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Auxin signalling and homeostasis in *Arabidopsis thaliana* during *Plasmodiophora brassicae* infection

Stefanie Mucha (1), Sabine Bergmann (1), Linda Jahn (1)

(1) Technische Universität Dresden

Auxin plays an essential role during plant growth and development. In plant cells, the IAA signal is recognized through two different types of receptors. The first one, ABP1, is responsible for activation of H^+/ATPases leading to acidification, cell wall loosening and finally cell elongation. In the second signalling pathway IAA binds to F-box proteins, e.g. TIR1, AFB1 and AFB2, which are part of an ubiquitin ligase pathway that degrades Aux/IAA repressor proteins. This affects the expression of auxin responsive genes, among them members of the *GH3* family.In addition to IAA signalling, conjugation of IAA plays an important role during the regulation of auxin homeostasis. The GH3 auxin conjugate synthetases remove active IAA from the total auxin pool and store it as amino acid conjugates. We investigate the role of auxin signalling and conjugation in the increased cell divisions and elongations taking place during the clubroot disease by expression analyses of *ABP1*, *TIR1*, *AFB2* and *GH3*s in *Arabidopsis* during the infection with *Plasmodiophora*. Infection tests with T-DNA knockout mutants for different GH3 genes show a higher susceptibility against *Plasmodiophora*. In addition, experiments with selected promotor::GUS lines will examine the influence of *Plasmodiophora* on IAA homeostasis.

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Comparative study of monoculture and mixed culture of the green algae *Oocystis marsonii* and the cyanobacteria *Microcystis aeruginosa*

Susanne Dunker (1), Christian Wilhelm (2)

(1) Plant Physiology; (2) University of Leipzig

Many studies deal with the culture of two or more algal species for example to understand phytoplankton dynamics, to analyse eco-toxicological effects or to optimise mass culture of algae. Promoted growth of one specie in phytoplankton community or a mixed culture of algae is strongly dependent on light and/or nutrient usage but also on the effect of info-chemicals. Therefore, the growth efficiency in a pluri-algal laboratory system can be studied only if the cell absorptivity is taken into account. Since smaller phytoplankton cells have a higher Chl a specific absorption coefficient (a^*_{Phy}) and a larger cell surface comparing to volume, we have performed a study where the competing organisms had similar cell sizes to ensure equal amounts of photons in the culture. Furthermore, natural Chl a-concentration under replete nutrient conditions were simulated to exclude as far as possible nutrient and light limitations. Interestingly, the study shows that growth of the *Microcystis aeruginosa* (cyanobacteria) squeezed out *Oocystis marsonii* (green alga) and actually M. aeruginosa grew better in mixed culture as well as in supernatant of mixed culture than in mono-algal culture. With the use of a bio-optical-model we tried to quantify the involved inhibiting effects.

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Iron as a determinant of virulence and resistance in the *Colletotrichum graminicola* – maize interaction

Fanghua Ye (1), Emad Albarouki (2), Holger Deising (3), Nicolaus von Wirén (4)

(1) Molecular Plant Nutrition, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany; (2) Institute of Agricultural and Nutritional Sciences, Martin-Luther-University Halle, Germany; (3) Institute of Agricultural and Nutritional Sciences, Martin-Luther-University Halle; (4) Physiology and Cell Biology, Molecular Plant Nutrition, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben

Iron (Fe) is an essential element for any forms of life. In order to overcome the low availability of Fe in hosts and to establish infection, plant pathogens have developed multiple Fe acquisition strategies. However, it is still unclear which plant Fe pools are utilized by pathogens and how Fe is involved in the plant immune system. The *C. graminicola* – maize system is used to uncover the plant resistance mechanisms and fungal virulence factors related to Fe. Our experiments showed that 3week-old (long-term) Fe-deficient maize plants are more susceptible to *C. graminicola* than Fe-sufficient plants. Previous studies suggested that Fe deficiency can strongly affect the leaf structure of field-grown pear or peach by reduction of cuticle weight and soluble cuticular lipids which can play active roles in plant-pathogen interactions. We are currently analyzing Fe nutritional dependent leaf structures and the components of cuticles and searching for a linkage between the change in Fe-dependent leaf structure and susceptibility to pathogens. To minimize the effect of changes in leaf structure under Fe deficiency, we are developing a short-term approach to assess the susceptibility of excised leaves fed over night (short-term) with a range of different Fe binding forms.

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New resistances to blackleg (*Leptosphaeria maculans*) transferred into *Brassica napus*

Hendrik Winter (1), Maja Mosch (1), Holger Budahn (2), Frank Marthe (2)

(1) Technische Universitaet Dresden; (2) Julius Kuehn Institute, Federal Research Centre for Cultivated Plants, Quedlinburg

Blackleg caused by *Leptosphaeria maculans* (*Phoma lingam*) is the most significant disease affecting oilseed rape (*Brassica napus*) worldwide.To widen the narrow base of oilseed rape resistance, offspring derived from somatic hybrids *B. oleracea* (+) *B. nigra* and *B. oleracea* (+) *B. carinata*, respectively, are currently characterised and developed towards the *B. napus* karyotype (genome AACC, 2n=38).The focus of this study is on blackleg resistance behaviour of selected selfing and backcross offspring produced using embryo rescue techniques. Adult plant resistant individuals of different generations, along with susceptible genotypes, were examined cytologically, e. g. by genomic *in situ* hybridisation (GISH). Furthermore, the most promising genotypes were self pollinated again and backcrossed with *B. napus* to obtain resistant plants with an AACC background.Moreover, a complete set of nine disomic *B. napus-Raphanus sativus* addition lines ($2n=38_{AACC}+2_{(R)}$) has been examined in blackleg resistance tests.GISH results are compared with those obtained earlier from blackleg resistant addition and putative recombination lines derived from interspecific, sexual hybrids between *B. napus* and *Sinapis arvensis*, *Coincya monensis* and *B. juncea*, respectively.