



Kaiserslautern,
7-9 September 2022



Symposium Molecular Biology of Fungi 2022

7th - 9th September, TU Kaiserslautern

14th Symposium of the VAAM Special Group 'Biology and Biotechnology of Fungi'
2nd joint meeting with the GeneAG 'Fungal Genetics' of the German Society of Genetics

Program and Abstracts

Wednesday, Sept. 7th 2022

14:00 Registration
16:00 Welcome address

16:10 - 18:10 Session 1: Plant Pathology

16:10 - 16:50 Keynote lecture: **Sylvain Raffaele**, Toulouse, FR: Evolutionary genomics of generalist parasitism in Ascomycetes

16:50 - 18:30 (15 min talks)

Arne Weiberg (LMU München): Small RNA communication in fungal-plant interaction

Weiliang Zuo (Univ. Köln): Sts2, a transcriptional activator-like effector secreted from *Ustilago maydis* regulates tumor formation on maize leaves

David Scheuring (TU Kaiserslautern): The *Botrytis* hypersensitive response inducing protein 1 triggers non-canonical PTI to induce plant cell death

Slavica Janevska (Univ. Amsterdam): The influence of epigenetic modifications on pathogenicity and chromosome transfer in tomato-infecting *Fusarium oxysporum*

Vera Göhre (Univ. Düsseldorf): Nuclear-localized effectors of the Brassicaceae smut fungus *Thecaphora thlaspeos*

Daniela Nordzieke (Univ. Göttingen): Spore types-specific infection of different maize tissues by *Colletotrichum graminicola*

Lukas Dorian Dittiger (Univ. Jena): Characterizing effector proteins of *S. reilianum* specifically targeting the phytoalexin response of *Sorghum bicolor*

18:30 - Get together with finger foods and drinks
Poster Session 1

Development of a Loop-Mediated Isothermal Amplification assay for rapid and specific identification of *Botrytis fragariae* on strawberry. (Poster PLANTPATH)

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Keywords: *Botrytis fragariae*, gray mold, strawberries, Loop-Mediated Isothermal Amplification, fungal identification.

Gray mold of strawberry is caused by multiple species of *Botrytis*, including *Botrytis cinerea*, *B. pseudocinerea*, *B. fragariae*, and *B. mali*. The species *B. cinerea* and *B. fragariae* are widespread in production regions of the eastern 30 United States and Germany and their distinction is important for disease management strategies. Currently, the only way to differentiate these species 32 field samples is by Polymerase Chain Reaction (PCR), which is time-, labour-, and cost-consuming. In this study, a Loop-Mediated Isothermal Amplification (LAMP) technique was developed based on species-specific NEP2 gene nucleotide sequences. The designed primer set specifically amplified *B. fragariae* DNA in less than 10 minutes excluding other *Botrytis* species (*B. cinerea*, *B. mali* and *B. pseudocinerea*) or plant pathogens. The LAMP assay was able to amplify fragments from an amount of 0.21 ng/μL DNA extracted from infected fruit using a rapid DNA extraction protocol, confirming its ability to detect a low amounts of *B. fragariae* DNA from field infected fruit. In addition, a blind test was performed to identify *B. fragariae* in 51 samples collected from strawberry fields in the eastern United States using the LAMP technique. The *B. fragariae* samples were identified with a reliability of 93.5%, not amplifying any of the *B. cinerea*, *B. pseudocinerea* or *B. mali* samples included in the test. Our results show that the LAMP technique is a specific and reliable method for the detection of *B. fragariae* from infected fruit tissue helping in the control of this important disease in the field.