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Detection of soybean major viruses by RT-LAMP

Y. Lee[1], D. Bae[2], Y. Yoon[1], H. Kim[1], S. Bae[1], I. Park[1], B. P. Mainali[1], S. Lee[2], H. Kang[1]
[1]*National Institue of Crop Science, Department of southern Area Crop Science, Miryang, Republic of Korea*
[2]*School of applied Bioscienes, Kyungpook National University, Daegu, Republic of Korea*
sky3832@korea.kr

Soybean mosaic virus (SMV) is a prevalent pathogen that causes significant yield reduction in soybean production worldwide. SMV belongs to *potyvirus* and causes typical symptoms such as mild mosaic, mosaic and lethal necrosis. SMV is seed-borne and also transmitted by aphid. Eleven SMV strains, G1 to G7, G5H, G6H, G7H, and G7A were reported in soybean varieties. Although *Soybean yellow common mosaic virus* (SYCMV) and *Soybean yellow mottle mosaic virus* (SYMMV) have been recently reported, they have occurred a lot with SMV in soybean field. SYMMV is a new member of the genus *Carmovirus* in the family *Tombusviridae*. SYMMV has a single stranded RNA genome of 4009 nucleotides with six putative open reading frames. SYCMV has a single stranded RNA genome of 4152 nucleotides with four putative open reading frames, the entire nucleotide sequence showed 31.2-71.3% nucleotide identity with the previously known eleven species of *Sobemovirus*. In this study, we designed RT-Loop mediated isothermal amplification (LAMP) primers named F3/B3/FIP/BIP from coat protein gene sequence of SMV, SYCMV, and SYMMV. After the reaction of RT-LAMP, each product was identified by electrophoresis and with the detective fluorescent dye, SYBR Green I. under daylight and UV light. Optimal reaction conditions were at 58, 63, and 58℃ for 60min and the primers of RT-LAMP showed the specificity for each SMV, SYCMV, and SYMMV tested in this study.

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Current impact and future directions of high throughput sequencing in plant virus diagnostics: the drivers of COST Action 1407

T. Wetzel[1], C. Büttner[2], S. von Bargen[2], A. Rumbou[2], A. Olmos[3], N. Boonham[4], T. Candresse[5], M. D. R. Felix[6], I. Font[7], M. Glasa[8], R. Jalkanen[9], P. Kominek[10], M. Laimer[11], T. Malinowski[12], V. Maliogka[13], A. Minafra[14], N. O. Parra[15], A. P. Poliverari[14], M. Ravnikar[16], D. S. Safarova[17], R. V. Vandervlugt[18], C. Varveri[19], J. W. Witzell[20], I. Z. Zagrai[21], S. Massart [22]
[1]*Dienstleistungszentrum Ländlicher Raum Rheinpfalz , Neustadt a. d. Weinstraße, Germany*
[2]*Humboldt University, Faculty of Life Sciences - Division Phytomedicine, Berlin, Germany*
[3]*Instituto Valenciano de Investigaciones Agrarias, Crop Protection, Virology, Moncada, Spain*
[4]*Fera Sand Hutton, York, United Kingdom*
[5]*INRA BP81, Campus INRA de la Grande Ferrade, Villenave d`Ornon cedex, France*
[6]*Universidade de Évora Laboratório de Virologia Vegetal, Departamento de Fitotecnia, Évora, Portugal*
[7]*UPV-IAM, Virology, Valencia, Spain*
[8]*Slovak Academy of Sciences, Institute of Virology, Bratislava, Germany*
[9]*Natural Resources Institute Finland , Rovaniemi Research Unit, Rovaniemi, Germany*
[10]*Crop Research Institute, Praha, Czech Republic*
[11]*University of Natural Resources and Life Sciences, Vienna, Austria*
[12]*Research Institute of Horticulture, Skierniewice, Poland*
[13]*Aristotle University of Thessaloniki, Faculty of Agriculture, Forestry and Natural Environment, School of Agriculture, Lab of Plant Pathology, Thessaloniki, Greece*
[14]*Institute for the Sustainable Plant Protection, Bari, Italy*
[15]*Scientia Terrae Research Institute, St.-Katelijne-Waver, Belgium*
[16]*National Institute of Biology, Ljubljana, Slovenia*
[17]*Palacky University, Olomouc, Czech Republic*
[18]*Plant Research International, Wageningen, Netherlands*
[19]*Benaki Phytopathological Institute, Athens, Greece*
[20]*SLU Southern Swedish Forest Research Centre, Alnarp, Sweden*
[21]*Statiunea de Cercetare Dezvoltare pentru Pomicultura Bistrita, Bistrita, Romania*
[22]*Université de Liège, Gembloux, Belgium*
thierry.wetzel@dlr.rlp.de; carmen.buettner@agrar.hu-berlin.de

The ability to provide a fast, inexpensive and reliable diagnostic for any given viral infection is a key parameter in efforts to fight and control these ubiquitous pathogens. The recent developments of high-throughput sequencing (also called Next Generation Sequencing - NGS) technologies and bioinformatics have drastically changed the research on viral pathogens. It is now raising a growing interest for virus diagnostics. This review provides a snapshot vision on the current use and impact of high throughput sequencing approaches in plant virus characterization. More specifically, this presentation highlights the potential of these new technologies and their interplay with current protocols in the future of molecular diagnostic of plant viruses. The current limitations that will need to be addressed for a wider adoption of high-throughput sequencing in plant virus diagnostics are

thoroughly discussed. This paradigm change gave rise to the COST Action 1407 which is currently launched. This Action, its objectives and expected impacts will be presented.

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Anti-quorum sensing activity of some medicinal plants in Iran

A. Mohammadrezaei[1,2], S. Ketabchi[2]
[1]*Young Researchers and Elite Club, Isfahan, Islamic Republic of Iran*
[2]*Shiraz Branch Islamic Azad University, Plant Pathology, Shiraz, Islamic Republic of Iran*
a.mohammadrezaei@gmail.com

In recent years, application of antibiotics against microbial pathogens has resulted both in microbial resistance against antibiotics and environmental pollution. Consequently, new therapeutic modalities and agents have received increased attentions. Bacteria often use small diffusible molecules called autoinducers to communicate between each other, also known as quorum is sensing (QS) that regulate the target gene expression and results in bacterial pathogenesis activity. In this work, 30 medicinal plants from Iran were screened for anti-QS activity using *Chromobacterium violaceum* CV026 as a biomonitor strain. Three of these plants showed QS inhibition including *Cuminum cyminum* L. (Apiaceae) zire sabz*, Thymus vulgaris* L. (Lamiaceae) avishan and *Rhus coriaria* L. (Anacardiaceae) somagh. These findings introduces a new mode of action and possible validation for traditional plant use, and also a potentially new therapeutic direction for the treatment of bacterial infections.

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Evaluation of mating disruption for controlling the grapevine moth, Lobesia botrana (Denis & Schiffermüller) (Lep.: Tortricidae)in Qazvin vinyardes

R. Shahsavari[1], A. Avane Faghih[2], S. Imani[2,1]
[1]*Science and Research Branch, Islamic Azad University, Tehran, Enthomology, Tehran, Islamic Republic of Iran*
[2]*Agricultural Entomology Research Department Iranian Research Institute of Plant Protection ., Agricultural Entomology, Tehran, Islamic Republic of Iran*
reza_shahsavari53@yahoo.com

Grapevine moth, Lobesia botrana, is a primary insect pest of vineyards. Hazards of insecticide application against this pest have encouraged the development of alternative control methods specially mating disruption by sex pheromone in the recent years. The efficiency of mating disruption with two kind of dispensers:Isonet-L dispensers, Shin-Etsu Co., Japan and dispensers of Russell, U.K., was compared with insecticide treatment (control). The capture rate of monitoring traps and the number of infested bunches were monitored in all treatments. The percentages of infestations were statistically compared. The monitoring-trap capture rate in mating disruption by both pheromone dispensers was 97% less than that in control. The number of infested bunches in mating disruption by Isonet-L and Russell dispensers were respectively 100% and 32% less than that in control throughout the experiment. The percentage of infested bunches in the mating-disruption by Isonet-L (0%) was significantly less than those in the mating disruption by Russell dispensers (2.72%) and control (4%).
Analysis of variance showed that the rates of damages were statistically different ($P \leq 0.01$) between central and marginal places of Russell treatment and control. The percents of infested bunches in three locations:southern margin, center and north in Russell-treated blocks were 4.5, 2.17 and 1.5respectively. More likely the movement of adult moths from adjacent grape gardens toward our experimental plots resulted in difference of infestation.The results showed that the mating disruption by Isonet-L was more efficient for reducing the damage of the pest in vineyards, when pest population level is low.

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Re-purposing bridging flocculation for on-site, rapid, qualitative DNA detection in resource-poor settings

H. Y. Lau[1], E. Wee[2], M. Trau[2], J. R. Botella[1]
[1]*The University of Queensland, School of Agriculture and Food Science, St. Lucia, QLD, Australia*
[2]*The University of Queensland, Australian Institute for Bioengineering and Nanotechnology, St. Lucia, QLD, Australia*
hanyih.lau@uqconnect.edu.au

Introduction: On-site, quick and cheap pathogen detection is the holy grail of disease diagnostics. Here we describe Single-Drop Genomics (SDG), a novel method to cheaply visualize amplified disease-specific DNA/RNA with minimal equipment via bridging flocculation. A key characteristic of flocculation is the abrupt transition from solution phase to flocculate which makes this phenomena ideal for binary yes/no applications. To the best of our knowledge, the detection of DNA/RNA has not yet been demonstrated via a DNA-mediated bridging flocculation mechanism which can be readily observed by the naked eye (Fig 1).