

EuroSciCon 

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Asian Journal of Plant Science & Research



PROCEEDINGS OF

5th EDITION OF INTERNATIONAL CONFERENCE ON

PLANT GENOMICS

JUNE 13-14, 2019 | BERLIN, GERMANY

Scientific Program

Agenda Day 1: June 13, 2019

Sylt 4-5

09:30-10:00 Registrations

10:00-10:25 Opening Ceremony

10:25-10:30 Introduction

Keynote Forum

10:30-11:20

Title: Genome editing in chilli pepper using a CRISPR/Cas9 cytidine base editing system

Raj Kumar Joshi, Rama Devi Women's University, India

Group Photo

Networking and Refreshments 11:20-11:50 @ Sylt Foyer

Session Introduction

Sessions: Plant Functional Genomics and Biotechnology | Plant Nutritional Genomics | Plant Breeding | Plant Genetics and Epigenetics | Plant Signaling and Chemical Signaling | Genome Sequencing

Session Chair: Ildiko Matusikova, University of St. Cyril and Methodius, Slovak Republic

11:50-12:20

Title: Nutrition effects on synthesis of plant defense proteins and tolerance to metals

Ildiko Matusikova, University of St. Cyril and Methodius, Slovak Republic

12:20-12:50

Title: The development of a novel SNP genotyping assay to differentiate cacao clones

Jocelyn De Wever, Ghent University, Belgium

Lunch Break 12:50-14:00 @ Restaurant Rienäcker

14:00-14:30

Title: Virulence of *Fusarium circinatum* is associated with perturbation of phytohormone homeostasis in *Pinus pinaster* seedlings

Laura Hernandez Escribano, National Institute of Agricultural and Food Research and Technology, Spain

14:30-15:00

Title: Establishment of regeneration protocol for Mongolian subendemic species *Oxytropis grubovii* Ulzij

Bolortuya Ulziibat, Institute of general and experimental biology, Mongolia

Panel Discussion

Day 2: June 14, 2019

Poster Presentations: 11:30-12:00 @ Sylt Foyer

Extended Networking and Lunch 12:00-13:00 @ Restaurant Rienäcker

Awards & Closing Ceremony



Mark your Calendar

6th Edition of International Conference on
Plant Genomics

February 26-27, 2020 Dubai, UAE

E-mail: plantgenomics@sciconmeet.com, plantgenomics@euroannualmeetings.org

Website: plantgenomics.euroscicon.com

CONFERENCES
2019

CONFERENCES
2019

2019

Fostering Collaborative Efforts of the Scientific Community to Promote Life Science Research Communication

Henderson, UK: Established in the year 2001, EuroSciCon is a UK based science Event organiser engaged in 'Life Sciences Communication' for over a decade through a series of science conferences across Europe. The uniqueness of the EuroSciCon lies in its ability to collaborate with renowned scientific agencies within UK and abroad and form ties with scientific societies to organize science events on Medical, Pharmaceutical, Life Science and Engineering streams.

Established with a view to organize independent life science events, EuroSciCon serves a vast business and academic clientele base that includes organizations indulged in medical science research, clinical practices and pharmaceutical industry. EuroSciCon could completely transform the traditional role of the science conference organizer that allowed interaction among the participants who are physically attending it. By harnessing the potentiality of the digital media, EuroSciCon also offers Online scientific events taking place across Europe. Colleagues, practitioners, clinical experts and enthusiasts can reap the benefits of live streaming of the events and can watch the conference sessions instantly in drawing rooms, libraries, class rooms and laboratories.

With renewed energy, EuroSciCon helps to achieve heightened levels of awareness through knowledge sharing. It stimulates the scientific temper among the participants from across the academic, corporate, and industry by making the best use of the technological innovations. Our conferences, with the technological know-how, would stick to the ethical principles and research integrity and set the highest standards within the scientific world.

EuroSciCon events transcend boundaries and geographical constraints in knowledge dissemination and reach out to a broad range of target groups, including market leaders; forming an excellent working relationship with major publishing groups. Our events remain ultimate destination for the major search engines of the globe.

EuroSciCon offers the opportunity to attend virtual as well as on-site conferences. The virtual conferences provide some advantages over the physical conferences, including reduced travel time, flexibility of accessing the event from preferred location, affordable registration fees, zero expenditure on accommodation, networking with global audience and reputed international speakers, feasibility of catching up with the missed talks during the free time, avoiding flight delays, fuel expenses, visa approvals and security checks.

All major meetings of EuroSciCon are accredited with Continued Professional Education (CPD), Continued Education (CE), and Continued Medical Education (CME) Credits. EuroSciCon takes the stand of a legitimate body, vested with the responsibility of assessing the scientific content and assures its quality as per the accepted standards. EuroSciCon encourages the early stage academicians and researchers to be part of the Young Research Forum, Best Poster Competition and E-Poster to collaborate for effective partnering, interaction with fellow young researchers and senior researchers, guidance on career prospects, fostering transcontinental cooperation, mutual agreement and engagement among young researchers. Our events help to gain visibility in the global context; in overall it's a key step in the production of new knowledge.

EuroSciCon organizes conferences and is a crucial player in over twenty European Countries (UK, Germany, Spain, Netherlands, Belgium, France, Austria, Portugal, Czech Republic etc.) in some of the top most conference destinations (London, Munich, Berlin, Madrid, Barcelona, Amsterdam, Brussels, Paris, Vienna, Lisbon, Prague etc.). It focuses on a wide array of subjects such as; Agriculture, Biochemistry, Cardiology, Chemical Engineering, Chemistry, Dentistry, Diabetes Endocrinology, Engineering, Environmental Sciences, Food, Gastro, Genetics & Molecular Biology, Geology Earth Science, Healthcare, Immunology, Infectious Diseases, Materials Science, Microbiology, Nanotechnology, Nephrology, Neuroscience, Nursing, Nutrition, Oncology & Cancer, Ophthalmology, Pediatrics, Pharmaceutical Sciences, Surgery, Vaccines, Veterinary among many others.



EuroSciCon CONFERENCE DIRECTORY 2019



Agri, Food Aqua & Veterinary

10th Edition of International Conference on

Food Safety And Regulatory Measures

May 23-24, 2019 Zurich, Switzerland

E: foodsafety@sciconmeet.com

W: foodsafety-hygiene.euroscicon.com

4th International Conference on

Agricultural Engineering and Food Security

June 17-18, 2019 Dubai, UAE

E: agrifood-security@foodspeakerexperts.org

W: agriculture-foodsecurity.euroscicon.com

11th Global Summit on

Aquaculture & Fisheries

August 22-23, 2019 Tokyo, Japan

E: aquaculture@sciconmeet.com

W: aquaculture-fisheriesconference.euroscicon.com

13th Edition of International Conference on

Oceanography & Marine Biology

September 26-27, 2019, London, UK

E: marinebiology@eurosciconmeetings.com

W: marinebiology-oceanography.euroscicon.com

4th International Conference on

Food Microbiology

November 11-12, 2019, Sydney, Australia

E: foodmicrobiology.foodtechconferences.com

W: foodmicrobiology.foodtechconferences.com



Alternative Healthcare

10th International Conference on

Acupuncture, Traditional Medicine & Healthcare

June 20-21, 2019 Rome, Italy

E: acupuncture@eurosciconmeetings.com

W: acupuncture.euroscicon.com

10th International Conference on

Alternative Medicine

August 20-21, 2018 Dublin, Ireland

E: acupuncture@eurosciconmeetings.com

W: alternativemedicine.euroscicon.com

9th International Conference on

Traditional Medicine

September 16-17, 2019 Sydney, Australia

E: traditionalmed@speakertalk.org

W: traditionalmed.euroscicon.com



Biochemistry

11th Edition of International conference on

Structural Biology

March 07-08, 2019 Berlin, Germany

E: structuralbiology@sciconmeet.com

W: structuralbiology.euroscicon.com

7th Edition of International Conference on

Modern Catalysis & Kinetics

June 06-07, 2019 London, UK

E: catalysis@sciconmeet.com

W: catalysis-kinetics.euroscicon.com



Cardiology

22nd International Conference on **New Horizons in**

Cardiology & Cardiologists Education

March 07-08, 2019 Berlin, Germany

E: cardiologyinsights@conferencesconnect.org

W: cardiologyinsights.euroscicon.com



Chemical Engineering

10th Edition of International Conference on

Biofuels and Bioenergy

March 04-05, 2019 Barcelona, Spain

E: biofuels@speakertalk.org

W: biofuels.euroscicon.com

4th Edition of International Conference and Exhibition on

Polymer Chemistry

March 28-29, 2019 Rome, Italy

E: polymers@bookmarkthedata.com

W: polymerchemistry.euroscicon.com

9th International Conference on

Petrochemistry & Chemical Engineering

May 27-28, 2019 Chicago, USA

E: petrochemistry@speakertalk.org

W: petrochemistryconference.euroscicon.com

10th Edition of International conference on

Biopolymers & Bioplastics

May 29-30, 2019 Singapore

E: biopolymers@scholarlymeetings.net

W: biopolymers-bioplastics.euroscicon.com

EuroSciCon CONFERENCE DIRECTORY 2019

5th Edition of International Conference on
Polymer Science and Technology
June 10-11, 2019 Berlin, Germany
E: polymerscience@scholarlymeetings.net
W: polymerscience.euroscicon.com



Chemistry

9th Edition of International Conference on
Chemistry Science and Technology
March 21-22, 2019 Dublin, Ireland
E: chemicalsciences@bookmarkthedata.com
W: chemicalsciences.euroscicon.com

7th Edition of International Conference on
Pain Management
March 25-26, 2019 Rome, Italy
E: painmanagement@bookmarkthedata.com
W: painmanagement.euroscicon.com

3rd Edition of World Chemistry Conference
June 25-26, 2019 Philadelphia, USA
E: worldchemistry@eurosciconmeeting.net
W: worldchemistryconference.euroscicon.com

10th Edition of International Conference on
Analytical Chemistry
June 28-March 01, 2019 London, UK
E: analyticalchemistry@eurosciconmeeting.net
W: analyticalchemistry.euroscicon.com

4th Edition Of International Conference on
Agriculture & Food Chemistry
July 08-09, 2019 Vienna, Austria
E: foodchemistry@bookmarkthedata.com
W: foodchemistry.euroscicon.com

8th Edition of International Conference and Exhibition on
Separation Techniques
July 29-30, 2019 Dublin, Ireland
E: separationtechniques@bookmarkthedata.com
W: separationtechniques.euroscicon.com

7th Edition of International Conference and Exhibition on
Organic Chemistry
August 26-27, 2019 London, UK
E: organicchemistry@bookmarkthedata.com
W: organicchemistry.euroscicon.com

9th Edition of International Conference on
Chemistry Education and Research
September 16-17, 2019 Brussels, Belgium
E: chemistryeducation@bookmarkthedata.com
W: chemistryeducation.euroscicon.com

22nd Edition of International Conference on
Green Chemistry and Technology
November 18-19, 2019 Frankfurt, Germany
E: greenchemistry@bookmarkthedata.com
W: greenchemistry.euroscicon.com



Dentistry

27th International Conference on
Dentistry and Dental Practice
January 28-29, 2019 Barcelona, Spain
E: dentalpractice@eurosciconmeeting.net
W: dentalconference.euroscicon.com

26th International Conference on **Dental Treatment**
August 26-27, 2019 Vienna, Austria
E: dentaltreatment@eurosciconconferences.com
W: dentaltreatment.euroscicon.com

27th International Conference on
Advanced Dental Care
September 16-17, 2019 Baltimore, USA
E: advanceddentalcare@eurosciconconferences.com
W: advanced-dentalcare.euroscicon.com

4th International Conference on
Advanced Dental Education
September 16-17, 2019 Sydney, Australia
E: advanceddentaleducation@sharerresearch.info
W: advanced-dental-education.euroscicon.com



Diabetes

3rd World Congress on **Diabetes and Obesity**
March 18-20, 2019 Rome, Italy
E: diabetesconference@eurosciconmeetings.org
W: diabetesconference.euroscicon.com

12th Edition of International Conference on
Endocrinology & Diabetology
September 02-03, 2019 Berlin, Germany
E: endocrinology@conferencesguide.org
W: endocrinology.euroscicon.com

15th International Conference on
Clinical Dermatology
September 26-27, 2019 Barcelona, Spain
E: clinicaldermatology@eurosciconmeetings.com
W: clinicaldermatology.euroscicon.com



EEE & Engineering

8th Edition of International Conference on

Big Data & Data Science

March 04-05, 2019 Barcelona, Spain

E: bigdata@euroannualsummit.com

W: big-data.euroscicon.com

2nd Edition of International Civil and Architectural Engineering Week

April 22-23, 2019 London, UK

E: architecture@bookmarkthedata.com

W: civil-architecture.euroscicon.com

7th European Congress & Business Expo on

Mechanical & Aerospace Engineering

May 06-07, 2019 London, UK

E: mechaero@conferencesguide.org

W: mechanical-aerospace.euroscicon.com

6th International Conference on Advancements in Graphic Design, Animation, Photography & Virtual Reality

June 19-20, 2019 Tokyo, Japan

E: graphicdesign@annualmeetings.org

W: graphicdesign.euroscicon.com

4th International Conference on

Power and Energy Engineering

June 17-18, 2019 Tokyo, Japan

E: powerengineering@shareresearch.info

W: power-energyconference.euroscicon.com

23rd Edition of International Conference on

Nano Engineering & Technology

November 11-12, 2019 Dubai, UAE

E: nanoengineering@eurosciconconferences.com

W: nano-engineering.euroscicon.com



Environmental Science

10th Edition of International Conference on

Water: Pollution, Treatment & Research

March 14-15, 2019 London, UK

E: waterpollution@sciconmeet.com

W: waterpollution.euroscicon.com

World Congress on Earth & Environmental Science

May 29-30, 2019 Singapore

E: earthscience@lifescienceevent.org

W: earthscience.euroscicon.com

5th Edition of International Conference on

Environmental Science & Technology

June 24-25, 2019 Moscow, Russia

E: environmentalscience@sciconmeet.com

W: environmentalscience.euroscicon.com

3rd Edition of Global Summit on

Renewable Energy & Emerging Technologies

October 24-25, 2019 Baltimore, USA

E: renewableenergy@lifescienceevent.org

W: renewableenergy.euroscicon.com

4th International Conference on

Climate Change and Environmental Disasters

October 21-22, 2019 Las Vegas, USA

E: climatechangeconference@europemeeting.org

W: climateconference.euroscicon.com



Gastroenterology

7th International Conference on

HEPATITIS & LIVER DISEASES

May 02-03, 2019 London, UK

E: hepatitis@conferencesguide.org

W: hepatitis.euroscicon.com

15th International Conference on

Gastro Education

June 17-18, 2019 Tokyo, Japan

E: gastroenterology@eurosciconmeetings.com

W: gastroenterology.euroscicon.com



Genetics and Molecular Biology

13th Edition of International Conference on

Advances in Tissue Engineering and Biomaterials Science

June 17-18, 2019 London, UK

E: tissuescience@euroannualconferences.org

W: tissuescience.euroscicon.com



Healthcare

5th Edition of International Conference on

Occupational Health and Public Safety

April 23-24, 2019 Berlin, Germany

E: occupationalhealth2019@conferencesguide.org

W: occupationalhealth.euroscicon.com

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2nd Edition of International Conference on

Ergonomics & Human Factors

April 29-30, 2019 London, UK

E: ergonomics@lifescience.events

W: ergonomics.euroscicon.com

9th Edition of International Conference on

Clinical & Medical CASE REPORTS

May 27-28, 2019 Barcelona, Spain

E: casereports@eurosciconconferences.com

W: casereports.euroscicon.com

15th Edition of International Conference on
Healthcare

May 27-29, 2019 Barcelona, Spain

E: healthcare@conferencesguide.org

W: healthcare.euroscicon.com

6th Edition of World Congress on **Health Economics, Health Policy and Healthcare Management**

June 17-18, 2019 Dubai, UAE

E: healthconomics@eurosciconmeeting.net

W: healthconomics.euroscicon.com

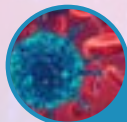
10th Edition of International Conference on

Preventive Medicine & Public Health

July 11-12, 2019 Vienna, Austria

E: preventivemedicine12@yandex.com

W: preventivemedicine.euroscicon.com



Immunology

23rd Edition of International Conference on

Immunology and Evolution of Infectious Diseases

April 29-30, 2019 London, UK

E: immunologyresearch@meetingscalendar.org

W: immunology-infectious-diseases.euroscicon.com



Infectious Diseases

12th Edition of International Conference on

Infectious Diseases

April 22-23, 2019 Rome, Italy

E: infectiousdiseases@sciconmeet.com

W: infectious-diseases.euroscicon.com

23rd Edition of International Conference on

Immunology and Evolution of Infectious Diseases

April 29-30, 2019 London, UK

E: immunologyresearch@meetingscalendar.org

W: immunology-infectious-diseases.euroscicon.com

11th World Congress on

Clinical Microbiology and Infectious Diseases

September 12-13, 2019 Baltimore, USA

E: infectiondiseases2019@eurosciconmeeting.net

W: infectiousdiseasesconference.euroscicon.com

15th Edition of International Conference on

Infectious Diseases Week

October 24-25, 2019 Baltimore, USA

E: infectiousdiseasesweek@Sciconmeet.com

W: infectious-diseases-week.euroscicon.com



Life Science

9th International Conference on

Ageing Research & Geriatric Medicine

April 22-23, 2019 London, UK

E: ageing@speakertalk.org

W: ageing.euroscicon.com



Materials Science

18th Edition of International Conference on **Emerging Trends in Materials Science and Nanotechnology**

January 28-29, 2019 Barcelona, Spain

E: nanomat@scholarlymeetings.net

W: nano-materials.euroscicon.com

4th Edition of International conference on

Advanced Spectroscopy, Crystallography and Applications in Modern Chemistry

April 25-26, 2019 Rome, Italy

E: crystallography@speakertalk.org

W: crystallography.euroscicon.com

8th International Conference on

Smart Materials and Structures

August 01-02, 2019 Dublin, Ireland

E: smartmaterialscongress@speakertalk.org

W: smartmaterialscongress.euroscicon.com

37th Edition of International Conference and Expo on

Nanoscience and Nanotechnology

June 19-20, 2019 Dubai, UAE

E: nanoscience@conferencesfinder.com

W: nanoscienceconference.euroscicon.com

3rd Edition of International Conference on

Materials Technology and Manufacturing Innovations

October 24-25, 2019 Baltimore, USA

E: materialstechnology@scholarlymeetings.net

W: materialstechnology.euroscicon.com

EuroSciCon CONFERENCE DIRECTORY 2019

2nd Edition of International Materials Science and Engineering Week

October 24-25, 2019 Sydney, Australia
E: materialsscienceweek@speakertalk.org
W: materialsscienceconference.euroscicon.com

23rd International Conference on Advanced Materials and Simulation

December 02-03, 2019 Barcelona, Spain
E: advancedmaterials@speakertalk.org
W: advancedmaterials.euroscicon.com



Medical

8th Edition of International Conference on Internal Medicine & Patient Care

March 25-26, 2019 Rome, Italy
E: internalmedicine@eurosciconconferences.com
W: internalmedicine.euroscicon.com

15th International Conference on Gastro Education

June 17-18, 2019 Tokyo, Japan
E: gastroenterology@eurosciconmeetings.com
W: microbiologyresearch.euroscicon.com



Microbiology

11th Edition of International Conference on Advances in Microbiology and Public Health

March 18-19, 2019 Vienna, Austria
E: advancedmicrobiology@conferencesguide.org
W: microbiologyresearch.euroscicon.com



NEPHROLOGY

20th Edition of International Conference on Clinical Nephrology

September 12-13, 2019 Sydney, Australia
E: clinicalnephrology@medicaleuroscicon.org
W: clinicalnephrology.euroscicon.com



NeuroScience

15th International Conference and Exhibition on Alzheimers Disease, Dementia & Ageing

April 22-23, 2019 Rome, Italy
E: eurodementia@neurologyspeakerexperts.org
W: dementiaconference.euroscicon.com

30th Edition of International Conference on Neurology and Neuroscience Week

May 27-28, 2019 Singapore
E: neuroweek@scholarlymeetings.net
W: neurologycongress.euroscicon.com

28th Euro-Global Neurologists Meeting

June 13-14, 2019 Barcelona, Spain
E: neurologists@neurologyspeakerexperts.org
W: neurologistsconference.euroscicon.com

25th International Conference on Neuroscience and Neurochemistry

June 13-14, 2019 Barcelona Spain
E: neurochemistry@neurologyspeakerexperts.org
W: neurochemistry.euroscicon.com

7th International Conference on Neurological Disorders & Stroke

October 07-08, 2019 Dublin, Ireland
E: stroke@scholarlymeetings.net
W: neurology.euroscicon.com



Nursing

5th World Congress on Polycystic Ovarian Syndrome

April 23-24, 2019 Berlin, Germany
E: pcos@lifescience.events
W: pcos.euroscicon.com

28th Edition of World Congress on Nursing Education & Research

April 25-27, 2019 London, UK
E: nursingeducation@eurosciconconferences.com
W: nursingeducation.euroscicon.com

29th Edition of International Conference on Nursing & Healthcare

October 24-25, 2019 Sydney, Australia
E: nursinghealthcare@eurosciconmeetings.com
W: nursingconference.euroscicon.com

6th World Congress on Midwifery & Womens Health

October 24-25, 2019 Baltimore, USA
E: euromidwifery@expertconferences.org
W: midwiferyconference.euroscicon.com

30th International Nursing and Primary Healthcare Professionals Congress

October 21-22, 2019 Las Vegas, USA
E: nursing-phc@lifescience.events
W: nursing-healthcareconference.euroscicon.com

**Nutrition****26th World Nutrition Congress**

June 17-18, 2019 London, UK

E: worldnutrition@euroannualmeetings.orgW: worldnutritioncongress.euroscicon.com**26th Global Nutritionists Week**

September 12-13, 2019 Sydney, Australia

E: nutritionweek@sciconmeet.comW: nutritionweek.euroscicon.com**23rd International Conference on****Nutritional Science, Health and Aging**

October 24-25, 2019 Las Vegas, USA

E: nutritionalscience@nutritionspeakerexperts.orgW: nutritionconference.euroscicon.com**Oncology & Cancer****5th Edition of International Conference on****Clinical Oncology and Molecular Diagnostics**

June 17-18, 2019 Rome, Italy

E: clinicaloncology@eurosciconmeetings.comW: oncology.euroscicon.com**7th International Congress on****Gynecology & Gynecologic Oncology**

June 20-21, 2019 London, UK

E: gynecologymeeting@eurosciconmeetings.comW: gynecologyconference.euroscicon.com**19th Edition of International Conference on****Dermatology and Melanoma**

August 19-20, 2019 Tokyo, Japan

E: dermatology@sciconmeetings.comW: dermatology.euroscicon.com**6th Edition of World Congress on****Cancer Research, Survivorship and Management**

August 22-23, 2019 Tokyo, Japan

E: cancerresearch@eurosciconmeetings.comW: cancer.euroscicon.com**13th World Biomarkers and Clinical Research Conference**

August 22-23, 2019 Vienna, Austria

E: biomarkers@eurosciconmeetings.comW: biomarkers.euroscicon.com**4th Edition of International Conference on****Colorectal cancer**

October 10-11, 2019 Dublin, Ireland

E: colorectalcancer@eurosciconmeetings.comW: colorectalcancer.euroscicon.com**9th Cancer Diagnostics & Treatment Conference**

November 11-12, 2019 Frankfurt, Germany

E: cancerdiagnostics@eurosciconmeetings.comW: cancerdiagnostics.euroscicon.com**Ophthalmology****26th Edition of World Congress of Ophthalmologists**

May 27-28, 2019 Singapore

E: ophthalmologists@scholarlymeetings.netW: ophthalmologists.euroscicon.com**4th Edition of International Conference on****Eye And Vision**

June 06-07, 2019 London, UK

E: eye@scholarlymeetings.netW: eye.euroscicon.com**24th Edition of Advancements on****Ophthalmology: Clinical & Surgical Practices**

October 24-25, 2019 Zurich, Switzerland

E: ophthalmologysurgery@scholarlymeetings.netW: ophthalmologysurgery.euroscicon.com**Pathology****19th Edition on World Pathology Week**

June 19-20, 2019 Tokyo, Japan

E: pathologyweek@sciconmeet.comW: pathologyweek.euroscicon.com**4th International Conference on Digital Pathology**

August 22-23, 2019 Zurich, Switzerland

E: marksscaroline@yandex.comW: digitalpathology.euroscicon.com**18th International Conference on****Pathology & Cancer Epidemiology**

October 21-22, 2019 Rome, Italy

E: pathologydoctor@yandex.comW: pathology.euroscicon.com



Pediatrics

4th Edition on **World Pediatrics**

June 21-22, 2019 Philadelphia, USA

E: worldpediatrics@eurosciconmeeting.net

W: worldpediatricsconference.euroscicon.com

25th Edition of International Conference on

Pediatric Cardiology and Health

April 22-23, 2019 Madrid, Spain

E: pediatriccardiology@eurosciconconferences.com

W: heart.euroscicon.com

23rd Edition of International Conference on

Neonatology and Perinatology

April 23-24, 2019 London, UK

E: neonatology@eurosciconmeetings.org

W: neonatology.euroscicon.com

3rd Edition of International Congress on **Pediatrics**

May 23-24, 2019 Zurich, Switzerland

E: pediatrics2019@eurosciconevent.com

W: pediatricsconference.euroscicon.com

31st Edition of International Congress on

Pediatrics and Neonatology

June 19-20, 2019 Tokyo, Japan

E: pediatricscongress@eurosciconevent.com

W: pediatrics-neonatology.euroscicon.com

8th International Conference on

Euro Pediatrics Week

November 11-12, 2019 Dubai, UAE

E: europediatricsweek@pediatricseuroscicon.org

W: pediatricsweek.euroscicon.com



Pharma

9th Edition of International Conference on

Mass Spectrometry

March 04-05, 2019 Berlin, Germany

E: massspectrometry@conferencesguide.org

W: adolescenthealth.euroscicon.com

Asia-Pacific Annual Congress on

Biopharmaceutics and Pharmacokinetics

June 25-26, 2019 Sydney, Australia

E: pharmaworld@bookmarkthedata.com

W: adolescenthealth.euroscicon.com

World Forum on

Advanced Clinical Research and Clinical Trials

June 25-26, 2019 Sydney, Australia

E: clinicalresearch@bookmarkthedata.com

W: adolescenthealth.euroscicon.com

7th Edition of International Conference on

Pharmacognosy and Medicinal Plants

March 11-12, 2019 London, UK

E: pharmacognosy@eurosciconmeeting.net

W: pharmacognosy.euroscicon.com

World Toxicology and Pharmacology Conference

August 22-23, 2019 Tokyo, Japan

E: worldtoxicology@lifescience.events

W: toxicologyconference.euroscicon.com

12th Edition of International Conference on

Nanopharmaceutics and Advanced Drug Delivery

August 29-30, 2019 London, UK

E: nanodrugdelivery@eurosciconmeeting.net

W: nano-drugdelivery.euroscicon.com

14th Edition of International Conference on

Clinical and Hospital Pharmacy

September 23-24, 2019 Copenhagen, Denmark

E: clinicalpharmacy@eurosciconmeeting.net

W: pharmacyconference.euroscicon.com

13th Edition of International Conference on

Pharma Research and Development

October 24-25, 2019 Sydney, Australia

E: pharmaresearch@eurosciconmeeting.net

W: pharmaresearch.euroscicon.com

14th Edition of International Conference on

Neurochemistry and Neuropharmacology

October 24-25, 2019 Sydney, Australia

E: neuropharmacology@eurosciconmeeting.net

W: neuropharmacology.euroscicon.com

18th Edition of International Conference and Exhibition on

Pharmaceutics and Novel Drug Delivery Systems

October 14-15, 2019 WARSAW, POLAND

E: pharmaceutics@conferencesguide.org

W: colorectalcaner.euroscicon.com

8th Edition of International Conference on

Antibiotics, Antimicrobials & Resistance

October 21-22, 2019 Rome, Italy

E: antibiotics@conferencesguide.org

W: colorectalcaner.euroscicon.com



Physics

7th World Congress on **Optics, Lasers and Photonics**

May 27-28, 2019 Chicago, USA

E: worldoptics@lifescience.events

W: opticsconference.euroscicon.com

EuroSciCon CONFERENCE DIRECTORY 2019

5th International Conference on
Condensed Matter and Materials Physics
September 02-03, 2019 Berlin, Germany
E: eurocondensedmatter@lifescience.events
W: condensedmatterphysics.euroscicon.com



Plant Science

5th Edition of International Conference on
Plant Genomics
June 13-14, 2019 Berlin, Germany
E: plantgenomics@eurosciconmeetings.com
W: plantgenomics.euroscicon.com

5th Annual Congress on **Plant & Soil Science**
June 28-March 01, 2019 London, UK
E: plant.soil@sciconmeet.com
W: plantscience-biology.euroscicon.com



Psychiatry

31st Edition on
World Psychiatrists and Psychologists Conference
June 17-18, 2019 Tokyo, Japan
E: psychiatrists@meetingscalendar.org
W: psychiatryconference.euroscicon.com

30th International Conference on
Sleep Disorders and Psychiatry
July 08-09, 2019 Vienna, Austria
E: sleepmedicine@eurosciconconferences.com
W: sleepmedicine.euroscicon.com

9th International Conference on
Addiction Psychiatry & Mental Health
September 16-17, 2019 Rome, Italy
E: addictionpsychiatry@meetingscalendar.org
W: addictionpsychiatry.euroscicon.com

30th International Conference on
Clinical Psychology & Neuroscience
November 11-12, 2019 Dubai, UAE
E: clinicalpsychology@eurosciconmeetings.com
W: psychology.euroscicon.com



Surgery

4th Edition of World Congress & Exhibition on
Vascular Surgery
March 28-29, 2019 Rome, Italy
E: vascularsurgery@eurosciconmeetings.com
W: vascularsurgery.euroscicon.com

2nd Edition of European Conference on
Otolaryngology, ENT Conference
May 27-28, 2019 Singapore
E: entconference@europemeeting.org
W: entconference.euroscicon.com

14th International Conference on **Neurology, Neuroscience
and Neuromuscular Disorders**
June 17-18, 2019 Tokyo, Japan
E: neuromuscular@eurosciconmeeting.com
W: neuromuscularconference.euroscicon.com

8th Edition of International Conference and Exhibition on
Surgery and Transplantation
July 01-03, 2019 Valencia, Spain
E: surgeryconference@medicaleuroscicon.org
W: surgeryconference.euroscicon.com

15th International Conference on **Clinical Dermatology**
September 26-27, 2019 Barcelona, Spain
E: clinicaldermatology@eurosciconmeetings.com
W: vascularsurgery.euroscicon.com

8th Edition International Conference on
Public Health, Nursing & Primary Care
October 10-11, 2019 Madrid, Spain
E: primarycare@eurosciconmeetings.com
W: phc-publichealth.euroscicon.com

4th Edition of Annual Congress on
Plastic, Aesthetic and Reconstructive Surgery
November 11-12, 2019 Frankfurt, Germany
E: plasticsurgery@eurosciconmeetings.com
W: plasticsurgeryconference.euroscicon.com

8th International Conference on **Otorhinolaryngology**
November 11-12, 2019 Frankfurt, Germany
E: otorhinolaryngology@eurosciconmeetings.com
W: otorhinolaryngology.euroscicon.com



Veterinary

14th Global Summit on **Veterinary and Animal Sciences**
September 12-13, 2019 Sydney, Australia
E: veterinariyscience@sciconmeet.com
W: veterinary.euroscicon.com

DAY 1

Keynote Forum



5th Edition of International Conference on

Plant Genomics

June 13-14, 2019 | Berlin, Germany

June 13-14, 2019
Berlin, Germany

Raj Kumar Joshi, AJPSKY 2019, Volume 09

Genome editing in chili pepper using a CRISPR/Cas9 Cytidine base editing system

Raj Kumar Joshi

Rama Devi Women's University, India



Anthraxnose, caused by *Colletotrichum* species complex is the most devastating disease of chili pepper (*Capsicum annuum*) in the tropical and subtropical regions of the world. Attempted management of chili anthracnose through conventional approaches hasn't met with tangible success. CRISPR/Cas9 based precise and predictable targeted point mutations has emerged as the most powerful alternative in plant breeding without the need for a foreign DNA donor or double stranded DNA cleavage. We have used a CRISPR/Cas9 fused Cytidine Base Editing (CBE) system for precise editing of NAC72 locus in Chili pepper using *Agrobacterium*-mediated transformation approach. The CBE efficiently edited the targeted cytidine bases leading to anthracnose resistance with precise base edition efficiency up to 69% in chili pepper. The outcomes from this study will be deliberated to demonstrate that base editing could facilitate precision molecular breeding in plants for specific trait improvement.

Biography

Raj Kumar Joshi is Associate Professor at the Dept. of Biotechnology, Rama Devi Women's University, India where he teaches graduate level courses on Plant Genomics and Genetic Engineering. He also serves as the Group Leader of the Plant Functional Genomics Group, and in that capacity he supervises the overall research activities on the functional aspects of molecular plant-microbe interactions. He has been awarded with the prestigious SERB early career grant and SERB extramural grant from the Dept. of Science and technology, Govt. of India and CREST award from Dept. of Biotechnology, Govt. of India. In collaboration with Prof. Nat Kav from University of Alberta, Canada, he is running a successful program on the delineation of molecular networks in the interaction between plants and fungal phytopathogens. His recent forays into genome editing and precise base editing towards improvement of these crops has been highly productive.

rkjoshi@rdwu.ac.in

DAY 1

Scientific Tracks & Abstracts



5th Edition of International Conference on

Plant Genomics

June 13-14, 2019 | Berlin, Germany

DAY 1

June 13, 2019

Sessions
Cancer Science
Cancer Therapies

Session Chair

Ildiko Matusikova

University of St. Cyril and Methodius, Slovak Republic

Session Introduction

Title: Nutrition effects on synthesis of plant defense proteins and tolerance to metals

Ildiko Matusikova, University of St. Cyril and Methodius, Slovak Republic

Title: The development of a novel SNP genotyping assay to differentiate cacao clones

Jocelyn De Wever, Ghent University, Belgium

Title: Virulence of *Fusarium circinatum* is associated with perturbation of phytohormone homeostasis in *Pinus pinaster* seedlings

Laura Hernandez Escribano, National Institute of Agricultural and Food Research and Technology, Spain

Title: Establishment of regeneration protocol for Mongolian subendemic species *Oxytropis grubovii* Ulzij

Bolortuya Ulziibat, Institute of general and experimental biology, Mongolia

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Ildiko Matusikova, AJPSKY 2019, Volume 09

Nutrition effects on synthesis of plant defense proteins and tolerance to metals

Ildiko Matusikova

University of St. Cyril and Methodius, Slovak Republic

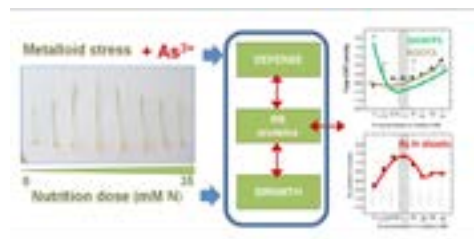
Under stress including metal toxicity plants synthesize defense components, including enzymes like β -1, 3-glucanases and chitinase. Since defense is costly the synthesis of these enzymes depends on nutrients availability. The situation is more complicated if nutrient dose itself represents stress several enzyme isoforms with peculiar response to either starvation or nitrogen excess have been identified. A comprehensive study on the impact of nutrition on defense enzymes under stress is missing. Therefore, responses of plants exposed to arsenic, combined with conditions of low, optimal as well as excessive N concentrations, were studied in more detail.

Methodology and Theoretical Orientation: Hydroponic wheat plants were grown in standard Hoagland media with different amounts of ammonium nitrate at the final nitrogen concentrations of 0, 0.75 and 5.25 mM N (suboptimal doses), 7.5 mM (optimum), and 15, 25, 30 and 35 mM N. After a week, As³⁺ at sub lethal dose was applied. The profile and activity of individual defense enzymes (β -1,3-glucanases and chitinases) as well as some morpho-physiological parameters were studied.

Findings: Nutrition conditions affect the responses of wheat plants to arsenic toxicity: Enzyme isoforms responsive to nitrogen concentration, metalloid, and to both were identified. Although (supra) optimal nitrogen concentrations positively activate the defense, the optimal dose appears not always the same for the individual parameters. Furthermore, at high doses of

nitrogen the plants accumulated less arsenic in the shoots; probably due to better ability to prevent the transport of toxic element to the aerial parts.

Conclusion and Significance: Nutrition availability affects accumulation and/or activity of defense-related compounds, and impacts uptake of arsenic by the wheat plants. Some chitinase and glucanase isoforms are candidates for screening of plants health in the context of fertilizer management and / or presence of toxic metals.



Biography

Ildiko Matusikova studies the physiology and biochemistry of, and gene expression changes in, stressed plants. She focuses on enzymes of chitinases and β -1, 3-glucanases in context of different scientific questions. Recently she extended her interests in studying the uptake, transport and accumulation of (toxic) metals in plants using radioanalytical approaches. She also does research on the molecular biology of *Drosera* and studies the role of hydrolytic enzymes in prey digestion by carnivorous plants.

ildiko.matusikova@ucm.sk

June 13-14, 2019
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Jocelyn De Wever, AJPSKY 2019, Volume 09

The development of a novel SNP genotyping assay to differentiate cacao clones

Jocelyn De Wever

Ghent University, Belgium

Plant genetic diversity studies are of high importance for efficient plant conservation and resource strategies (eg. tackling mislabeling, conserving valuable genetic material, parentage analysis, and genetic diversity studies) as they contribute to an increased knowledge on the genetic background and diversity of specific plants. These studies are most commonly analyzed through simple and effective genotyping methods making use of genetic markers, such as SSRs, however SNPs are gaining more interest. Recently, a cost-effective qPCR-based method has been proposed for SNP genotyping purposes, coined double-mismatch allele-specific (DMAS) qPCR as cheap alternative to other methods. It's an accurate and fast multi-sample and multi-locus method, based on straightforward readout of DNA-binding dye based qPCR technology. Its design, optimization, validation and application on *Theobroma cacao* L., an important cash crop involved in the chocolate production, has shown successful. It offered valuable knowledge on the background of cocoa which is often plagued by mislabeling and inefficient and limited management resources. The method, optimized here, showed 98.05% efficient in calling the right cacao genotype and identified 15.38% off-types and two duplicates in an internationally recognized cacao population (n=65), using a limited amount of markers (n=42). Furthermore, only 13 markers were needed to differentiate all analyzed accessions. Notably, the described method can easily be optimized and implemented in any molecular biology lab for a wide range of objectives and organisms e.g. mutation detection and to facilitate gene mapping and marker-assisted selection for breeding purposes.

Methodology and Theoretical Orientation: In this study, first the need for more genotyping in plant specific studies with focus on cocoa is elucidated, focused on the available markers and methods, together with their advantages and disadvantages. DMAS-qPCR SNP genotyping seems a cheap and reliable alternative for such analysis and has been analysed. In this study, the design (PrimerX1), optimization and validation (sequencing and database dependent) of the DMAS qPCR SNP genotyping method is pointed out specifically for cocoa. In addition, several genotyping models have been optimised, of which two can be automated, to translate the retrieved Cq values from DMAS qPCR assay to allele calls and finally a genotype. Thereafter, its applicability on cocoa genetic diversity and mislabelling studies, using GenAIEx v6.5, has been analysed and confirmed on a Vietnamese cocoa population.

Findings: Cocoa DMAS-qPCR based SNP genotyping method has been optimized and consist of 42 SNP markers, which showed 98.05% as efficient in calling correct genotypes. In addition 15.38% off-types and two duplicates have been identified in an internationally recognized cacao population (n=65). Furthermore, three genotyping models have been proposed, of which two could be used in an automated set-up starting from the qPCR data retrieved. Thereafter, key descriptive analysis of the markers, representing the applicability of this method in cocoa genetic diversity studies, using GenAIEx v6.5 has been described in more detail. From this analysis it has been concluded only 13 SNP markers from the DMAS- qPCR assay were needed to differentiate all accessions individually.

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Conclusion and Significance: In conclusion, we have developed a robust and accurate method for cacao genotype identification using a limited set of SNPs. The ease of use and cost-efficiency of the method without the need of specialized instruments can contribute to the adoption of routine-based genotyping to prevent mislabeling in germplasm collections and select optimal breeding parents in cacao and other organisms. The described method can easily be implemented in any molecular biology lab in the context of genotyping, genetic diversity studies, parentage analysis, mutation detection and to facilitate gene mapping and marker-assisted selection for breeding purposes.

Biography

Jocelyn De Wever is a, soon finishing, PhD student with synergistically combined technical (lab technician) and theoretical (bio-engineering) background on applied genetics. She developed a passion in trying to understand the encrypted secrets of flavor in the cocoa its genetics. Thereafter she gained several on-field experiences concerning the cocoa cultivar selection and post-harvesting treatment. Furthermore, she is the main actor on the optimized hands-on DNA and RNA extractions from the difficult and highly contaminated cocoa tissues, and aided in the development of several cocoa genotype and transcriptome based studies.

Jocelyn.deweever@ugent.be

June 13-14, 2019
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Laura Hernandez Escribano, AJPSKY 2019, Volume 09

Virulence of *Fusarium circinatum* is associated with perturbation of phytohormone homeostasis in *Pinus pinaster* seedlings

Laura Hernandez Escribano

National Institute of Agricultural and Food Research and Technology, Spain

Plants have developed complex molecular strategies to face the attack of a pathogen in order to maintain their survival, and phytohormones are known to play a crucial role in plant-pathogen interactions. The aim of this study is to elucidate the role of phytohormones in *Fusarium circinatum* virulence, the causal agent of pitch canker disease, known as one of the most important pathogens of conifers worldwide.

Methodology and Theoretical Orientation: For this purpose, by a dual RNA-sequencing approach, we determine the expression profiling of both organisms during the interaction at 3, 5 and 10 days post-inoculation.

Findings: *Pinus pinaster* showed moderate resistance at the early time points. This may be explained, at least in part, by the early recognition, the induction of pathogenesis-related proteins and the activation of complex phytohormone signaling that involves crosstalk between three main protagonists: Salicylic acid, jasmonic acid and ethylene. Moreover, we hypothesise the key steps where the pathogen could be manipulating host phytohormone balance to its own benefit, contributing to pathogen virulence. Upon examination of the pathogen

transcripts, we propose that *F. circinatum* prevents salicylic acid biosynthesis from the chorismate pathway by the synthesis of isochorismatase family hydrolase (ICSH) genes, perturbs ethylene homeostasis in the host by expression of genes related to ethylene biosynthesis, and could be blocking jasmonic acid signalling by COI1 suppression.

Conclusion and Significance: Targeted functional testing using *F. circinatum* mutants in future studies would be needed to support this hypothesis.

Biography

Laura Hernández Escribano is currently a PhD student in the National Institute of Agricultural and Food Research and Technology, Center for International Forestry Research (INIA-CI-FOR), working in the field of plant pathology with the thesis named "Fusarium circinatum – host interaction: Ecological and molecular aspects of the pathogenic and endophytic association". She has a degree in Biology and masters in "Applied Vegetable Biology", by the Complutense University of Madrid.

hernandez.escribano@inia.es

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Bolortuya Ulziibat, AJPSKY 2019, Volume 09

Establishment of regeneration protocol for Mongolian subendemic species *Oxytropis grubovii* Ulzij

Bolortuya Ulziibat

Institute of general and experimental biology, Mongolia

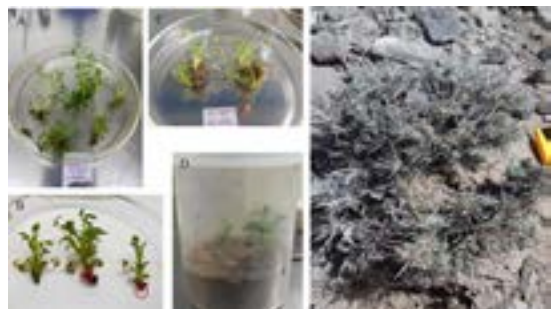
One of the Mongolian subendemic species, *Oxytropis grubovii* Ulzij., grows as a perennial woody shrub and registered in endangered plant list of Mongolia. It distributed in Mongolia gobi desert area with high content of underground wealth. Even it could be regenerated by seed and vegetative organs; it did not produce the seeds during last decade due to the lower rain-falling. Plants growing in a part of the gobi, desert ecosystem drastically damaged by off-road vehicles, mining and pollution depend on mining activity. Since, these native plants are endangered and difficult to propagate by conventional method, conservation and mass propagation in *in vitro* condition can play an important role in the rehabilitation of mining site.

In this study, our research group established tissue culture system for *Oxytropis grubovii* Ulzij. Contamination was highly occurred during the *in vitro* culture and general reagents for sterilization could not work on that woody shrubs. Washing in PPM solution together with supplemental PPM in growth medium was reduced the contamination rate until 60%. In the process of shoot development, medium with combinations of BAP and NAA, Kin and NAA, or BAP, TDZ and 2iP separately investigated step by step. In a result, shoots were effectively regenerated on the medium with 2iP (2.0 mg/l) and produced 15 shoots per explants within four weeks. For rooting of these proliferated shoots, only auxins of IBA, IAA, NAA or combinations of 2iP with IBA tested consistently and results revealed that roots were induced on the medium containing IBA and IAA (2.0mg/l) with 20-30 percent. Produced root's branching

in IBA supplemented medium were higher, however, root length was too short. Whereas, roots were effectively elongated when combining IBA with 2iP (5.0:1.0mg/l) on the medium and root induction percentage were about 50percents.

As indicated in these results, shoot and roots of *Oxytropis grubovii* Ulzij. Can be regenerate *in vitro* condition and this regeneration protocol is first time developed for the species. Preliminary test for *ex vitro* adaptation also executed a time, however, results not identified yet.

Regeneration steps of *Oxytropis grubovii* Ulzij. A. Proliferated shoots on the medium supplemented 2iP, B. IBA effect for shorter root generation, C. Combination of 2iP and IBA induced longer and actively elongated roots, D. Adaptation in *ex vitro* condition, E. Naturally growing plant.



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Biography

Bolortuya Ulziibat works as a researcher in the Plant biotechnology laboratory of Institute of General and Experimental Biology, Mongolian Academy of Sciences. She graduated her Ph.D course in Tohoku University, Japan in 2016. During her doctoral course, she conducted the research work to identify cold tolerance gene of Yunnan landrace 'Lijiangxintuanheigu' in rice during booting stage. Her current research work is tissue culture system development and gene

identification for rhizome development of Mongolian very rare, and endangered plants used in traditional and modern medicine *A. calamus* through the transcriptome analysis. She is also working on the project that identifies the possibility to establish micropropagation protocol for rare and endangered plant species in the mining field and to apply them for rehabilitation after mining exploitation.

jabo_2002ca@yahoo.com

POSTERS

Abstracts



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Marek Szklarczyk, AJPSKY 2019, Volume 09

Conversion of GBS polymorphisms into CAPS markers for a fertility restoring gene in carrots

Marek Szklarczyk

Krakow Agricultural University, Poland

Breeding of carrot hybrids is based on Cytoplasmic Male Sterility (CMS) and CMS lines are reproduced using the so called maintainer lines which should be devoid of fertility restoring alleles. Therefore, the development of DNA markers for such alleles would greatly facilitate production of new hybrids. For this purpose we mapped carrot restorers in the context of DNA polymorphisms detected via Genotyping By Sequencing (GBS). In the present work we selected a few GBS polymorphisms, which were linked to fertility restoration, and subjected them to conversion into Cleaved Amplified Polymorphic Sequences – CAPS markers.

Methodology and Theoretical Orientation: The GBS datasets were screened for possible CAPS markers with the VCF2CAPS software developed by Wojciech Wesołowski. The respective PCR primers were designed manually. PCR was followed by restriction with a tetra-cutter and routine electrophoresis in agarose. Genotyping was performed for plants from population 170 which segregated into male-sterile and male-fertile (restored) plants.

Findings: Conversion was performed for four GBS polymorphisms from chromosome 9 where the restorer gene from population 170 was mapped. For two GBS polymorphisms the respective CAPS

polymorphisms were not detected. The remaining two GBS polymorphisms translated into polymorphic CAPS markers named pe098/RsaI and pe106/TaqI. Both polymorphic CAPS markers showed co-segregation with the sterility/fertility phenotype. Co-segregation reached the value of 84 and 89 % for pe098/RsaI and pe106/TaqI, respectively. For both markers the male-fertile plants were homozygous and the male-sterile-plants were heterozygous.

Conclusion and Significance: The results show that some GBS polymorphisms may be negatively verified with the use of CAPS markers. Likely, it is related to low coverage of DNA sequencing during GBS which results in low quality of the identified polymorphisms. Nevertheless, two GBS polymorphisms were converted into useful CAPS markers which can be used for identification of the restorer from chromosome 9 in segregating populations.

Biography

Marek Szklarczyk is a faculty member at the Institute of Plant Biology and Biotechnology, Krakow Agricultural University, Poland. His main scientific interests are cytoplasmic male sterility (CMS) and fertility restoration. He studies these traits in carrots, beets, onions and rye.

marek.szklarczyk@urk.edu.pl

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Marija Kostadinovic, AJPSKY 2019, Volume 09

Marker assisted selection for β -carotene rich maize: Validation of the gene-specific marker in BC₁ generation

Marija Kostadinovic

Maize Research Institute Zemun Polje, Serbia

Worldwide, modern grain breeding programs widely implement Marker Assisted Selection (MAS). Molecular markers are being used in two ways: To control the target gene (foreground selection) and to accelerate the reconstruction of the recurrent parent genotype (background selection). Marker analysis allow breeders to discard plants without alleles of interest prior to pollination, reducing the size of breeding population. Marker assisted selection for the qualitative traits, which are regulated by the action of a single or several genes and are clearly phenotypically defined, achieved the best results. The improvement of β -carotene content using crtRB1-specific molecular marker is one of the successful examples of MAS. The introgressed inbreds possessing favourable allele of crtRB1 and improved hybrids with increased β -carotene can be used in the biofortification program.

The results presented herein are a part of the breeding program conducted at the Maize Research Institute "Zemun Polje", with the aim to convert the standard maize to β -carotene rich genotypes adapted to temperate regions. The utility of SSR marker specific to the crtRB1 gene in foreground selection has been already tested on parental lines and distinct marker polymorphism was observed between the donor and recurrent parents. The objective of this study was to validate the ability of

the same SSR marker to detect homozygous dominant and heterozygous plants separately in BC₁ generation. Heterozygous individuals were clearly distinguishable, therefore they will be selected and backcrossed with the recurrent parent to produce BC₂ generation. Percentage of heterozygous plants identified in BC₁ generation was approximately 50%, which is in accordance with the expected Mendelian ratio of 1 O2O2 : 1 O2o2. The use of the crtRB1-specific marker will be extended in the next generation of MAS for β -carotene enriched lines for growing in temperate regions.

Biography

Marija Kostadinovic has completed her PhD in Genetics at University of Belgrade, Serbia. At present, she is working as a Research associate in the Laboratory of Molecular Genetics and Physiology at the Maize Research Institute "Zemun Polje", where she is engaged in the project "Improving the quality of maize and soybean by conventional and molecular breeding" funded by the Ministry of Education, Science and Technological Development of Republic of Serbia. Her research focus is on the marker assisted selection for improvement of the maize protein quality. Also, she is included in genetic characterization of maize lines, hybrids and populations, as well as in biochemical testing of the grain quality.

kmarija@mrizp.rs

E-POSTERS

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Jimena Cascales et al., AJPSKY 2019, Volume 09

Survey of differentially methylated and expressed genes in vegetative and reproductive organs of two Ilex species

Jimena Cascales, Mariana Julia Garberoglio and Alexandra Marina Gottlieb

University of Buenos Aires, Argentina

Ilex paraguariensis and *I. dumosa* (Aquifoliaceae) are dioecious perennial trees native to southern Brazil, northwestern Argentina, northeastern Paraguay and Uruguay. The aerial parts of *I. paraguariensis* the 'yerba mate' are used to prepare the 'mate' infusion which has a great cultural and socio-economic value in many southern South American countries. This species produces several secondary metabolites, many with nutraceutical properties. *Ilex dumosa* is a valuable gene/allelic reservoir as it produces significantly lower contents of such compounds and shows resistance to an *I. paraguariensis*' hemipteran plague. The mechanisms of sex determination are unknown in *Ilex*, while metabolic and defense pathways have been proposed only for *I. paraguariensis*. The knowledge derived from intra- and interspecific comparisons could be applied in genetic improvement programs of the 'yerba mate' crop, as well as to enhance the harvest period. The present comparative study focused in detecting epigenetic and gene expression differences between sexes and species, by screening flower buds and vegetative organs (young and adult leaves). For this, MSAP Methylation Sensitive Amplified Polymorphism and cDNA-AFLP techniques

were used. A total of 103 isolated differential fragments were effectively characterized with bioinformatic tools, considering $\leq 10^{-5}$ E-value. Of these, 46.6% derive from *I. paraguariensis* and 53.4% from *I. dumosa*; 63% were recovered from reproductive and 37% from vegetative organs. Thirty-five percent of the fragments were identified as related to: metabolism (7.8%), regulation of gene expression (7.8%), biotic/abiotic stress resistance (3.9%), and other cellular processes (15.5%). Additionally, three groups of genes were distinguished: a) potentially involved in sexual determination (9 sequences), b) secondary metabolite production (3 sequences), and c) biotic stress resistance (6 sequences). The methodological approach allowed detecting differentially represented genes, which would be worth validating in qPCR studies.

Biography

Jimena Cascales is a postdoctoral scholar with expertise in population genetics, epigenetics and gene expression analysis of *Ilex paraguariensis* and *I. dumosa*.

jcascales@ege.fcen.uba.ar

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Maria Krzakowa et al., AJPSKY 2019, Volume 09

Complex analysis of genetic differentiation in *Lolium westerwoldicum* European collections revealed by biochemical and molecular markers

Maria Krzakowa, Zbigniew Celka and Michał Ronikier

Adam Mickiewicz University, Poland

Polish Academy of Sciences, Poland

L*olium westerwoldicum* Break a very important forage grass was initiated in Westerwolde (Netherlands) and this is why its name was created by the place where the species has been selected. This annual grass can exist as diploid or tetraploid form. Thirty tetraploid cultivars originated from different European countries were examined according to phosphoglucose isomerase (PGI, EC5.3.1.9). PGI as one of the most important enzyme systems, catalysis the reversible isomerization of glucose-6-phosphate and fructose-6-phosphate and have an influence on starch production in chloroplasts. Individual plants were genotyped from one-month old seedlings cultivated in the uniform greenhouse conditions. Electrophoresis was performed on horizontal, 11% starch gels (Sigma) in Ashton buffer system pH 8.1 and staining procedure from Vallejos with some minor modifications. Electrophoretically detected PGI band patterns show four alleles in one locus. Because of its dimeric structure, PGI is very polymorphic in all *Lolium* species. Investigated cultivars were described by such genetic parameters as observed and expected heterozygosity, fixation indices and polymorphic indices of genotypes. Similarities between populations, based on allele frequencies were illustrated by dendrogram constructed using the unweighted pair of group method UPGMA. All investigated populations (=cultivars) show oscillation in polymorphism level from Pg=0.1267 for almost monomorphic cultivar Gonzales to the most

polymorphic cultivar Kaja (Pg=-.9025). Molecular biology offers a wide range of markers that can be utilized in crop breeding. Besides these mentioned above investigations, ten other populations composed of individuals belonging to the two species: *L. westerwoldicum* and *L. multiflorum* were simultaneously compared according to PGI and AFLP markers and show spectacular separation of these species in question.

Biography

Maria Krzakowa works as Professor Senior at Adam Mickiewicz University in Poznań, Poland. Some years ago, she spent one-year training as Post Doc at the University of California Davis. She learned there allozymes detection by horizontal electrophoresis. First of all, her scientific activity was concerned about genetic variation of natural populations of Bryophytes (different species of Hepatics and Mosses) and later on forest trees: Scots pine (*Pinus sylvestris*), beech (*Fagus sylvatica*) and ash-tree (*Fraxinus excelsior*). In the meantime she developed investigations on grasses, for example *Apera spica-venti* and *Alopecurus myosuroides*. Her main achievement was the first description of dimeric peroxidase in reed (*Phragmites australis*). It was some kind of discovery, as dimeric peroxidase was known earlier only from the rice (*Oryza sativa*). Now, she is working on European collection of Italian and Westerwolds ryegrasses (*Lolium* spp.) considering biochemical and molecular polymorphism of these important forage grasses.

jcascales@ege.fcen.uba.ar

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Abstracts



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AJPSKY 2019, Volume 09

The Role of Epigenetics and Environmental Stimuli in the Inheritance of Freezing Tolerance in Wheat

Jamin Smitchger

Washington State University, USA

The field of epigenetics has discovered that the genome is affected by environment, and it is possible to use the idea of epigenetics in plant breeding by exposing plants to various environmental cues such as frost, drought, or hot temperatures. The progeny that result from these epigenetic changes often have slightly higher frost, drought, or heat tolerance. These principles were first discovered by the eminent Russian biologist Trofim Lysenko in the 1940's, but the underlying mechanism for such observations was not previously known. At this current time, this phenomenon has not been extensively studied and the potential role of DNA methylation in plant breeding has not been thoroughly explored. In this

research, 43 wheat varieties were subjected to freezing temperatures in a randomized complete block design during four site years. The subsequent generation of wheat after the freezing treatment was ~15% more tolerant of freezing temperatures than the previous generation, indicating significant epigenetic changes were caused by the freezing treatment in the previous generation. We conclude that environmental stimuli can shape the phenotype of wheat, and that these epigenetic changes can be heritable in subsequent generations. This potentially could have an enormous impact on the breeding of varieties that can withstand abiotic stresses.

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High-Density Linkage Map Construction and Mapping of Salt-Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing

Latyr Diouf

Institute of Cotton Research, China

Over 6% of agricultural land is affected by salinity. It is becoming obligatory to use saline soils, so growing salt-tolerant plants is a priority. To gain an understanding of the genetic basis of upland cotton tolerance to salinity at seedling stage, an intra-specific cross was developed from CCRI35, tolerant to salinity, as female with Nan Dan (NH), sensitive to salinity, as the male. A genetic map of 5178 SNP markers was developed from 277 F2:3 populations. The map spanned 4768.098 cM, with an average distance of 0.92 cM. A total of 66 QTLs for 10 traits related to salinity were detected in three environments (0, 110, and 150 mM salt treatment). Only 14 QTLs were consistent, accounting for 2.72% to 9.87%

of phenotypic variation. Parental contributions were found to be in the ratio of 3:1, 10 QTLs from the sensitive and four QTLs from the resistant parent. Five QTLs were located in At and nine QTLs in the Dt sub-genome. Moreover, eight clusters were identified, in which 12 putative key genes were found to be related to salinity. The GBS-SNPs-based genetic map developed is the first high-density genetic map that has the potential to provide deeper insights into upland cotton salinity tolerance. The 12 key genes found in this study could be used for QTL fine mapping and cloning for further studies.

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Genetic Diversity of Some Quality Protein Maize Lines (Genotypes) As Revealed By Molecular Markers

Mansir Yusuf

Ahmadu Bello University, Nigeria

Unmasking of genetic diversity in maize breeding populations can greatly assist in designing appropriate breeding strategies. Six quality protein maize inbred lines (parents) together with their respective progenies were characterized using molecular (RAPD) markers primarily to determine the genetic diversity within the population and to establish the genetic relationship between the parents and their progenies at molecular level. The primer; OPERON- AF 13 gave the highest number of DNA polymorphic bands , suggesting that it could be used

as an effective marker in more detailed genetic studies involving these lines and possibly other maize lines. The results of the Dendrogram revealed the relationships between the parents and their respective single cross hybrids with 33.33% of the progenies resembling more like the female parents and 60.67% resembling more like the male parents respectively, this may indicate less maternal effect within the maize population under study which is often desirable in breeding work.

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Genomic Reshuffle Among Hybrids Offers Strategies for Survival of Segregates In Nature: *I. Ophioglossum L.* (Pteridophyta)

Mitesh Patel

Veer Narmad South Gujarat University, India

Modern plant biology research is getting totally trapped in laboratories but on making field surveys and population enumeration over several years we have encountered too many variations and evolutionary mechanisms within the species and many species of the same genus. One of the major reasons which is becoming now popularly known and studied is the incidence of natural hybridizations. Population biology studies conducted (during 1970-2018) by one of us (HKG) have presented such unusual features exhibited by the genomes of the pteridophytic genera *Ophioglossum L* and *Isoetes L* that have become unknown and unique among the related genera and species. Lately, a similar attempt has been under operation in Gujarat, in search of intragenomic variations within the genus *Ophioglossum* in the Western part of India. We have not only discovered unique and hitherto unknown features in several species of *Ophioglossum* but also on the basis of morphological and phylogenetic studies conducted on DNA isolation-sequencing and comparative genomics have identified

new species. A few of them appear to be natural hybrids. While in Central India and Rajasthan, *Ophioglossum costatum* has been identified to be a one of the putative parents, in Gujrat populations, the genus indicates genetic involvement of *O. vulgatum*. Obviously, participation of species depends upon their closer occurrence within the ecological niche. Major but consistent variables are some of the attributes of biological evolution to ascertain the survival. Obviously, natural hybridizations abruptly disrupt meiotic selections of the species; male-gamete contribution remains unaffected; but female parent or the diploid (Zygote) faces partial threat, because, the product-hybrid undergoes survival tests at many stages. Briefly, evolution of certain designated “new genomes” tagged as new species, viz. *Ophioglossum malviae* Patel & Reddy; *O. eliminaum* Khandelwal & Goswami; *O. indicum* Yadav & Goswami; *O. chaloneriei* Goswami et al; *O. aletum* Patel, et al; and *O. hitkishorei* Patel & Reddy will be presented.

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Transmission *Xylella fastidiosa*: Evidence from European countries

Nadhem Selmi

University of Sfax, Tunisia

The plant *Xylella fastidiosa* causes a diverse range of host plant species and olive. The bacterium *Xylella fastidiosa*, transmitted and carried by insect vectors, attacks a very broad spectrum of plants: vines, olive trees, fruit trees (Prunus), citrus fruits, coffee trees, oaks, alfalfa, etc. The severity of its impacts varies according to the strain, the plant and the ecosystem concerned. Thus, there is a great diversity of situations in the world. *Xylem bacterium*, *Xylella fastidiosa* prevents the plant from feeding by hindering the movements

of the raw sever. The symptoms of its manifestations are not very specific (wilting, leaf burns) and make it difficult to detect. Currently, there are no curative ways to fight against this bacteria. The European decision to prevent the introduction and spread of the bacterium on the territory, advocates the uprooting and destruction of contaminated plants. Our results show that transmission of *Xylella fastidiosa* to 3-year-old wood and olive in Italy and Spain.

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De Novo sequencing and hybrid assembly of biofuel crop *Jatropha curcas* Ls Insights on gene annotation, comparative genomics and transcriptome analysis with identification of quantitative trait loci for geminivirus resistance

Nagesh Kancharla

Reliance Industries Limited, India

J*Jatropha curcas* is an important perennial, drought tolerant plant identified as a potential biodiesel crop. We report here the hybrid de novo genome assembly of *Jatropha curcas* generated using Illumina and PacBio sequencing technologies and identification of quantitative loci responsible for geminivirus resistance. In this study, we generated scaffolds of 265.7 Mbp in length which is corresponding to 84.8% of the gene space using BUSCO analysis. Additionally, 96.4% of predicted protein-coding genes were captured in corresponding tissues transcriptome data, which reconfirms the accuracy of the assembled genome. The genome was utilized to identify 12,103 dinucleotide repeat SSR markers, which were exploited in genetic diversity analysis to identify genetically distinct lines. A total of 250, polymorphic SSR markers were employed to construct a genetic linkage map for Jatropha Mosaic Virus (JMV) resistance using

interspecific F2 mapping population involving *Jatropha curcas* and *Jatropha integerrima* as parents. QTL analysis showed the identification of three minor Quantitative Trait Locus (QTL) for JMV resistance and validated in an alternate recipient genetic background F2 mapping population. These validated QTLs were utilized in Marker Assisted Breeding (MAS) for developing *Jatropha Mosaic Virus* resistance hybrids in *Jatropha*. Comparative genomics of oil-producing genes across selected oil producing species revealed 27 conserved genes and 2,986 orthologous protein clusters in *Jatropha*. This reference genome assembly gives an insight into the understanding of the complex genetic structure of *Jatropha* and serves as source for the development of agronomically improved virus resistant and oil producing species.

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Genetic analysis of Seed Quality Traits and Concentrations of Zinc and Iron in Maize Topcross Hybrids

Richard Akinwale

Obafemi Awolowo University, Nigeria

Adequate knowledge about the genetic control of iron (Fe) and zinc (Zn) concentrations as well as seed quality in maize (*Zea mays L.*) is important in improving the crop for both traits thereby combating malnutrition and food insecurity in sub-Saharan Africa. Twenty-six maize genotypes comprising 16 topcross hybrids were evaluated for seed quality traits and Fe and Zn concentrations in maize kernels to study their inheritance pattern. The experiment was laid out using randomized complete block design with three replicates. Data collected were subjected to analysis of variance. Genotypic effect was significant for all traits except Germination Index (GI) and shoot length. When genotypic effect was partitioned into its genetic effects, both General Combining Ability (GCA) for line and Specific Combining Ability (SCA) mean squares were significant for all traits except shoot length, shoot fresh and dry weights. Similarly, GCA for tester was

significant for all traits except GI, number of roots, and SL. General combining ability was relatively more important for germination rate index, primary root length, root fresh and dry weights, as well as shoot fresh and dry weights indicating that additive gene action is in control. In contrast, SCA was relatively more important for Fe and Zn concentrations, indicating that non-additive gene action is in control. Inbreds TZEEI82 and TZEEI64 had superior GCA effects for conductivity, In terms of germination percentage, TZEEI81 and TZEEI 82 had the best GCA. For Fe concentration, varieties DTE-STRYSYNPOPC3, 2009TZEEI-OR1STR, and 2009TZEE-OR1STRQPM and inbreds TZEEI81 had superior GCA effect while inbreds TZEEI58 and TZEEI64 had outstanding GCA effects for Zn.

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Morpho-physiological and molecular Assessment for foliar disease and oleic acid content using gene based SSR markers in groundnut (*Arachis hypogea L.*)

Tiwari Sushma

Rajmata Vijayaraje Scindia Krishi Vishva Vidyalaya, India

Cultivable groundnut (*Arachis hypogea L.*), is an important oilseed crop with an allotetraploid genome (AABB, $2n=4x=40$), which is being cultivated and practiced widely. It is self-pollinated legume and excellent cash crop, cultivated in more than 100 countries for edible oil and food uses. Like other crops, several biotic and abiotic factors affect yield of groundnut including foliar fungal diseases. Rust (caused by *Puccinia arachidis*) and Late Leaf Spot (LLS) (caused by *Cerco sporidium personatum*) are two major foliar fungal diseases of groundnut and can cause yield loss upto 70%. Developing advance varieties resistant to various stresses is the best and viable option to minimize economic losses for farmer and is Eco-friendly also. Integration of molecular breeding is the best option to improved variety with trait of interest. In current study, genetic diversity was studied in Forty two germplasm lines and four cultivars of diverse groundnut set using 7 morphological traits and Simple Sequence Repeat (SSR) markers. Morphological characters were taken for yield related traits were observed i.e., Days to Maturity, Number of Pods/ Plant, 100 Pod weight (gm), Karnel Yield (gm/plant), 100 Karnel Weight (gm), Shelling percentage and Sound Mature Karmel. In this study morphological analysis has been conducted with 7 parameters and genetic distance was measured by NTSYS2.0 to show diversity. Gene based markers were used for screening of oleic acid and foliar diseases. Total 5 germplasms were identified having foliar disease resistance and 16 germplasms have been

identified having high oleic acid content using gene based markers. Molecular characterization along with morphological analysis show an authentic result and identified highly diversified lines of Groundnut along with some germplasms lines having foliar disease resistance and high oleic acid content. Molecular characterization along with morphological analysis identified several lines having resistance for late leaf spot and rust along with higher yield performance which can further be utilized in crop improvement programme.

Methodology and Theoretical Orientation: Measurement of Morphological Traits

A set of 42 germplasms and four varieties were evaluated for 7 morphological traits. Days to Maturity, Number of Pods/ Plant, 100 Pod weight (gm), Karmel Yield (gm/plant), 100 Karmel Weight (gm), Sound Mature Karmel and Shelling % were observed for five plants and there mean value was considered for further analysis. The Analysis Of Variance (ANOVA) of morphological traits for Standard Error (S.E.), Critical Difference (CD) and Coefficient of Variation (CV) was performed. The coefficient of correlation among all morphological traits at maturity was calculated using SPSS ver19.0 software. The similarity matrices were used to construct a dendrogram for all the germplasm lines and genotypes using NTSYS-pc 2.0

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Meta QTL (mQTL) Analysis Using Three Connected Mapping Populations in *Sorghum bicolor* for Drought Tolerance Related Traits

Techale Birhan

Jimma University, Ethiopia

Identifying Quantitative Trait Loci (QTL) of considerable effects that are expressed in diverse genetic backgrounds across different drought stress regions can significantly complement the conventional breeding efforts. The purpose of this study was therefore to map consistent QTL related to drought tolerance using three connected mapping populations of different genetic backgrounds.

Methodology and Theoretical Orientation: All QTL identified in the individual populations using CIM were projected on the consensus linkage maps using the chromosomal position, LOD score, confidence interval and proportion of phenotypic variance (R^2) explained by each QTL. For each chromosome, meta-QTL analysis was used to estimate the numbers and positions of the mQTL. Meta QTL was declared only when it was common to all the three populations or when one region harbored an elevated number of QTL derived from a minimum of two populations.

Findings: A total of 106 QTL were identified from the three individual population QTL analysis for all traits studied. All the 106 QTLs identified in individual populations were projected on the combined consensus map for Meta QTL analysis. The meta-analysis then reduced the total number of QTLs from 106 to 16 mQTLs. As a result, 4 mQTL for grain yield per plant, two for days to maturity, one for days to flowering, two for leaf senescence and three for plant height were detected.

Conclusion and Significance: The final consensus map developed would allow us to map a larger number of markers than possible in any individual map and to obtain a more complete coverage of the sorghum genome. Therefore, the consensus map can be used as a reference resource for genetic studies in different genetic backgrounds and the QTL identified in this study could be used for marker assisted breeding programs in sorghum.

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Heterologous expression of a barley homologue Na⁺/K⁺ transporter from *Leptochloa fusca* showed ion permeability and salt tolerance

Zaheer Ahmed

University of Agriculture, Pakistan

The aminoglycoside antibiotic hygromycin (hyg), inhibits yeast growth by hyperpolarization of cell membrane. Wild type and *trk1*, *trk2* yeast (*Saccharomyces cerevisiae*) strains growing on solid Yeast Peptone Dextrose (YPD) media showed growth sensitivity when supplemented with hyg. Growth of potassium uptake deficient yeast strain deprived of its two major K⁺ transporters; *Trk1* and *Trk2*, was used to show the K⁺ uptake activities on expression of *LfHKT2;1*. Loss of growth activity of *trk1*, *trk2* yeast was observed on expression of empty control vector in the presence of hyg while expression of *LfHKT2;1* complemented the growth

activity of *trk1*, *trk2* yeast cells. Increased concentration of Na⁺ resulted in cellular Na⁺ toxicity which elevated on supplementing hyg in the media. Hypersensitivity of *trk1*, *trk2* yeast cells to Na⁺ on expression of *LfHKT2;1*, clearly showed an additional Na⁺ uptake system operating on membrane as confirmed by transient GFP expression studies. Relative abundance of transcripts under low K⁺ concentration revealed the high affinity K⁺ uptake system on expression of *LfHKT2;1*. This study demonstrated the hyg sensitivity of yeast cells as the most powerful screen to functionally characterize membrane transporters and channels.

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Fine mapping and marker development of major quantitative trait loci that confers resistance against Hessian fly in Wheat

Nida Ghori

Kansas State University, USA

Hessian fly (HF) is a major invasive wheat pest in North Africa, southern Europe, North America, and northern Kazakhstan that cause massive economical damage and reduce the grain yield and quality every year. At least 35 different HF-R genes, from H1 to H34 and Hdic, have already been genetically identified. Most of them have been mapped within cluster of NB LLR encoding genes but no HF-R genes have yet been cloned. H34 is a Hessian fly resistance gene, confers high level of resistance against many Hessian fly biotypes. So, it is need of time to develop resistant wheat cultivars adapted to this region to minimize the losses caused by HF.

Methodology and Theoretical Orientation: Previously, it was detected on distal end of short arm of chromosome 6BS using recombinant inbred lines (RILs) from a cross between Ning7840 x Clark. After that, another RIL F5

population was developed from a cross between two of the RILs (RIL118 and RIL 115) to fine map H34. The RIL 118 carries H34 from Clark whereas RIL115 carries the susceptibility allele. Initially, two flanking SNPs were identified at the H34 region using the new RIL population and heterozygous RILs were identified to generate a new F2 population. After screening >3000 F2 plants using the flanking markers, >100 F2 recombinants were selected. Their F3 families were phenotyped to further narrowing the flanking region of H34 to the minimum.

Findings and Conclusion: This study resulted in development of diagnostic markers linked to H34 gene for marker-assisted selection that will lead to the cloning of H34.

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