COST Action CA16107
EuroXanth: integrating science on *Xanthomonadaceae* for integrated plant disease management in Europe

Minutes of the WG1 Meeting

Zagreb, Croatia, 11-12 September 2018

Minutes of the WG1 Meeting written by J. Costa, N. Skandalis, E. Dermic, V. Catara and R. Koebnik, and reviewed by all participants

Attending: Miroslav BARANEK (CZ), Claude BRAGARD (BE, EFSA representant), Daiva BUROKIENE (LT), Vittoria CATARA (IT, Action Vice Chair), Joana COSTA (PT, WG1 Leader), Jaime CUBERO DABRIO (ES), Edyta DERMIC (HR), Sara GODENA (HR), Marie-Agnès JACQUES (FR), Ralf KOEBNIK (FR, Action Chair), Aleksa OBRADOVIC (RS), Françoise PETTER (FR, EPPO representant), Joël F. POTHIER (CH, WG2 Leader), Maria SAPONARI (IT), Nicholas SKANDALIS (GR, WG1 Vice Leader), Fernando TAVARES (PT), and Joana VICENTE (UK)

On 11 September at 8:30 am in Zagreb (Croatia), a special task force two-day meeting between participants of WG1 "Diagnostics & Diversity – Population Structure" of the COST Action CA16107 EuroXanth was organised. The meeting was divided into four sessions (two sessions per day) and each participant was assigned a theme presented in a talk of 15-20 minutes. Each session ended with a discussion period and wrap-up by the session chair. Additional presentations were given by representants of EPPO and EFSA. A total of 17 scientists (53% female and 41% ITC members) working in the field of *Xanthomonadaceae* took part in this two-day meeting. The goals of this special task force meeting were to organize COST activities for the upcoming grant period and to launch preparatory work for tangible deliverables of WG1. These latter correspond to:

- Deliverable 5: Protocols for detection of *Xanthomonadaceae* listed as quarantine organisms in Europe (EPPO A1 and A2 lists of pests recommended for regulation as quarantine pests) due at month 24
- Deliverable 6: List of molecular markers useful to study the genetic diversity and population structure of plant-associated *Xanthomonadaceae*, due at month 24
- Deliverable 7: Curated, internet-accessible database for molecular typing of plant-associated *Xanthomonadaceae* essentially for epidemiological purposes, due at month 24
- Deliverable 8: Personnel from ITC (Inclusiveness Target Countries) and non-ITC trained in the use of software, databases and websites relevant for detection, molecular typing and epidemiology of bacterial pathogens, due at month 30.

Thanks to the initiative of C. Bragard and R. Koebnik, several of the attendees had already met on the evening before the kick off of the meeting during dinner. Aside from being a very good icebreaker opportunity this allowed to prepare the meeting and also discuss different aspects of the Action.

Funded by the Horizon 2020 Framework Programme of the European Union

At the first day of the meeting, after a welcoming and quick opening by the Chair of Local Organizing Committee, E. Dermic, the Action Chair, R. Koebnik presented a slideshow with COST rules and Action goals. This introduction was more relevant for non-MC Members and participants that are not familiar with COST Action functioning. Afterwards all attendees were asked to introduce themselves briefly.

V. Catara chaired the first session "*Xanthomonas* detection methods" that included three presentations. J. Cubero gave the first presentation on "PCR-based methods", emphasizing the problems related with the viability state of the detected cells by these methods and its impact on seed trading. Another raised point focused the inability of commonly used PCR-based methods to discriminate between pathogenic and non-pathogenic bacteria. The second presentation on "LAMP" methodology was given by J. Pothier with a brief introduction about the molecular basis of the technique and associated bias followed by a follow up on its practical/field application. J. Pothier proposed to confirm the specificity of the existing LAMP primers for *Xanthomonas* detection, a key issue confirmed by all the participants. This research will be an output for WG1. F. Tavares gave the third talk describing the hybridising-based methods using his research work has an example of the applications, bias and scope. F. Tavares raised important questions related with constructions of epidemiological studies and their importance.

The second session - "*Xylella* detection methods" - was chaired by WG1 Leaders, J. Costa and N. Skandalis. M. Baranek presented the theme "PCR-based methods" with a detailed timeline-based description for *Xylella* sp. detection and identification. M. Saponari gave an overview on the constrains that we currently have regarding *Xylella fastidiosa* detection. Then she made a critical overview of the methods currently used, namely isolation, serologic-based methods, molecular based-methods, LAMP, remote-sensing and subspecies specific methods.

In order to determine how could EuroXanth contribute to European duties and policies, two representants from European agencies were invited, namely Francoise Petter (Invited member) from EPPO and Claude Bragard (WG1 member) from EFSA. During the afternoon session, C. Bragard presented a slideshow with EFSA organization, challenges, goals and work flow system. Participants were challenged with a questionnaire raising key questions and fostering a brainstorm discussion period. In F. Petter's presentation, the EPPO story, organization and goals were described along with several databases. F. Petter identified ways in which EuroXanth members can contribute with their expertises. The issue of isolation of a pathogen being a prerequisite for its detection was particularly discussed. The participants wrapped up the day meeting by summarizing the outcome of the different topics that had been discussed.

The day ended with a guided city tour followed by a dinner in a nice atmosphere where future opportunities were evaluated. R. Koebnik, M. Baranek, A. Obradovic and J. Costa discussed several aspects related with the organization of the next two EuroXanth Annual Conferences in the Czech Republic and in the Republic of Serbia.

On the second day, R. Koebnik chaired the third session on "*Xanthomonas* diversity" that included three presentations. J. Vicente gave the first presentation on "MLSA/MLST" with a timeline-based description of these methodologies. J. Vicente raised concerns related to the absence of curated databases and the lack of overlapping between the existing methods that prevents exchanging information between studies and labs. A scheme was proposed and discussed for the initial identification of *Xanthomas* based on the partial sequence of two genes, *rpoD* and *gyrB*. R. Koebnik gave the second presentation on "VTNR/MLVA", starting with describing the methodologies followed by a detailed analysis of their application in the *Xanthomas* field. D. Burokiene presented papers found on PubMed related with "other methods" for studies of *Xanthomonas* diversity.

Funded by the Horizon 2020 Framework Programme of the European Union

The fourth session on "*Xylella* diversity" was chaired by M. Saponari. In this session M. A. Jacques gave an introduction into *Xylella* taxonomy and host range, followed by a critical overview on the currently used methods to study *Xylella* diversity, focusing on the MLSA/MLT scheme and associated databases. Afterwards, M. Saponari presented several other used methods, always referring in which context they should be applied, and their advantages and drawbacks. She also presented recent work from the "PonTE" project on the pangenome of this genus.

The participants discussed about the different tools available for collaborative work and for sharing information in order to realize and valorise efficiently the WG1 deliverables. These included the completion of the form (in Excel format) in which all the relevant literature for the deliverables has been collected and shared online. Possible peer-reviewed publications were also discussed. Additionally, the scientific opinion of the participants towards several points raised by the EPPO and EFSA representants will be collected, compiled and made available to them in order to be used in their duties. Finally, the attendees discussed possible activities for the upcoming grant periods, including the proposition of a training school on software, databases and websites relevant for detection, molecular typing and epidemiology of bacterial pathogens (WG1).

The two-day meeting was characterized by lively discussions and a strong cohesive effect among the 17 WG1 participants could be clearly perceived. This result can certainly be attributed to several previous encounters fostered by COST CA16107, which contributed highly to the "small family/network feeling" and can thus be considered as a very positive and valuable output of this COST CA16107 special task force meeting.

Special task force in front of the Agriculture Faculty, Zagreb. From left to right, first row: F. Tavares, J. Cubero, V. Catara, F. Petter, D. Burokiene, E. Dermic, J. Costa, M. A. Jacques, J. Vicente, S. Godena. From left to right, second row: J. F. Pothier, C. Bragard, M. Baranek, M. Saponari, R. Koebnik, N. Skandalis, D. Dermic and A. Obradovic.

Funded by the Horizon 2020 Framework Programme of the European Union