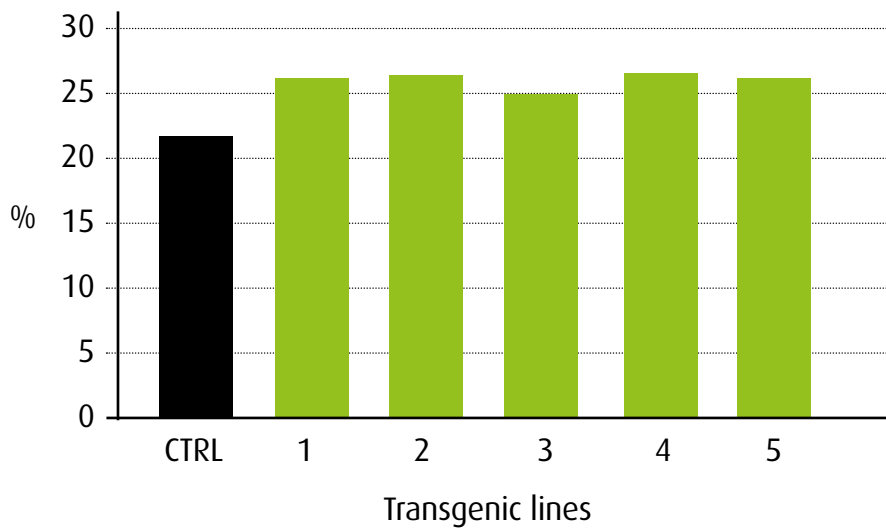


Fig.1a. The oil content (in % based on seed dry weight) of some transgenic lines expressing hemoglobin genes. CTRL= Wild type. 1-5: transgenic lines.

Enzymatic fractionation of oils from new crops

2012

Vegetable oils are attractive renewable raw materials for the chemical industry. A particularly interesting component of some vegetable oils is erucic acid, which is used in the production of plastics and other technical applications. Erucic acid is present in natural oils, but to make it industrially useful, it should be separated from other fatty acids and other components of the oil. The aim of the project is to combine the development of new varieties of oil crops with increased erucic acid content with enzymatic enrichment of the oil to obtain very long chain fatty acids, especially erucic acid, with high purity. New varieties of **Crambe** have been developed with erucic acid contents of about 76 % compared to about 59 % in the oil from the wildtype **Crambe**. Furthermore, it has been found that several enzymes are useful for the enrichment of erucic acid. They convert other fatty acids more rapidly, thereby leaving erucic acid in its original form. The most promising enzyme is the lipase from the microorganism **Candida rugosa**, with which erucic acid contents of up to 90 % have been achieved.

The results so far show that the methodology works, but still further enrichment is needed to achieve the 98 % purity which is desired for some applications. There are different possible ways to achieve this:

- Further plant breeding.
- Protein engineering of a lipase to further improve its fatty acid selectivity.
- Combination of the enzymatic enrichment with physical fractionation, such as fractional crystallisation.

The first approach would give the lowest production costs, if sufficient purity would be achieved. However, this is considered very difficult and combinations with other approaches will still be needed. The protein engineering approach is attractive, but probably requires rather large resources.

Publications from this project

Kaki, S.S. and Adlercreutz, P (2013) Quantitative analysis of enzymatic fractionation of multiple substrate mixtures. *Biotechnol. Bioeng.* 110, 78-86 (2013)

Volkova, N., Li, X., Zhu, L.-H. and Adlercreutz, P. (2016) Combination of modern plant breeding and enzyme technology to obtain highly enriched erucic acid from *Crambe* oil. *Sustainable Chemical Processes* 4(1):1-5

Participants

Patrick Adlercreutz,
Dept of Biotechnology, LU
Sten Stymne and Li-Hua Zhu,
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Tripartite Plant-Yeast-Insect Interactions

2012

Ceci n'est pas une pomme («This is not an apple»), a painting by René Magritte, shows an apple. The painting is, as indicated by its title, an incomplete description of an apple. It also illustrates our past attempts to understand interactions between insects and their host plants by studying insect and plant, only.

What we have now learnt is that microbes are involved in »tri-partite« interaction between insects and plants, and that microbes interface all animal herbivores with their food plants. Studies of the olfactory apparatus of the fruit fly *Drosophila melanogaster* in our laboratory demonstrated that the flies mainly use yeast signals - and not plant signals - to locate fermenting fruit for feeding. Moreover, yeast, and not fruit, is necessary for larval growth and survival. Codling moth *Cydia pomonella* (Lepidoptera, Tortricidae) is a typical plant-feeding insect, and an economically most important pest of apple. When studying the olfactory receptors of codling moth, we became aware that many of them are tuned to microbial signals and this led us to hypothesize the role of microorganisms in codling moth host finding.

In this study, we showed that yeast, found in codling moth larval galleries, is an essential part of the larval diet and that egg-laying females of codling moth sense and respond to yeast volatiles. Codling moth larvae dig galleries in the apple in order to grow the yeasts on which the larvae feed. Yeasts associated with codling moth further promote larval survival by reducing the incidence of fungal infestations in the apple. Larval feeding, on the other hand, enables yeast proliferation on unripe fruit and yeast dispersal. Chemical, physiological and behavioral analyses demonstrate that codling moth senses and responds to yeast aroma: moths and larvae are attracted to fermenting yeast. Beyond the PlantLink project, we have now demonstrated that yeast can be used to bait an insect pathogenic virus, codling moth granulovirus. A combination of yeasts with codling moth virus significantly increases larval mortality.

The finding that yeast enhances larval ingestion of an insect-pathogenic virus is accordingly opportunity for the development of a novel plant protection technique. The method is widely applicable to a range of pest insects and a patent for this method has been obtained. We expect that the combination of yeasts and insect pathogens will essentially contribute to future insect management.

Publications and patent from this project:

Witzgall P, Proffit M, Rozpedowska E, Becher PG, Andreadis S, Coracini M, Lindblom TUT, ReamLJ, Hagman A, Bengtsson M, Kurtzman CP, Piskur J, Knight A. 2012. »This is not an apple« - yeast mutualism in codling moth. *J chem Ecol* 38:949-957.

Witzgall P, Bengtsson M. 2014. A method for controlling insects, using an insect pathogen and a microorganism that is naturally associated with the larvae of the insects. WO2014182228-A1; SE201350560-A1

Participants

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»Ceci n'est pas une pomme«
(René Magritte, 1964)

Identification of glycerophosphocholine acyltransferase (GPCAT) genes in yeast and plants

2013

The aim of this project was to identify and clone the enzyme glycerophosphocholine acyltransferase (GPCAT)-gene(s) in yeast and plants and to further characterize the function of this enzyme. We successfully identified the gene encoding GPCAT in yeast by using the yeast deletion strain collection. With sequence homology we could further identify homologs in Arabidopsis and other plant species. Interestingly GPCAT belong to a family of proteins with no known function and is not related to other known acyltransferases. GPCAT was earlier not known to exist in plants and the work with characterizing GPCATs role in lipid metabolism in plants is now in progress. We have identified deletion mutants and created over-expressors of GPCAT in Arabidopsis and they are now being analyzed for the physiological function of this novel enzyme in plants. The characterization of GPCAT is one of the missing links in understanding lipid metabolism in plant cells and the identification of the gene encoding GPCAT has been crucial for further work within this field. This Plantlink financed project is a steppingstone towards further work with GPCAT in plants, where GPCATs role and importance in the large network of other related lipid enzymes will be investigated. A publication leading up to this project, with biochemical data about GPCATs function in plants was recently published:

Participants

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Publications from this project:

Lager, I, Glab, B., Eriksson, L., Chen, GQ., Banas, A. and Stymne, S. (2015) Novel reactions in acyl editing of phosphatidylcholine by lysophosphatidylcholine transacylase (LPCT) and acyl-CoA:glycerophosphocholine acyltransferase (GPCAT) activities in microsomal preparations of plant tissues. *Planta* 241 (2):347-35

Glab, B, Beganovic, M, Anaokar, S, Hao, MS, Rasmusson AG, Patton-Vogt, J, Banas, A, Stymne, S, and Lager, I. (2016). Cloning of Glycerophosphocholine Acyltransferase (GPCAT) from Fungi and Plants A NOVEL ENZYME IN PHOSPHATIDYLCHOLINE SYNTHESIS. *Journal of Biological Chemistry* 291:(48)25066.

Devising a morphodynamic computational model for hyper- sensitive reaction development

2013

Phytophthora infestans causes late blight, the most destructive disease on potato worldwide in particular, and Phytophthora species are the most aggressive on dicotyledonous plants in general. Together with increased restrictions on fungicides and potential risk of increasing epidemics of Phytophthora due to climate change, there is an immediate need for novel sources of genetically based plant resistance to this disease. In many pathogen defense responses, plants induce localized cell death at the infection site, termed hypersensitive response (HR), which is widely correlated with pathogen resistance.

The main objective of this project was to develop a dynamical, two-dimensional model of HR in resistant potato leaves infected with *Phytophthora infestans* and to identify environmental and genetic factors important for HR development. Due to the successful collaboration between biologists and theoretical physicists (modelers) we have established a computer model that mimics the natural development of HR and identified environmental factors and a gene with a novel function in HR development. The main applicable advantage of the model is that it is able to predict the effect of pathogen load on HR spread. Additionally, this project also led to two successful project applications.

Participants

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Biogas digestate promotes plant production but reduces mycorrhizal abundance

2013

Mycorrhiza and nitrogen-fixing root nodules are symbiotic interactions between plant roots and soil microorganisms, which have important functions for plant nutrient acquisition and soil fertility. Residues after biogas production from e.g. animal manure or food waste provide easily available nitrogen and phosphorous which promote crop productivity, but such biogas digestates may have less beneficial effects on mycorrhizal and nitrogen-fixing symbioses. This project has evaluated the plant and symbiotic performance of the legume lucerne (*Medicago sativa*) and the grass cocksfoot (*Dactylis glomerata*), grown alone or together, with and without fertilization with a biogas digestate provided by Sysav.

The effects of fertilization with the biogas digestate were similar to what would be expected from fertilization with inorganic nitrogen and phosphorous fertilizers: Fertilization enhanced aboveground growth of cocksfoot grown alone but it decreased the abundance of arbuscular mycorrhizal fungi (AMF) in cocksfoot (alone and in mixture) as well as in lucerne grown alone. Surprisingly, lucerne showed a competitive advantage over cocksfoot when fertilized and grown in mixture, in contrast to the expectation that cocksfoot would be a strong competitor for added nutrients in the species mixture. Furthermore, growth and nodulation of lucerne grown alone was unaffected by fertilization. Our findings suggest that the mycorrhizal symbioses in lucerne and cocksfoot are more sensitive to fertilization with biogas digestate than the root nodule symbiosis in lucerne.

Participants

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Stig Edner, Sysav

Ann Thorén, Sysav

The project has contributed to the following publication:

Zhao M, Jones CM, Meijer J, Lundquist P-O, Fransson P, Carlsson G and Hallin S (2017) Intercropping affects genetic potential for inorganic nitrogen cycling by root-associated microorganisms in *Medicago sativa* and *Dactylis glomerata*. *Applied Soil Ecology* 119: 260-266.

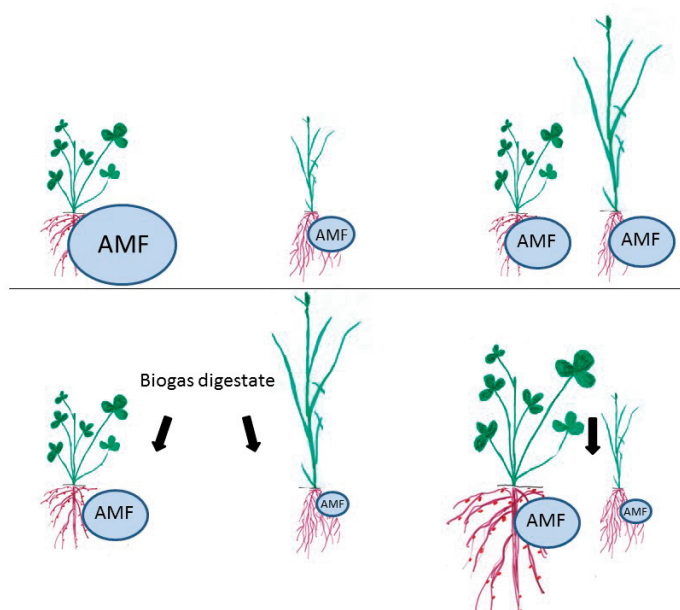


Figure 1. Schematic illustration of plant growth (relative size of shoots and roots) and root colonization of mycorrhizal fungi (relative size of blue »AMF« ellipses) in lucerne grown alone (left), cocksfoot grown alone (center) and the two species grown together (right). The part above the horizontal line represents unfertilized treatments, and the lower part represents fertilization with biogas digestate (indicated by black arrows).

2013

Towards the ecological meaning of Streptomyces-produced and induced volatiles in plant-insect-microbe interactions

Volatiles produced by **Streptomyces soil bacteria** are responsible for the characteristic smell of the earth. Especially the terpenes geosmin and 2-methylisoborneol (MIB) are detectable at extremely low doses by most humans. In recent years we have shown that the vinegar fly **Drosophila melanogaster** has a sensitive olfactory circuit dedicated to the perception of geosmin only. Other organisms are expected to also sense the earthy smelling volatiles. Despite their distinctive smell, low detection thresholds and global presence, the biological functions of the two compounds are not understood. Molecular genetic studies have for the first time elucidated the regulatory pathways and transcriptional regulators that control the biosynthetic genes for geosmin and MIB. The data show that production of these characteristic earthy odorants is developmentally regulated and occurs specifically in sporulating cells, which is different from most other **Streptomyces** secondary metabolites that are produced in non-growing mycelium. This finding, and the fact that geosmin biosynthesis is a completely conserved feature among all studied **Streptomyces** species, raise the question about what evolutionary advantage streptomycetes have of sporulation-associated geosmin and MIB production. This PlantLink project facilitated collaboration between two groups working on plant-insect-microbe interactions (SLU) and microbial genetics and developmental biology (LU) to approach the ecological meaning of geosmin and MIB, and in addition to study the effect of potential **Streptomyces**-induced plant volatiles.

The project has been successful and resulted in two major outcomes:

(i) Investigating possible ecological roles of **Streptomyces**-produced volatiles, we revealed that volatile compounds from streptomycetes serve as attractants for springtails, which are a major group of soil-inhabiting micro-arthropods. In field tests we found that springtails more than any insect were attracted to **Streptomyces** volatiles. Further, electrophysiological antennal recordings showed that the springtail *Folsomia candida* does sense and respond to both geosmin and MIB. Behavioural assays revealed that **F. candida** is attracted to both compounds. We have also demonstrated that **Streptomyces** spores adhere very well to springtail cuticula, and that the animals appear to graze on the **Streptomyces** bacteria.

Overall our data suggest the earth-smelling volatiles mediate a mutually beneficial interaction between **Streptomyces** bacteria and soil micro-arthropods like springtails, in which the animals act as vectors for spore dispersal at the same time as they graze on the **Streptomyces** mycelium. Investigations of the microflora of wild springtails provide further support for this ecological interaction (manuscript in prep.). Based on these findings we successfully applied for a project grant at the Crafoord foundation. This funding now allows us to perform final experiments. ►

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Dept of Biology, LU

-
- **(ii)** We established an Arabidopsis-growth assay and discovered a previously unknown effect of **Streptomyces** odours on plant growth. We found that volatiles of **S. coelicolor** significantly inhibit the development of **A. thaliana**. However, plants exposed to a wild type strain differ in root development from plants exposed to a mutant strain deficient in geosmin synthesis. Our preliminary results indicate that geosmin has a positive effect on root development, which is in contrast to an overall plant growth inhibitory effect induced by the complete headspace volatiles emitted by **Streptomyces**. Such plant growth-modulating effects have not yet been described for **Streptomyces** volatiles. Hydrogen cyanide (HCN) has been suggested as a bacterial volatile inhibiting plant growth. However, cyanide production is restricted to a few specific groups of Gram-negative bacteria, and we have strong indications that the effect caused by **Streptomyces** (Gram-positive) is different as we were not able to detect HCN in our headspace samples, find no indications for HCN biosynthesis genes in the **S. coelicolor** genome and furthermore see a different pattern of growth in wild type **Streptomyces**-exposed plants (no root development) than in plants exposed to HCN positive bacteria or to HCN (root development). These findings led to a new PlantLink seed money project (»Aboveground-effects of volatiles produced by **Streptomyces** soil bacteria on plants and insects«, Becher, Flårdh, Rasmusson) .

In addition to the collaboration between Paul Becher and Klas Flårdh the project helped to further develop our existing project collaborations within our home universities and with the John Innes Centre, and to widen our research network by creating contacts to research groups in Greece and Denmark for future collaboration.

Funding

A major goal of the seed money project was to acquire additional funding. Crafoord granted our project proposal »Chemical communication in **Streptomyces** bacteria: a study on the smell of earth« with 300 000 SEK.

Manuscript in preparation:

Gkounti, Vasiliki, Maureen J. Bibb, Elisabeth Barane, Mahmoud Al-Bassam, Mark J. Buttner, Paul G. Becher and Klas Flårdh. Developmental regulation and possible function of the earthy odorants geosmin and 2-methylisoborneol in **Streptomyces**. (in prep.).

Selection of plant defense against natural enemies: Induced defense and environmental effects within and between generations

2013

In recent years, it has been understood that inheritance of properties is not only determined by genetic factors but also by non-genetic factors, such as epigenetic regulation of genes expression. Our knowledge of non-genetic inheritance comes today mainly from a few model types. In order to gain deeper knowledge about the importance of non-genetic factors under natural conditions, it is important to study wild plants as well. In this study we investigated the incidence of non-genetic inheritance in relation to plants' defense against pathogens of the wild annual *Solanum physalifolium*. This plant grows wild in Sweden and is related to potatoes. Like potatoes, it is infected with *Phytophthora infestans*, an oomycete that produces potato late blight, which leads to multimillion costs for cultivated potatoes.

We conducted experiments where plants were treated with a harmless chemical that can trigger the immune system in potatoes. These plants were compared with controlled plants. We were able to see that the immune system of *Solanum physalifolium* is initiated using this chemical. We collected seeds from these plants and studied the immune response in the next generations. Although these plants had not been directly treated with the chemical, they had a stronger immune response. This finding shows that there is a non-genetic component of the plant's defense even in wild plants, where epigenetic inheritance is a possible mechanism. This is the first time this is shown on wild collected material.

This project has helped us get started with studies of plants' defense of *Phytophthora infestans* in wild potato plants. Such studies are important as it can provide opportunities for developing new types of defense strategies in farmed potatoes through increased knowledge of how defense works in natural systems. Today we have several ongoing projects that investigate the plant's defense and pathogen's infectivity in both *Solanum physalifolium* and in *S. dulcamara*, another wild potato relative (funding from PlantLink, Crafoordska Foundation, Carl Tryggers Foundation, CF Lundström Foundation). We hope to further develop these and seek additional financing. A future development opportunity for this PlantLink project is to study in more detail mechanisms involved in non-genetic inheritance. In addition, *S. physalifolium* is very interesting to study because it is even more sensitive to potato late blight than cultivated potatoes. We hope to isolate »sensitivity genes« of this species, which are then mutated into cultivated potatoes, thereby creating resistance to potato late blight.

Participants

Åsa Lankinen
Kibrom Abreha
Erik Alexandersson

Erik Andreasson,
Plant Protection Biology, SLU

Stefan Andersson,
Dept of Biology, LU

Presentations at international conferences

Abreha KB, Alexandersson E, Andersson S, Lankinen Å and Andreasson E. Non-genetic inheritance of induced resistance in a wild annual plant. OMGN Oomycete molecular genetics network, Annual meeting 15-17 June 2016, Malmö, Sweden (oral presentation).

Lankinen Å, Abreha KB, Masini L, Alexandersson E, Andersson S, Grenville-Briggs L, Råberg L and Andreasson L. Learning about plant defence from natural interactions between *Phytophthora infestans* and wild potato relatives. EAPR Triennial Conference 0-14 July 2017, Versailles, France (oral presentation).

Publications from this project

Lankinen, Å, Abreha, K, Alexandersson, E, Andersson, S, Andreasson and E. (2016). Non-genetic inheritance of induced resistance in a wild annual plant. *Phytopathology* 106(8): 877-883.

Unravelling Fusarium-Oat interaction mechanisms by proteomics

2014

The overall aim of this project was to improve the understanding of the mechanisms underlying resistance against Fusarium in oats. This was achieved using controlled infection assays of the susceptible cultivar Belinda and the partially resistant cultivar Argamak and three partially resistant oat lines from CropTailor AB. The infected tissue was analysed for mycotoxin levels in the grains. Quantitative proteomics of infected oat flowers in cultivars Belinda and Argamak was then performed.

In total, 526 proteins were identified of which 107 were significantly differentially expressed only in the resistant cultivar Argamak. Of these 107 proteins, 73 proteins were upregulated upon infection and 34 were downregulated. Functional annotation of the differentially expressed proteins highlighted various biological mechanisms that are potentially important for resistance to Fusarium (Figure 1).

Based on toxin tests, Belinda and Argamak were chosen for a scanning electron microscopy study. The surfaces of lemma and glumes were compared for the structure and for the presence of hyphae. The results suggest that Argamak has a thicker wax layer in lemma than Belinda.

In conclusion, the project led to successful setups for Fusarium infection assays for controlled infection of the oat plants, phenotypic evaluation, toxin measurement, protein extraction and analysis. The proteins identified as differentially expressed during infection, and those differing between the resistant and susceptible lines, will help for deciphering of the infection process and resistance mechanisms, and could guide development of Fusarium resistant Swedish oat.

A master thesis student was involved in the project and completed his thesis based on the work, and a manuscript is in preparation for publication of the results.

Participants

Fredrik Levander, LU
Salla Marttila, SLU
Olof Olsson, CropTailor AB
Aakash Chawade, LU
Erik Andreasson, SLU

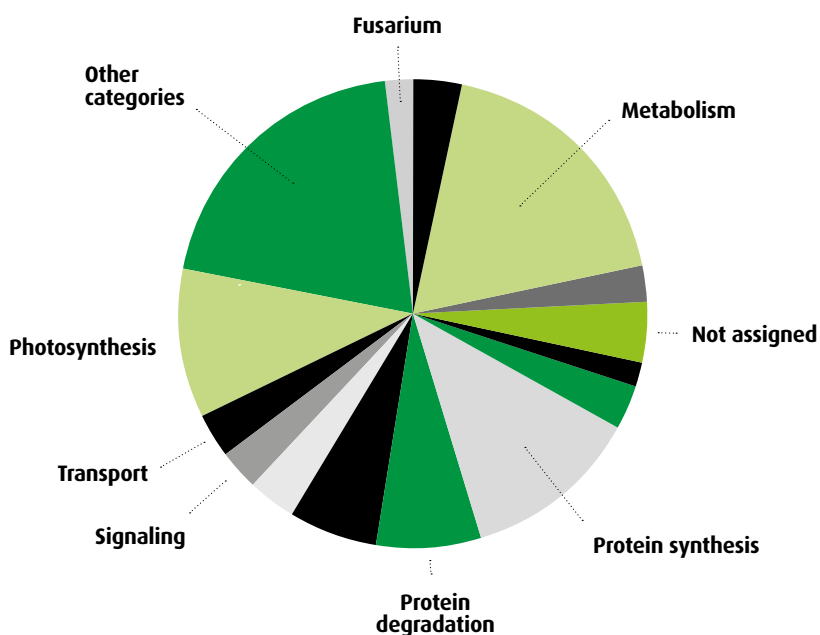


Figure 1. Number of differentially expressed proteins during infection and functional annotation. (3)

Pollinators – How attractive is the colour, odour and shape of clover flowers?

2014

The red clover seed yield in Sweden is very variable between farms and between years. The reason for the unpredictable seed yield is not fully understood, but it is clear that tetraploid cultivars show lower seed yield than diploids. Tetraploid cultivars are important as they produce more biomass and persist longer in leys. Red clover is outcrossing and totally dependent on pollinators to set seeds, particularly bees and bumblebees. Tetraploid flowers are larger than diploid flowers and it could be more difficult to reach the nectar in the corolla tube of the flower and this could promote robbing nectar without pollination. Recent studies have also showed a decline in wild long-tongued pollinators that can reach the nectar. We investigated the interaction between pollinators and the flowers of different red clover species. We moved two varieties (50 of each) of diploid, (SWRK1151 and Ares) and two of tetraploid (Dagny and Vicky) red clovers from red clover fields in Svalöv (Svalöv Weibull) to Alnarp Trädgårdslaboratoriet. We measured the colours of the red clover flowers and collected odours from the different growing stages (Fig 1).

The colours are almost the same of the different flowers, but the tetraploid are brighter than the diploida flowers. The first peak is in the blue-green area, next is a yellow peak and there are several peaks in the red area of the spectrum. There are only very small variations, but the bumble bees can probably see the differences and learn which colour that gives most nectar.

The four examined red clover varieties differed in seed set, with diploid varieties producing more seeds than tetraploid varieties. We predicted that this difference was caused by traits related to both the clover varieties and to the pollinators. We expected the long tongued bumble bees to select tetraploid varieties to a higher extent compared to the short tongued species, due to the difference in corolla depth. However, our results indicated that the bumble bee density was higher in the diploid clover varieties, independent of bee tongue length (Fig. 2a). Although no interaction between ploidy and bee group, the short tongued bumble bees took longer time to visit a tetraploid compared to a diploid clover flower, while the flower handling time did not differ between ploidy levels for the long tongued bumble bee species (Fig 2b). The results we have received in the PlantLink project will be a start for the new ECO-Formas project with Åsa Lankinen, Maj Rundlöf, Göran Birgersson and Mattias Larsson.

Participants

Anna Balkenius & Åsa Lankinen,
Plant Protection Biology, SLU

Maj Rundlöf,
Department of Biology, LU

Presentations at international conferences

Hederström V. Pollinator traits are not the main cause of low seed set in tetraploid red clover. Scape annual meeting 13-16 October, Abisko, Sweden (poster)

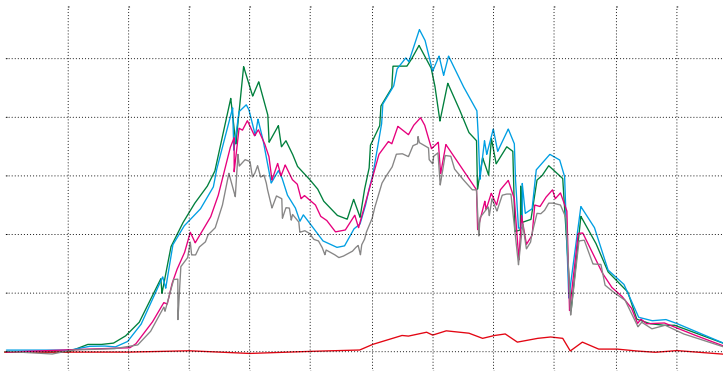


Figure 1. The colours of the different flowers from the different species (SWRK-blue, Ares-green, Vicky-purple and Dagny-grey). The colours are almost the same of the different flowers, but the tetraploid are brighter than the diploid flowers.

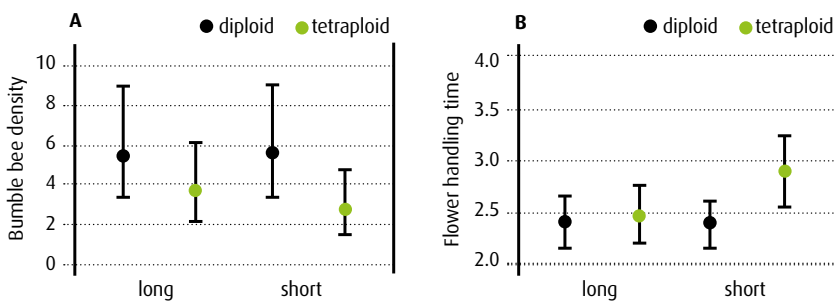


Figure 2. Bumble bee density (a) and flower handling time (b) in relation to clover ploidy (diploid or tetraploid) and bumble bee tongue length (long (>7 mm) and short (<7 mm)). Circles represent means and error bars 95% confidence limits, which both are based on back-transformed, model-estimated least square means.

Variability in sugar beet for impact of *Trichoderma* biocontrol

2014

Sugar beet is an important crop in the region, and stand for one fifth of the world sugar production. However, fungal infections like ‘damping off’ during the seedling phase reduce harvests, and is thus controlled by fungicide application to the seed. Future use of fungicides may be restricted and alternative approaches are therefore needed. It has been known for many years that the fungus *Trichoderma* spp. provide a beneficial effect on plant growth. This has led to development of *Trichoderma* strains, which are used as biocontrol agents, e.g. the strain *Trichoderma harzianum* T-22. Plant defence against pathogens involve several pathways of responses, including for example jasmonic acid, and salicylic acid.

The aim of this investigation was to determine how the genetic variation in sugar beet influences its interaction with *T. harzianum*, strain T-22. First, we followed the effect of T-22 on plant growth. Six in-bred genotypes of sugarbeet, representing a spectrum of pathogen sensitivities were grown on soil as well as under sterile conditions and with or without T-22. When grown on soil, T-22 stimulated growth of several genotypes, whereas under sterile conditions growth was generally inhibited. From these results, genotype A and genotype F were chosen for further experiments, since these showed most opposite behaviour (F was much less negatively affected than A in sterile culture). In the second part of the project, RNA was collected from sterile grown plants at 8, 24 and 48 h after infection with T-22. The samples were subjected to real time RT-PCR using primers for sugarbeet orthologues of Arabidopsis marker genes for salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) signalling pathways. We found that there was a fast and large response for genotype A to JA/ET compared to SA signalling that was not as observed in genotype F. This agreed with that genotype A was the one that was more affected by T-22 as seen from the growth studies.

No difference was found in infection degree between genotype A and genotype F. This suggests that the variation in defense gene response between genotype A and F was due to signaling differences rather than a variation in physical interaction.

In summary, we have shown that the effect of T-22 depend on the sugarbeet genotype, and that biocontrol competence may be a valuable trait in breeding. This investigation has initiated collaborations between the different universities and the industry. We have also established a connected project on quinoa financed by SIDA.

Manuscript in preparation:

Schmidt J, Schmiderer L, van Tour A, Kumar B, Marttila S, Fredlund KM, Widell S, Rasmusson AG (-)
Genotypic variation in sugar beet (*Beta vulgaris*) affects growth-stimulation and gene expression induced by *Trichoderma harzianum* T-22.

Participants

Susanne Widell,
Dept. of Biology, LU

Salla Marttila,
Dept. Plant Protection, SLU

Kenneth M. Fredlund, Syngenta
Seeds AB, Landskrona

Allan G. Rasmusson, Dept. of
Biology, LU

Novel mass spectrometrical analyses for the identification of potato pathogens on potato leafs and their targets in the leaf apoplast

2014

The apoplast has a number of important roles for the plant. One of these roles is that it is the compartment where the first interaction between the plant and a pathogen occurs. As a first line of defense, the plant secretes a number of proteases into the apoplast, in order to hydrolyze protein from the pathogen. An infecting pathogen likewise secretes proteases into the apoplast. We hypothesized that an analysis of the peptides present in the apoplast would give important information about the first plant proteins that become targets of the pathogen during early infection.

The analysis of apoplastic non-tryptic peptides turned out to be quite technically challenging. We were unable to get peptides to analyze from the apoplast of infected leaves, i.e. the most interesting ones. In order to elucidate the reason for this we analyzed larger proteins and compared the result of digesting these with trypsin in solution as opposed to first separating them on a short SDS-PAGE and then performing the tryptic digests. There was no difference between the two methods when analyzing apoplast from uninfected plants, but for the infected plants the result of the in solution digestion was much superior. We concluded that the presence of proteases or other compounds that inhibited the analysis hampered the analysis of peptides directly from apoplastic fluid. Thus, this is likely the reason for our inability to satisfactorily analyze non-tryptic peptides from infected potato leaves.

However, we have continued to collaborate, and we are now participating (together with a number of other researchers) in another project, where we are comparing the leaf proteome of potatoes grown in southern (Lund) and northern Sweden (Umeå), with the goal of identifying markers for properties that make potatoes suitable for cultivation in northern Sweden. In the preliminary data we can identify 2350 proteins per sample and detect interesting clustering between varieties and growing locations.

Participants

Svante Resjö, SLU Alnarp
Staffan Nilsson, LU
Sven Kjellström, LU

Figure 1. Isolation of apoplastic fluid





Aboveground-effects of volatiles produced by *Streptomyces* soil bacteria on plants and insects

2015

Volatile compounds are essential long distance communicators between organisms. *Streptomyces* spp. are ubiquitous soil microbes in all plant inhabited ecosystems. Prior to this project we discovered that *Streptomyces* volatiles modulate the growth of *Arabidopsis thaliana* seedlings. A main goal of this project was to elucidate the mechanisms of this previously unknown plant-microbe interaction. Moreover, we planned to investigate possible bacterial-induced consequences at higher trophic levels by studying the behaviour of herbivorous insects.

We could confirm that volatiles of *S. coelicolor* influence growth of *Arabidopsis* seedlings and alter root architecture. Both RNA_{seq} and *Arabidopsis* hormone mutant analysis indicated altered cytokinin/auxin homeostasis, possibly by novel mechanisms. Notably we have observed altered growth programming and large increases of fresh weight in both roots and shoots. Gen ontology of transcript analysis identified significant induction of auxin response genes. Interestingly, this is accomplished without induction of classic auxin response genes (ARFs). Instead, we have identified unidirectional induction of a family of genes called KISS ME DEADLY (KMD), which has been shown to suppress positive cytokinin signalling. In addition we have identified candidate compounds emitted by *S. coelicolor* that when applied to *Arabidopsis* seedlings were able to account for most of the plant responses to *Streptomyces* volatiles.

Based on the PlantLink seed money project we successfully acquired additional 132 tSEK from the ICE-3 Strategic fund (Chemical Ecology Unit, Dept. Plant Protection Biology).

Final experiments will evaluate the performance of herbivorous insects (*Spodoptera littoralis*) when feeding to *Arabidopsis* previously exposed to bacterial volatiles.

Moreover, this project was essential for the preparation of three grant applications within this SLU-LU collaboration.

Dissemination

We presented our findings within seminars at SLU and LU, the PlantLink day 2015 and at the Plant Biology Europe EPSO/FESPB conference in Prague (CZ) and 8th European Symposium on Plant Lipids conference in Malmö (SE). A manuscript on this project is under preparation:

Manuscript in preparation

Dotson B., Verschut V., Flårdh K., Becher P. and Rasmusson A. *Arabidopsis* F-box proteins modify auxin/cytokinin program in response to *Streptomyces* volatiles.

Participants

Paul G. Becher, Plant Protection Biology, SLU

Klas Flårdh and Allan Rasmusson, Department of Biology, LU

Evaluating a multi-scale structural-mechanistic modeling approach of plant protein based materials with interesting properties: tuning structure with functionality

2015

A main challenge for the future is to decrease dependencies on non-degradable materials in everything from packaging to various industrial products e.g. car interior panels. Recent advancement in materials based on wheat gluten (WG), where high strength or flexible-extensible material properties has been achieved with chemical additives. These materials consist of supra-molecular assemblies, and predicting the material properties is currently impossible. We have combined micro-stretching experiments for quantifying material properties, synchrotron X-ray scattering experiments (i.e. SAXS) for measuring structural properties in the material, and finite element method (FEM) mechanical models with the aim to develop a predictive description of the material properties from the material constituents. We mapped how the mechanical and nano-structural properties differ in WG protein films produced using different variables (additives etc.). We used SAXS experiments to quantify the complexity of the hierarchical structure of the material and material strength was measured by stretch tests. Strikingly, we found a correlation of 76% between these parameters indicating that the most complex hierarchical structure is greatly correlated with the mechanical strength (Figure 1a). To understand if differences in internal microscopic structure of the WG protein materials had an influence of the macroscopic viscoelastic properties of materials, we extracted detailed maps of force vs displacement in successively applied uniaxial force experiments. These tests consisted of stretching the WG protein samples to predefined length and measuring the forces and nano-structure during the process. We developed a FEM mechanical model to simulate the uniaxial stretch experiments, where we used an accurate 3D description of the patch geometries (Figure 1b). We used the model to test a range of hypotheses for the material elasticity and plasticity and optimized these parameters by direct comparison to the stretch experiments. We found that by using a non-linear Mooney-Rivlin material model with Poisson ratio of 0.3 and plastic yield stress response we can match the stretch displacements up to the third stretch release cycle (Figure 1c). The stress-strain diagram of this material reveals the nonlinear properties of the material with at least two types of linear like response, which suggests that two different structures or components of the material are responsible for elastic response in different strain regimes.

Our multidisciplinary approach has provided a first step towards bridging the gap from molecular to composite material properties. The detailed measurements using advanced technologies are integrated with multi-scale computational models will provide an unprecedented methodology for the future design of biodegradable material with optimized material properties. ►

Participants

Henrik Jönsson, Computational
Biology & Biological Physics, LU

Ramune Kuktaite,
Dept of Plant Breeding, SLU

Figure 1a. The mechanical and nano-structural properties in WG protein films produced using different variables.

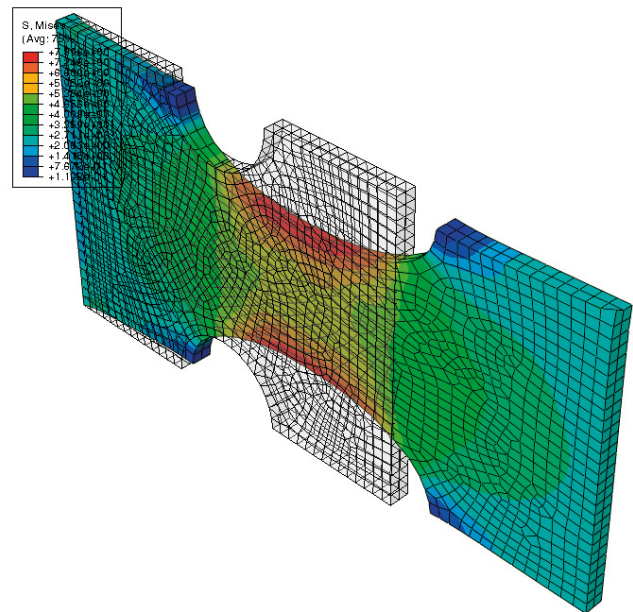
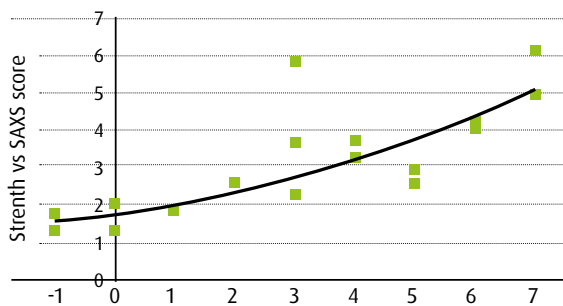


Figure 1b. A step from FEM simulation of the test on the sample. The color map on the deformed shape shows von Mises stress measure. The wire frame shape shows undeformed sample shape.

► Future perspectives/planned activities

While we are excited that we have been able to characterize material properties sufficient to explain experiments using FEM models, we have identified additional complexity of the material and the long term goal of adding multiple mechanical structures into the models is still in progress for extending our results into a manuscript.

Publications (directly/indirectly linked to this project; PlantLink is acknowledged for the support):

Kuktaite, R., Muneer, F., Rasheed, F., Newson, W. R., Plivelic, T.S., Hedenqvist, M.S., Jönsson, H., Krupinski, P., Johansson, E. Modelling plant protein structures and interactions: impact on quality in biofilms and foods. 12th International Gluten Biotechnology Workshop, September 2015, Perth, Western Australia, pp. 50-51.

Kuktaite, R., Newson, W. R., Rasheed, F., Plivelic, T. S., Hedenqvist, M. S., Gällstedt, M., E. Johansson, 2016. Monitoring nano-structure dynamics and polymerization in glycerol plasticized wheat gliadin and glutenin films: relation to mechanical properties. *ACS Sustainable Chemistry and Engineering*, 4 (6), 2998–3007.

Kuktaite, R., Rasheed, F., Hall, S., M.S., Bozorg, B., Krupinski, P., H. Jönsson. Multiscale structural-mechanistic modelling of wheat gluten proteins: a novel approach to predict future materials behavior, (manuscript in preparation).

Genetic variation and gene expression analysis of tolerance to infection by *Phytophthora infestans* in a wild *Solanum* species

2015

Cultivated potato is infected by the oomycete *Phytophthora infestans*, which leads to late blight and multimillion costs. The introduction of new resistant potatoes has not been a sustainable plant protection strategy, as *P. infestans* can quickly adapt their disease-inducing ability to existing resistance. An interesting possibility is to use tolerance mechanisms where the plant instead of killing the pathogen can minimize its damage. Unlike the case of resistance, tolerance does not adversely affect the pathogen, and is therefore not expected to cause a breakdown of the defense. Despite this advantage, we know very little about tolerance mechanisms and which genes that control them. In this project, we have studied tolerance in *Solanum dulcamara*, which is a wild relative of potatoes. We infected the wild relative *S. dulcamara* with *P. infestans* in a greenhouse environment. After a number of days, we investigated the degree of infection and at the same time measured a number of fitness characteristics of the plant to understand how the infection rate affects growth of the plant. If growth is high despite the fact that the plant is infected, the plant exhibits a higher tolerance than if the growth is lower at the same level of infection. The results show that there are clear differences between different genotypes in how sick the plants become. A surprising result was that the length of the shoots increased in infected plants. This indicates that infected plants exhibit overcompensation, which other studies have mostly seen after attack by herbivores. In summary, we have developed a method for studying tolerance mechanisms in a wild potato relative that we can now use for more in-depth studies.

The project has given us a unique opportunity to initiate studies of tolerance mechanisms and genes that control these in *S. dulcamara*. Since we have now developed a method that gives us the chance to investigate variation in infection rate and fitness, we have good opportunities to develop this project towards studying genes and mechanisms that control tolerance. Very few studies have the goal of separating resistance and tolerance, and today no study in either plants or animals has found genes that control tolerance. A development of the project in this direction has begun. We have funding from the Crafoordska Foundation and Carl Trygger Foundation. We are also planning to apply for larger funding for more in-depth studies. Increased knowledge of plant-pathogenic interactions in natural systems can help us develop more sustainable control strategies. We also have several ongoing projects that investigate the plant's defense and pathogen's infectivity in *S. dulcamara* and two other wild potato relatives in Sweden. An interesting result is that we have found that *P. infestans* can overwinter near the roots of *Solanum dulcamara*. This indicates that the presence of this plant in the cultivation landscape can have consequences for the epidemiology of *P. infestans*.▶

Participants

Åsa Lankinen, SLU Alnarp

Lars Råberg, Department of Biology, LU

► **Manuscript in preparation**

Laura Masini, Laura Grenville-Briggs, Erik Andreasson, Lars Råberg and Åsa Lankinen. Tolerance and overcompensation to infection by *Phytophthora infestans* in a wild *Solanum* species (in prep.)

Presentations at international conferences

Masini, L, Vetukuri, R, McDougall, R, Panda, P, Williams, N, Abreha, KB, Alexandersson, E, Råberg, L, Grenville-Briggs, L, Andreasson, E and Lankinen, Å. Non-genetic inheritance of induced resistance in a wild annual plant. OMGN Oomycete molecular genetics network, annual meeting 15-17 June 2016, Malmö, Sweden (talk)

Masini, L, Alexandersson, E, Råberg, L, Vetukuri, R, Grenville-Briggs, L, Andreasson, E and Lankinen, Å. Unravelling the defence arsenal of the wild *Solanum dulcamara* to *Pythophthora infestans*. Wild Plant Pathosystems, 2nd international meeting 29-31 August 2016, Helsinki, Finland (talk)

Lankinen, Å, Abreha, KB, Masini, L, Alexandersson, E, Andersson, S, Grenville-Briggs, L, Råberg, L and Andreasson, L. Learning about plant defence from natural interactions between *Phytophthora infestans* and wild potato relatives. EAPR Triennial Conference 9-14 July 2017, Versailles, France (talk)

Interview with PlantLink researcher Docent Åsa Lankinen, SLU Alnarp

Asa Lankinen works with ecological and evolutionary aspects of pollination and plant resistance to disease, and has participated in 3 seed money projects. PlantLink interviewed Åsa to get her picture of how the seed money has benefitted her research.

Could you give us some background on the seed money projects?

– I participated in 3 seed money projects. They were on pollination, seed set and flower scent in red clover, and nongenetic inheritance, resistance and tolerance to disease in wild potato relatives.

What was the main outcome of the seed money projects?

– The economic outcome was that the project on red clover gave very nice pilot data, which resulted in a successful application to Formas on red and white clover. The other projects have also resulted in new applications. Scientifically, the seed money projects gave us the opportunity to form new collaborations and investigate more long-term risky, research questions.

Åsa has herself moved from LU to SLU, and thinks that the seed money projects have enabled her to link her previous research with new projects. In general, Åsas experience is that it is difficult to get funding for new ideas, and that there is a need to provide pilot data with the application. This first, crucial funding for pilot studies is difficult to get, and the seed money filled an important function here. Seed money provided funding to test new ideas, which provided data that were the foundation for new grant applications.

What was the seed money used for?

– Generally speaking, it is easier to get funding for equipment and analyses, than for salaries as the latter costs are so much higher. It was very good to be able to use the seed money for salaries, for example for assistants.

One of the core aims of PlantLink is to encourage new research collaborations in Skåne. Was this achieved in the projects you were involved in?

– First, it was valuable to work in the seed money projects in order to incorporate evolutionary biology and ecological aspects into agronomical research, and to have the agronomical background when working on evolutionary questions in crops. For example, the project on wild potato relatives and tolerance benefitted a lot from the new cooperation with functional zoology.

Are there other benefits of the seed money projects?

The seed money has provided a continuity, allowing senior researcher to work together for a longer period of time. This has resulted in new ideas, and we are currently involved in writing an EU Horizon 2020 application based on the seed money cooperations.

Interview



»The seed money has provided a continuity, allowing senior researcher to work together for a longer period of time.«

Åsa Lankinen, SLU Alnarp



PLANTLINK



from **FARM** to **FORK**

March 21st 2013

Plant molecular breeding and post-harvest research in the 21st century.

A seminar day organized by PlantLink, Food Technology (Lund University) and Department of Plant Breeding (SILU Alnarp) the 21st March 2013 in the Blue Hall, Ecology Building, Lund.

This seminar day will highlight the possibilities with novel techniques in plant breeding and post-harvest research. It is an excellent opportunity to meet researchers from both these areas in the region. We invite participants to bring posters presenting their research.

To meet dynamic consumer preferences, industry needs and challenges imposed by climate change, rapid development of new plant cultivars with improved characteristics combined with advanced post-harvest technologies are crucial.

For free registration, full schedule and more information go to: www.plantlink.se



Examples of PlantLink activities

From the top right a guided tour during the »Fascination of Plants Day« which every second year put the focus on the importance of plant research for society to the general public, »From farm to Fork« one of the over 30 seminars and meetings arranged over the past six years, in the snow we visited MAXIV and ESS facilities together with colleagues at Copenhagen Plant Science Centre in 2017 and finally the coffeebreak during the vivid debate on genetically modified plants held in Lund in 2014.

Contact and more information

Follow us on Facebook and Twitter to get continuous updates from PlantLink.
For more information also check our homepage: www.plantlink.se

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