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# Accepted Abstracts

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## *Plant science 2022*



4<sup>th</sup> International Conference on  
**Plant Science and Agriculture**

March 09, 2022 | Webinar

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**Studying the molecular physiology of auxin during the grafting process in *Carya cathayensis***

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Application of various hormones improves the grafting process and among which auxin plays a vital role for the formation of vascular reconnection. Auxin role in the grafting process was analysed by studying the differential expression pattern of auxin-associated genes (ARF, GH3) and transporter genes (ABC and Aux:Hyd) under auxin- and NPA- (an auxin inhibitor) applied conditions at 0,3,7 and 14 days after grafting (dag). Analysis shows that the expression of GH3, ARF and Aux:Hyd genes were found to be low at the time of grafting but increased at 3 and 7 dag and again get reduced at 14 dag. While the expression of ABC gene was found to be high at 14 dag and got reduced at 3 and 7 dag. Further the application

of IAA or NPA to the grafted sample is not influencing the gene expression in a concordant way. With the availability of rough draft unigene library for Hickory tree species to our group, 34 different ARF genes were identified and analysed for their expression level at 0, 7 and 14 dag. Among the 23 genes analysed, 15 genes expression level are not affected at various time of analysis and 5 of the genes expression were not detected in the grafted plants. While 3 of the gene expression level got drastically reduced at 7 and 14 dag when compared with 0 dag which shows that these ARF genes have specific role in the grafting process which has to be studied in detail in the future.

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**Counterfeits in food; dietary supplements and herbal medicines- A global issue-quality and safety**

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FDA has identified an emerging trend where over-the-counter herbal products, frequently represented as dietary supplements, contain undeclared /hidden active ingredients that could be harmful. The global dietary supplements industry was valued more than USD 96 billion in 2017, and it is expected to reach USD XX billion by 2023, at a CAGR of 6.9%, during the forecast period. The purpose of this talk is to describe the food ,herbal medicine & dietary supplement fraud i.e. deliberate substitution, addition, tampering or misrepresentation of ingredients or packaging about a product for economic gain, based on practical laboratory experiments and using authenticated plant samples and standard chemicals/medicines .Fraud involving foods & dietary supplements consist of substitution with cheap, less potent and spurious materials or diluting the valuable ingredient with an inexpensive one . Food items being used daily e. g. honey, olive oil, cranberry, pomegranate and spices particularly saffron & cinnamon also in chocolates,

some of it have been found to contain PDE-5 inhibitors which may cause fatal side effects particularly with nitrates.

Some estimates place the cost of food fraud globally as high as 10-15 billion dollars per year. Furthermore, Quite a number of these herbal medicines & dietary supplements—promoted mainly for weight loss, sexual enhancement, diabetes and bodybuilding—that are found to contain hidden or deceptively labeled ingredients, such as synthetic steroids,PDE-5 inhibitors or their analogs (closely-related drugs).These products look like dietary supplements but they do not qualify as dietary supplements/ ingredients. Some of these products contain hidden prescription ingredients at levels much higher than those found in an approved drug product and are dangerous to public health.

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## **FlowerPhenoNet: Deep learning based flower detection using image sequences for 2D and 3D temporal phenotyping analysis**

**Sruti Das Choudhury**

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A phenotype is the composite of an observable expression of a genome for traits in a given environment. The trajectories of phenotypes computed from an image sequence and timing of important events in a plant's life cycle can be viewed as the temporal phenotypes and indicative of the plant's growth pattern and vigor. This research introduces a taxonomy of 2D and 3D temporal flower phenotypes. To achieve this, we introduce a novel method called FlowerPhenoNet which uses deep neural networks for detecting flowers from multiview image sequences for high throughput temporal plant phenotyping analysis. Following flower detection, a set of novel flower-based phenotypes are computed, e.g., the day of emergence of first flower in a plant's life cycle, the total number of flowers present in the plant at a given time, the highest number of flowers bloomed in the plant, growth trajectory of a flower and the blooming trajectory of a plant. Plants are not static but living organisms that change in shape and topology over time. The occlusions of flowers by the leaves, drooping of petals, and change in orientation of flowers in accordance with the incident

sunlight pose challenges to the accurate computation of flower size from 2D images. Thus, we compute 3D model of a flowering plant based on voxel-grid reconstruction, and use color and texture properties to segment the flowers from the 3D reconstructed model. The volume of a flower, i.e., flower size, is computed as the total number of voxels constituting the flower. We use the well-known space carving technique for voxel-grid reconstruction and aims to achieve the fully automatic reconstruction of a large number of plants without requiring any manual intervention on an individual plant basis. To develop a new algorithm and facilitate performance evaluation based on experimental analysis, a benchmark dataset is indispensable. Thus, a benchmark dataset called FlowerPheno has been introduced which comprises of image sequences of three flowering plant species, e.g., sunflower, coleus and canna, captured by a visible light camera in a high throughput plant phenotyping platform from multiple view angles. The experimental analyses on the FlowerPheno dataset demonstrate the efficacy of the FlowerPhenoNet..

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### **Bio char and wood distillate for a sustainable agriculture**

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In agriculture, the use of natural products to replace synthetic fertilizers and pesticides will be fundamental, without however affecting the yield, but rather, if possible, increasing it, as expressly envisaged by the Farm to Fork Strategy of the European Union. We have several projects underway aimed at testing the application in agriculture of biochar and wood distillate, two by-products of the use of waste wood biomass for the production of electrical and thermal energy through pyrolysis, thus offering a formidable example of circular economy. These projects will assess the potential to reduce the use of synthetic chemicals in agriculture, while providing high yield, nutraceutical value and crop quality. Furthermore, both the positive impact on biodiversity and

the ecosystem, and the possible environmental side effects of ecotoxicological interest will be assessed.

In particular, biochar is tested with the aim of counteracting the effects of climate change, improving the characteristics of the soils and the productivity of agroecosystems, thanks to its ability to counteract salinity and promote water retention, as well as to remediate polluted soils and make them available to agriculture. Wood distillate is tested both as a biostimulant and as a biopesticide (inducer of endogenous resistance) in some of the main plants of agronomic interest grown in the Mediterranean.

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**Global analysis of RNA-dependent RNA polymerase-dependent small RNAs reveals new substrates and functions for these proteins and SGS3 in Arabidopsis**

**Xia Hua, Nathan D Berkowitz, Matthew R Willmann, Xiang Yu, Eric Lyons and Brian D Gregory**

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RNA silencing pathways control eukaryotic gene expression transcriptionally or post transcriptionally in a sequence-specific manner. In RNA silencing of *Arabidopsis thaliana*, small RNAs (smRNAs) are often derived from long double-stranded RNA (dsRNA) molecules synthesized by one of the six genomically encoded RNA-dependent RNA Polymerase (RDR) proteins. However, the full complement of the RDR-dependent smRNAs and functions that these proteins and their RNA-binding cofactors play in plant RNA silencing has not been fully uncovered.

To address this gap, we performed a global genomic analysis of all six RDRs and two of their cofactors to find new substrates for RDRs and targets of the resulting RDR-derived siRNAs to uncover new functions for these proteins in plants. Based on these analyses, we identified new substrates for six RDRs as well as the RDR2 cofactor RNA-directed DNA methylation 12 (RDM12) and the RDR6 cofactor suppressor

of gene silencing 3 (SGS3). These findings revealed that the target substrates of SGS3 are not limited to those solely utilized by RDR6, but that this protein seems to be a more general cofactor for the RDR family of proteins. Additionally, we found that RDR6 and SGS3 are involved in the production of smRNAs that target transcripts related to abiotic stresses, including water deprivation, salt stress, and ABA response, and as expected the levels of these mRNAs are increased in  *rdr6*  and  *sgs3*  mutant plants. Correspondingly, plants that lack these proteins ( *rdr6*  and  *sgs3*  mutants) are hypersensitive to ABA treatment, tolerant to high levels of PEG8000, and have a higher survival rate under salt treatment in comparison to wild-type plants. In total, our analyses have provided an extremely data-rich resource for uncovering new functions of RDR-dependent RNA silencing in plants, while also revealing a previously unexplored link between the RDR6/SGS3-dependent pathway and plant abiotic stress responses.

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