



Nederlandse Vereniging voor Plantenbiotechnologie en -Weefselkweek
Netherlands Society for Plant Biotechnology and Tissue Culture

KvK nr. 40121960 NL42INGB0004240007 www.nvpw.nl info@nvpw.nl

Summaries of the lectures on the NVPW autumn symposium, Friday, December 8th 2017
Hotel de Nieuwe Wereld, Marijkeweg 5, 6709 PE Wageningen.

The battle in the apoplast, the rat race between plants and intercellular plant pathogens.

Prof. dr. ir. Pierre J.G.M. de Wit – Wageningen University & Research – Laboratory of Phytopathology

An overview will be presented of the search for effectors secreted into the apoplast by different intercellular pathogens to facilitate infection, and the response by plants to prevent infection by development of an array of different immune receptors.

Genetic aspects of tissue culture responses

Prof. dr. ir. Maarten Koornneef – Wageningen University & Research – Laboratory of Genetics / Max Planck Institute for Plant Breeding Research

It is well known that species differ in their capacity to regenerate from tissue cultures. Such variation can also be found within species, as well as between related species. The latter allows one to transfer this trait into another genotype. This is especially relevant when efficient regeneration is required e.g. for gene transfer experiments. In the early days of transformation of crop plants tomato was not easy to transform. However, it was known that some related wild species regenerated much more efficiently from tissue culture. Therefore, we used an available species hybrid between the cultivated tomato and the wild *Lycopersicon* (now *Solanum*) *peruvianum* and further backcrosses to introgress the regeneration trait into the cultivated tomato (Koornneef et al. 1986, 1987, 1993) as well as performing mapping experiments to identify the loci underlying the variation for this trait. This resulted in the identification of a major gene controlling regeneration ability. This gene was, later on, discovered, together with additional loci, in other studies and it was also introduced in model tomato cultivars such as Microtom. The molecular follow-up of this locus is now better possible with the advancement of genetics and genomics and it is expected that the underlying gene(s) will be identified in the near future. References: Koornneef et al 1986 Plant Sci 45: 201-208, Koornneef et al. TAG 74: 633-641, Koornneef et al. TPJ 3: 131-141

Agrobacterium-Mediated Transformation (AMT): DNA transformation facilitated by virulence protein co-delivery and host factors.

Prof. dr. Paul J.J. Hooykaas - Institute of Biology, Leiden University

Soon after the discoveries of the Ti plasmid and the presence of part of it as T-DNA in crown gall cells, *Agrobacterium* was converted into an efficient plant vector. The binary vector system developed in the 80s Leiden still is in use as the preferred plant vector nowadays. Much more insight into the process of AMT has been obtained over the years. Thus the *Agrobacterium* vector system could branch out to other organisms such as yeasts and fungi. It has become clear that virulence proteins, which are co-delivered into host cells by *Agrobacterium*, play an essential role in transformation. Otherwise, host factors play a dominant role in the steps leading to T-DNA integration. Nowadays there exist still many mysteries around *Agrobacterium* and AMT. Future studies will no doubt lead to further optimization of *Agrobacterium* as a genome editor and protein therapist.

Tomato fruit ripening, an interplay between hormones, RNA molecules, transcription factors and epigenetics.

Prof. dr. ir. Gerco C. Angenent – Wageningen University & Research - Plant Developmental Systems

Tomato fruit ripening is an important agronomical trait that has been studied intensively during the last two decades. These studies, mainly based on mutants, yielded a number of genes and factors that play an essential role in this process. Despite our knowledge about the individual components of the ripening process, the interactions between these components starts to be unveiled only recently. The regulatory network that controls ripening in tomato involves transcription factors, small RNA molecules, ethylene and epigenetic regulation. Surprisingly, we observed that a very similar network is active in the transition to flowering. Using CRISPR/CAS9 mutagenesis we aim to understand the contribution of the different factors and to manipulate the ripening process in a quantitative manner.

Seaweeds as commodities for the future; sea lettuce as model plant for plant biotechnology.

Dr. Willem A. Brandenburg – (formerly) Wageningen University & Research – Plant Research International

In order to warrant food security in the near future alternative protein sources are key. Seaweeds are then an interesting source without a drop of fresh water. Besides that, they are recycling phosphate and are a source of hydrocolloids and trace elements and they contribute to the restoration of the marine ecosystem by fixation of carbondioxyde, methane and nitrogen compounds. Looking at its life cycle, sea lettuce offers unrivalled opportunities to study plant metabolism mechanisms, especially the conservative ones and may shed light on new ways to improve stress tolerances in future crop plants.

Plant roots and their microbiomes

Prof. dr. Ton A.H.J. Bisseling - Wageningen University & Research – Laboratory of Molecular Biology

Plant roots have intimate interactions with numerous microbes. Examples that have been studied extensively are the interactions of rhizobia and Frankia bacteria that result in N fixing root nodules as well as arbuscular mycorrhiza. The latter resulting in extraradical mycelia connected to intracellular structures by which nutrients (phosphate) are translocated to the host plant. During the last decades a diversity of approaches has been used to obtain insight in molecular mechanisms underlying these interactions. This brings us also the possibility to assess the potential of future applications. In addition to these endosymbiotic interactions plants interact with thousands of microbes that are hosted on the root surface (rhizosphere) as well as inside plant (endosphere). These microbial communities become now accessible among other because of novel sequencing methods. These communities can contribute to plant growth/development, (a)biotic stress tolerance and nutrient uptake. Examples from microbiomes from desert areas will be discussed.

Technology development at Naktuinbouw to facilitate the Dutch horticulture

Dr. ir. Maarten Toonen – NAKTuinbouw

Healthy and reliable starting material (seeds and young plants) is the key to production of high quality products for food, feed and ornamental products. The Netherlands being one of the key players in the production of starting material, have the unique position as one of the world leading horticultural nations. Naktuinbouw safeguards the quality of Dutch starting material. This facilitates seed and young plant producers in trading their products worldwide. To maintain this position, Naktuinbouw develops and implements novel technologies to ensure the quality of starting material. This covers development of novel disease testing methods, authenticity of plant material and molecular tools to identify plant pathogens and plant varieties.

Modern aspects of potato breeding

Prof. dr. ir. Evert Jacobsen – Wageningen UR – Laboratory of Plant Breeding

Potato breeding started in the second half of the 19th century by using directed crosses between breeding parents. At the beginning of the 20th century Mendelian genetics was added to the breeding tools. At the start of scientific potato breeding many varieties were selected by pioneers like Geert Veenhuizen (cv Eigenheimer) en Kornelis Lieuwes de Vries (cv Bintje). Many wild species are diploid, so part of classical breeding is made at this ploidy level to introduce all kind of resistance traits. In practise, a restricted frequency of new varieties will be popular and partly replace existing potato varieties. The phenomenon of true potato seed varieties (TPS) will be discussed in the past and its future perspectives as F1 hybrid seed varieties at diploid and tetraploid level. Improvement of existing popular varieties will be shown by adding R-genes and silencing S-genes for resistance to late blight. The loss of function mutation to come in one step to amylose free (amf) potato starch at tetraploid level will be discussed as first example of Crispr-Cas9 gene editing in potato.

Exhibitors:

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