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Biologisk Markkartering

-Integrerad analys av jordburna växtsjukdomar och markkemi i olijeväxter och stråsäd - FAS II

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BioSoM

Preface

The thematic programme *Biological Soil Mapping* (BioSoM) was initiated in 2008 and has been operational since 2009. The overall goal of the programme was to develop diagnostic tools for selected soilborne plant pathogens of specific importance for Swedish agriculture, and to implement and communicate the information gained to farmers and associated decision makers.

The dynamic network with complementary competences created in this programme has helped increase awareness and knowledge of the biological complexity represented by soilborne plant pathogens. The research performed has in all respects fulfilled the initial intentions and in some cases the work has been more successful than anticipated. The scientific achievements and visibility of the programme are obvious from the scientific publications and from the substantial number of national and international presentations. For further information, visit www.biosom.se.

The strategic importance and value to growers of avoiding propagation and spread of soilborne pathogens cannot be underestimated. What remains to be achieved is development of control measures, a component not included in the BioSoM programme.

Objectives of the programme

Soilborne plant pathogens can be a major limitation in production of marketable produce and are adapted to grow and survive in the bulk soil, causing root diseases. Soilborne pathogens are confined within the soil, but some of these pathogens present on infected crop debris or soil can be spread by the wind. Several soilborne pathogens produce aerial sexual spores that are also spread by the wind. In addition, these pathogens can spread above ground with irrigation water or rain runoff. The long persistence and the complex distribution pattern of a number of soilborne pathogens make it relevant and financially justifiable to develop systems for mapping the distribution of disease inoculum. Soilborne pathogens include bacteria, fungi, oomycetes, protists and nematodes and are generally characterised by hardy and long-lived resting structures.

The overall objectives of the BioSoM programme were to provide scientific background and to design procedures for mapping soilborne pathogens that can be used in optimising crop rotations in Sweden. The work was divided into the following areas:

- Development and validation of PCR-based detection methods for important soilborne pathogens.
- Development of sampling methods and routines for determining the distribution of pathogen inocula. Correlation of infection level with soil characteristics.
- Increased knowledge of pathogen biology, forecasting economic impacts of disease and investigations of the effect of crop management on plant pathogens.
- Initiation and advancement of the implementation process in agriculture.

History of the programme

The Faculty of Natural Resources and Agricultural Sciences (NJ Faculty) at the Swedish University of Agricultural Sciences (SLU) announced a call on thematic research in spring 2008 that was intended to generate highly relevant research activities in collaboration with stakeholders in the Swedish agricultural sector. The BioSoM programme started officially on 1 January 2009, but in practice the work gained pace about eight months later. Phase I was reported and sent for external evaluation in March 2013. In parallel, an updated application on Phase II was prepared and approved. In Phase I, the following pathogens were included: *Plasmodiophora brassicae* (clubroot), *Verticillium longisporum* (Verticillium wilt), *Sclerotinia sclerotiorum* (stem rot), *Phytophthora* species on pea (pea rot), *Aphanomyces euteiches* (pea rot root), *Fusarium avenaceum, Phoma exigua, Cylindrocarpon destructans*

(clover root rot), *Gaeumannomyces graminis* (take-all), *Aphanomyces cochlioides* (rot root sugar beet) and *Rhizoctonia solani* (Rhizoctonia root rot, sugar beet). Following an instruction from NJ Faculty to concentrate the work on a smaller number of pathogens and crops, work on clover, cereal and sugar beet pathogens was omitted in Phase II. Development of multiplex analysis of several pathogens was also excluded in Phase II.

The programme was funded by NJ Faculty, SLU (50% of funding), and by the following stakeholders and foundations: Foundation of Swedish Farmers Research (SLF), Västsvenska Lantmännen (VL) and Skånska Lantmännen (SL) Foundations, Swedish Seed and Oilseed Growers Research Foundation (SSO), Eurofins Food and Agro AB, Intertek Semko AB (Scanbi Diagnostics AB), Findus R&D, Rural Economy and Agricultural Society/HS Konsult AB, Lantmännen (SW Seed), Nordic Beet Research (NBR), Syngenta Seed AB and YARA AB. The large number of stakeholders reflects the extraordinary importance of soilborne pathogens and associated research questions scrutinised in the BioSoM programme. The following departments at NJ Faculty took part in the programme: Soil and Environment (Division of Precision Agriculture and Pedometrics), Plant Biology, Forest Mycology & Plant Pathology, and Urban and Rural Development.

Project organisation

The research tasks were organised into different work packages (WP) during the programme period.

Work packages in Phase I (2009-2012)

WP 1a. Sampling and detection of pathogens
1b. *Phytophthora* sp. on peas
WP 2. Forecasting, based on bioassay and field trials
WP 3a. Pathogen biology: Resting structures and applied genomics
3b. *Beta vulgaris-Rhizoctonia solani* interaction
WP 4. Soil characteristics and infection by pathogens
WP 5. Implementation and use in R&D and practice.

Work packages in Phase II (2013-2015)

WP 1. Pathogen detection
WP 2. Presence, suppression and decline of soilborne pathogens
WP 3. Implementation and use in precision agriculture
WP 4. Communication, synthesis and programme management.

Programme staff

Dr. Anders Jonsson, Dr. Ann-Charlotte Wallenhammar, Prof. Christina Dixelius, Dr. Katarzyna Marcez-Schmidt, Dr. Arne Schwelm, Dr. Fredrik Heyman, Dr. Sarosh Bejai, Dr. Gerogios Tzelepis and PhD students Charlotta Almquist, Louise Andersson and Christina Lundström.

Scientific results of the programme

Procedures for soil sampling and milling and homogenisation of soils have been developed. To extract DNA from soils, various commercial DNA isolation kits were used in this development work. Cell disruption was achieved either by bead beating or by freeze-thaw cycles. Density flotation of soil samples was in some cases carried out prior to DNA extraction to further enhance yield.

A standard operating procedure (SOP) was formulated for soil sampling in practice, including routines for a ‘W-pattern’ transect and point sampling in the field, handling and storage of samples before DNA extraction. To prevent cross-contamination among soil samples, an

aseptic method for milling and homogenisation of soil samples was developed. Quantitative real-time polymerase chain reaction (PCR) methods for quantification of *P. brassicae* (clubroot), *S. sclerotiorum* (stem rot), *A. euteiches* (pea root rot), *A. cochlioides* (sugar beet root rot) and *V. dahliae*/*V. longisporum* (Verticillium wilt on sugar beet and oilseed rape) have been developed and can now be used to analyse field soil samples and plants. A similar approach has been developed for studying root rot pathogens in red clover.

Low clay content and high sand content in soil samples may compromise the accuracy of quantitative PCR (qPCR) assay, as exemplified during analysis of *A. cochlioides* in the BioSoM programme In the *P. brassicae* PCR assay, no significant effect on accuracy was observed with different clay contents (clay 3-63%, organic matter (OM) 2.5-15%, sand 4-77%). We concluded that using the dedicated kit for DNA extraction from soil samples and an additional cleaning procedure is sufficient to obtain good quality, pure DNA from soil samples.

The work on development of PCR methods ready for use at commercial laboratories included observations of precision, repeatability and inter-assay variation determined at stakeholder laboratories, and observations of reproducibility in joint work by stakeholder laboratories and the laboratories at SLU departments. The repeated field sampling performed indicated that the sampling technique devised for use has satisfactory accuracy and acceptable repeatability, although more replicates of field sample can always improve the results.

Phytophthora pisi was found on infected roots of peas and faba beans and its pathogenic effects can be confused with visual disease symptoms caused by *A. euteiches*. The problem of confused disease symptoms may also be one explanation for the high disease index observed on sugar beet and attributed to *A. cocchlioides*.

The PCR methods can also be used directly on plant material to monitor pathogen infections. Infection by *P. brassicae* was monitored in winter oilseed rape seedlings during the early stages of growth and the presence of DNA from *P. brassicae* was demonstrated only four days after emergence (cotyledon stage) in clubroot-susceptible (cv. 'Compass') and resistant (cv. 'Alister') cultivars. However, symptoms of clubroot disease were not visible on the roots until 21 days after sowing (3-4 true leaf stage). It is worth noting that roots of resistant plants also showed symptoms of the disease, but the disease severity index (DSI) of resistant plants was lower than that of susceptible plants. Hence, a new generation of resting spores was produced rapidly in both susceptible and resistant plants.

In the BioSoM programme and associated projects, three genomes have been sequenced; those of *V. longisporum*, *R. solani* AG2-2IIIB and *P. brassicae*. In addition, the transcriptome of the potato powdery scab pathogen *Spongospora subterranean*, which is closely related to *P. brassicae*, has been sequenced. In simplified terms, the *V. longisporum* genome is comprised of two different *V. dahliae* genomes, a feature that had to be clarified in order to design species-specific primers. The basidiomycete *R. solani* AG2-2IIIB causes crown and root rot and seedling damping-off in sugar beet. Comparative genomic analyses with four other sequenced *R. solani* isolates representing different anastomosis groups revealed differences regarding predicted secreted proteins and enrichment of cell wall-degrading enzymes in *R. solani* AG2-2IIIB, suggesting host specialisation. Purification of high quality DNA from the obligate biotroph *P. brassicae* (and *S. subterranea*) remained a challenge until 2015, when the genomes of the chlorarachniophyte *Bigelowiella natans* and the foraminifer *Reticulomyxa filosa* became available. Our recently published *P. brassicae* genome and transcriptome and the *S. subterranea* transcriptome represent the first genomic data on a pathogenic member of the Rhizaria and a new plant pathogenic organism group in the genomic era. The reference genome of *P. brassicae* sequenced in the project is currently being used in a comparative genomic project with seven additional *P. brassicae* genomes. One of the aims is to identify Single Nucleotide polymorphisms (SNPs) that in next step can be linked to different pathotypes and thereby form a resource for more informative diagnostic analysis. However,

mechanisms behind genetic variation are as yet largely unknown.
The susceptibility to plant pathogens is influenced by plant nutrients. One aim of the BioSoM programme was to study the effect of selected macronutrients and micronutrients on plant susceptibility to clubroot and pea rot. In general, the effect of a particular nutrient was found to vary considerably depending on plant species and target pathogen. For studying the effect of nutrients on *P. brassica*, a micromethod was developed and used together with pot experiments and field experiments on both clubroot and pea rot. The most significant and repeated observed was an effect of boron (B) on disease severity index of both clubroot and pea rot. Amounts equivalent to 10 kg B/ha applied as water solution at sowing brought about a decrease in clubroot disease severity index from 64 to 35 (0-100 scale, where 0 = healthy plants and 100 all plants severely infected) in Chinese cabbage plants. In pea plants attacked by *Aphanomyces euteiches*, positive effects of boron were observed on applying 5 and 10 kg B/ha in all three naturally infested field soils tested. Moreover, Rhizobia nodules were larger on the roots of pea plants treated with boron. However, there appears to be a narrow window between positive and toxic effect of boron on plants. In some experiments, we observed a slight toxic effect of boron, but only on the oldest leaves (boron is not very mobile) and it did not influence plant growth and size negatively. We also tested decreasing the amount of boron applied per hectare by seed priming or seedling dipping with boron solution. In some test soils naturally infected with *A. euteiches* we recorded a decrease in disease severity index for clubroot in cabbage after dipping plantlets in boron solution, whereas no decrease was observed after seed priming of oilseeds.
A common problem with implementation of new technology and knowledge in practice is that the full potential determined in laboratory conditions is seldom fulfilled. This relates perhaps to farmers' decision-making but research on this issue is very scarce, and a holistic research perspective including biological, economic, technical and social factors is often lacking. In the BioSoM programme, we identified new possibilities to combine existing models on decision making by farmers (AgriDSS), diffusion of innovation and IT-based decision support systems built on knowledge on natural decision making (NDM) and the theoretical framework of distributed cognition (Dcog). This work was conducted in close integration with stakeholders such as NBR and Hushållningssällskapen in an interactive research approach involving participatory technology development and focus group interviews.

Value of the programme

Impact of the programme on industry and society
In 2012, one of our stakeholders (Eurofins Food and Agro Sweden AB) launched a service for clubroot detection based on progress made in the BioSoM programme. The Swedish Seed and Oilseed Growers association (also a BioSoM stakeholder) has used the method since 2012 to test soil from experimental sites intended for field trials with oilseed rape. Furthermore, growers have been encouraged to identify infected fields using this DNA-based diagnostic. During 2014-2015, approximately 300 soil farm samples were analysed each year by Eurofins. Eurofins has also received enquiries and samples from Germany.
The methods developed for detection and quantification of soilborne pathogens have also been extensively used in field experiments within the BioSoM programme. An important first use was in determination of *P. brassicae* in the *Svensk Raps* field experiment with oilseed rape. In 2012 we reported infection (>5 pf g^{-1}) in 15 out of 49 (31%) field plots tested. Fields used by YARA for development of oilseed rape fertilisation regimes were also included and analysed for the presence of soilborne pathogens. *P. brassicae* was detected in 7 of 15 (44 %) experimental sites. In fact, analysis of experimental sites for the presence of *P. brassicae* DNA has become a necessary measure prior to establishing oilseed rape experiments.

Soil samples from the Swedish long-term fertilisation trials (*Bördighetsförsöken*) that were started in 1957 were tested for detection of *P. brassicae* DNA. These field experiments, which are located in southern Sweden, have a four-year rotation of oilseed rape and *P. brassicae DNA* was observed in four out of seven samples tested in 2007. The field plots were sampled once in the rotation and when all samples from 1970 were analysed, an increase in the level of *P. brassicae* infection was observed over the period. The peak of *P. brassicae* DNA correlated well with observed severe infections of clubroot. One important conclusion was that the increase in infection that precedes clubroot attack can be detected in samples years before actual severe disease symptoms. This indicates that the observed amount of *P. brassicae* DNA can be used to estimate risk of attack and yield loss. The 'death $rate_{50}$' calculated from the decline in DNA supports earlier observation of high risks of severe clubroot infection even 15-20 years after the last outbreak of clubroot disease.
The effect on the development of soilborne pathogens of short rotation time was obvious in an experiment with oilseed rape supported by our partner stakeholder SSO. The level of *P. brassicae* DNA was much higher in the soil after four oilseed rape crops in six years (oilseed rape each second year) than after two crops in six years.
The method developed for *P. brassicae* quantification has resulted in a soil testing service that identifies fields where the prevalence of soilborne inoculum guides the choice of a susceptible or partly resistant cultivar. The results of monitoring on research farms and research stations have been used to identify test sites with high inoculum/infection levels for testing new cultivars and to avoid to repeat oilseed rape crops in practical crop rotations.
The methods developed for *Aphanomyces euteiches* and *A. cochlioides* have high specificity and precision, and consequently have the potential to replace bioassays and to be used in practice by farmers, as well as by researchers. For soils with a high amount of *A. cochlioides* DNA, high disease severity index was generally found in bioassays. However, in some soils with high disease index in bioassays we detected low or no A. *cochlioides* DNA. These 'false negative' observations, i.e. low amounts of DNA but high disease severity, make it impossible at present to formulate statement such as 'low DNA equals low risk of infection'. However, our finding about high levels of DNA from *Aphanomyces* spp. and high infection potential of *A. cochlioides* is important information that can be used to decide between a resistant and partly tolerant sugar beet cultivar, since the tolerance varies between different cultivars. The present method actually has the potential to support cultivar choice and one stakeholder (Nordic Beet Research) is considering future use.
In canning pea production, the aim of the qPCR method is to replace the bioassay used to identify fields with a low risk of infection. Considerable efforts have been made to lower the detection limit, but with the protocols available there are still problems detecting the pathogen in soils with low infection potential. However, in pea and sugar beet production, the method has high practical potential to identify fields with a high risk of severe infection and yield loss.

The real time qPCR assay developed for *S. sclerotiorum* where the incidence of *S.sclerotiorum* DNA on leaves reveals the field-borne inoculums have a similar potential to improve disease risk assessment while sampling of airborne inoculum of *S. sclerotiorum* will help to understand the influence of local environmental conditions on disease development.
The methods developed for detection and quantification of *Verticillium* spp. and *Phytophthora pisi* and are specific and well suited for efficient laboratory work. However, knowledge concerning the relationship between level of pathogen DNA and risk of soil disease severity in the field is still lacking. More applied research and development is needed to establish guidelines for these pathogens. At present, however, the qPCR methods are excellent tools for identifying the presence of the pathogen in arable soils. For example the method for *Phytophthora pisi* is instrumental for epidemiological studies in faba bean (*Vicia faba*).

Root rot is a major constraint to yield and persistence in red clover. DNA of *Fusarium avenaceum, Fusarium culmorum, Phoma* spp and *Cylindrocarpon destructans* was quantified in field infected clover roots in a range of cultivars over time. These assays can be implemented in breeding programs and used for identification of sites for testing resistance of clover

Mapping the spatial distribution of pathogen infection on all fields on a farm can be an efficient way to establish and employ adequate crop management schemes in a more site-specific way. Three farms involved to varying degrees in agricultural research were analysed according to the protocol proposed by BioSoM. Fields showing a high infection level with *P. brassicae* and *A. euteiches* were found on all three farms, indicating the importance and possibility to identify experimental sites that are heavily infected for use in trials testing resistance or sites 'free' from a specific pathogen.

Access to Precision Agriculture (PA) techniques and Geographic Information Systems (GIS) enables farmers and researchers to keep track of and display infection levels of soilborne pathogens in a way that is easy to grasp and enables site-specific management. Treatments that could suppress multiplication and survival of soilborne pathogens are needed. One possibility is to adjust fertilisation to include nutrients that improve crop tolerance to pathogen infection. An interesting effect observed in greenhouse experiments was that different nitrogen sources such as nitrate, urea and ammonia inhibited development of clubroot differently at low levels of pathogen inoculum in the soil. However, corresponding field experiments remain to be performed.

A strengthening effect of boron against pea rot and clubroot was observed in greenhouse experiments. In field experiments, this beneficial effect of boron was confirmed in green peas. In oilseed rape/cabbage, problems with practical execution of the experiments disturbed the evaluation, but encouraging observations were made for both cabbage and oilseed rape indicating pathogen inhibitory activity of boron.

The research work for a better understanding of farmers' decision-making was intergrated in stakeholder activities. In co-work with Nordiv Beet Research the focuses mainly on investigating the possibilities to approach sustainable intensification by cultivating social learning among experienced sugar beet farmers, to whom new ICT solutions with production data is provided by an AgriDSS as well as physical and virtual learning groups. The contribution is a better understanding of how farmers learning and decision making can be facilitated to increase sustainability in farming practices.

A main focus is to investigate and discuss the *problem of implementation* and the related *gap of relevance* as well as identifying pros and cons in the shift of ICT system design methodology, from a more technology-centred approach to a more user-centred approach in the design, implementation and diffusion of AgriDSS. The Precision Agriculture Sweden (POS) AgriDSS development process was used as an illustrative case to raise these issues. we made suggestions on how to decrease the implementation problem by presenting some beginners pitfalls and suggestions on how to avoid them. The new knowledge about decision-making and understanding of the implementation process was also used to construct new ways to present the BioSom-analysis results to farmers.

Remaining knowledge gaps & outlook

Today, many farmers use a 'free' crop rotation based on an *ad hoc* choice depending on the current market price of products and opportune moments for sowing (i.e. early harvest). The possibility to actually measure and evaluate the infection level of major critical soilborne pathogens can improve the potential to optimise the crop rotation and enable more efficient use of break crops to obtain a secure time lapse between susceptible and profitable crops.

The BioSoM programme has been instrumental in starting the process to create a new toolbox for developing basic information on soilborne pathogens and procedures for stakeholders, not least analytical companies aiming to develop diagnostic services for farmers, advisory workers and plant breeders. It is currently not known how these steps will be fully implemented. There have been many calls for multiplex analyses, i.e. quantification of several pathogens from the same soil sample, and methods and technologies are now available for such analyses.

The extraction methods used have enabled diagnosis of *P. brassica* and adjustment of the relevant guidelines. However, for pathogens such as *Aphanomyces euteiches* and *A. cocchlioides*, fields with a high risk of infection can be identified but not fields with a low risk because of too high a limit of detection. Improved methods for extraction and preparation of DNA from these pathogens are therefore needed.

One other important issue of high priority is the much-awaited replacement of the rather imprecise and tedious pathotyping systems for *P. brassicae* into fast and more precise molecular diagnostic tools.

Discrepancies between bioassays (scoring extent of disease on plants growing in the soil on which the qPCR assay is based) and qPCR assays have been noted. This highlights the inaccuracy of bioassays and disease indexing based on wilting phenotypes, which are difficult to make unbiased as wilting in these phenotypes is most likely caused by several microorganisms. This problem can be solved by so-called community sequencing based on next-generation sequencing technology or, if the target microorganisms are known, a multiplex PCR approach.

Knowledge gaps between end-users and various technical achievements are wide. In order to close such gaps, basic training is needed but also good knowledge of human decision making and willingness to apply new technologies. The gap could be reduced by the development and use of new ITC applications, such as so-called 'serious games' covering the question of effects of sub-optimal crop rotation on yields and economic outcome.

There is huge demand for varieties harbouring resistance to the soilborne pathogens studied in the BioSoM programme. Pre-breeding activities to identify new genetic resources is a prerequisite for success on developing durable resistance, but knowledge of the pathogens cannot be ignored in such work

In order to meet new climate-related challenges and regulatory frameworks, for example regarding integrated pest management (IPM) (EU Directive 2009/128/EC), there is an urgent need to strengthen cooperation and to develop methods for improved implementation of new knowledge between academia and agricultural-associated stakeholders. Furthermore, it is essential to improve communication to farmers and advisors and to find new possibilities for disseminating knowledge of all available information technologies through collaboration with scientists and other expert groups.

Publications

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Reports – internal

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Information about soil sampling on youtube:

https://www.youtube.com/watch?v=Upv_mYq6_VY

Presence in the media and at fairs

Articles in media

- Klumprotsjuka tas på allvar. In Arvensis, no. 4 2013, by Nils Yngveson, HS.
- Ny metod mäter smittan i vilsporer. In Lantmannen no. 6 2013, by Anders Fällman, Lantmannen
- Biologisk markkartering – för ökad säkerhet. In Lantbrukets Affärer no. 6/7 2010, by L. Wikström, and article on the BioSoM programme.
- Klumprotsparasit på kål genetiskt kartlagt. 2015. Viola 8: 9
- Andersson O, Hemmesåker S. 2014. Klumprotsjuka. Varför drabbas vissa lantbrukare hårdare än andra? Examensarbete lantmästarprogrammet

National Meetings and Exhibitions

Elmia Lantbruk, 23-26 October 2010, Jönköping. Poster in collaboration with LOFT/SLF (Lantbrukare och Forskare Tillsammans) (AJ).
Borgeby Fältdagar, 30 June-1 July 2010, in collaboration with SLU; two posters (AJ, CD).
Borgeby Fältdagar, 29-30 June 2011, in collaboration with Svensk Raps; three posters (AJ, CD).
Logårdsdagen, Grästorp, 24 June 2011; two posters (AJ).
Rotröta i ärt och åkerböna - *Phytophthora pisi*. Poster by A.-K. Arvidsson, F. Heyman, L. Persson and M. Wikström, presented at Borgeby Fältdagar 2011 in Jordbruksverkets booth and 2012 in Findus booth.
Logårdsdagen, Grästorp, 3 July 2012; two posters (AJ).
Brunnby Lantbrukardag, Västerås, 7 July 2011; three posters (A-CW).
Logårdsdagen, Grästorp, 3 July 2012; two posters (AJ).
Brunnby Lantbrukardag, Västerås, 5 July 2012; two posters (A-CW).
Borgeby Field Days 26-27 June 2013; poster, film, and seminar (A-CW).
Logården and Brunnby Farmer Days, July 2013; posters, display, film (A-CW).
Sveakonferensen, 14 January, 2013; oral presentation (A-CW).
Uddevallakonferensen, 10 January, 2013; two oral presentations (AJ, A-CW).
Växjö möte 3 December 2013; two oral presentations (AJ, A-CW).
ÖstraSverige (ÖSF) Konferensen, Linköping 28 November; oral presentation (A-CW).
Field day, Nybble gård 9 June 2014; display (A-CW).
Brunnby Farmer Days, 3-4 July 2014; demonstration (A-CW).
Borgeby Field Days, 24-25 June 2015; with Svensk Raps, posters. (AJ, A-CW).
Brunnby Farmer Days, 1-2 July 2015; with HS poster (A-CW).
Smedjeveckan, SLU, Skara, 24 September 2015; presentations (AJ, A-CW).
Svenska Växtskyddskonferensen, Uppsala 10-11 November 2015; posters, presentations (CD, AJ, A-CW).
ÖSF-konferensen, Vreta Kloster, 25 November 2015; oral presentation (AJ).
Uddevallakonferensen, 15th January, 2016; oral presentations (AJ. A-C W).
Borgeby Field Days 28-30 June 2016; with Svensk Raps, posters. (AJ).
Borgeby Field Days 28-30 June 2016 with Svensk Raps, posters. (AJ, A-C W).
Brunnby Farner Days 6-7 July 2016 with Svensk Raps, posters, two seminars on Biological Soil Mappinng (A-C W)

Meeting with scientists and stakeholders

Contact Day, 30 September 2015, Landskrona. Participants (20) from Germany, Denmark and Sweden. Representing breeding companies (NPZ, KWS, Syngenta, Lantmännen), NBR, JKI, SJV, HS, SEGES (DK), Eurofins, Berlin Univ. Copenhagen University and SLU. Discussions on joint EU collaborations (COST-network, EU-projects) are on-going, seen as a continuation of the BioSoM programme.

Biologisk markkartering i praktiken, 18-19 November 2015, Lund. The final BioSoM seminar for advisors, farmers and stakeholders, summarising the results from the BioSoM programme and proposing future use of the findings. In total, 55 registered participants including, farmers, advisors, researchers and scientists.

International congresses & workshops (oral presentations and posters)

The program has been presented at conferences with 39 posters!

For further information about BioSom and results from the program see: www.biosom.se