

Instructions for Abstracts

Deadline for abstract submission: April 18, 2025

Select Session

Please choose the session in which you wish to present:

- **Session 1:** Exploiting Plant-Microbiome molecular crosstalks: diversity, distribution and evolutionary perspectives
- **Session 2:** Crop-Microbiome assembly dynamics under specific environments
- **Session 3:** Crop microbiomes and plant diseases: from dysbiosis to increased defenses
- **Session 4:** From current microbial inoculants to synthetic communities
- **Session 5:** Communication and engagement with the society

Oral Presentation or Poster

When you submit your abstract, please indicate if you wish to present an oral presentation or a poster.

Submission Format (sample abstract below)

1. **450 words maximum** (ca 3000 characters, including spaces)
2. **Title in bold font**
3. For each author of the abstract provide: **first name, surname and affiliation (as short as possible, i.e., name of the institute, town, country)**
4. The **presenting author** should be the first or the last author with his/her name underlined.
5. The authors' affiliations should be indicated with numbers as superscripts, e.g.:
Ralf Koebnik^{1*}, Claude Bragard²
and identified as follows, including the e-mail address of the corresponding author:
¹ Plant Health Institute of Montpellier (PHIM), Univ Montpellier, Cirad, INRAe, Institut Agro, IRD, Montpellier, France (ralf.koebnik@ird.fr)
² Earth & Life Institute, UCLouvain, Louvain-la-Neuve, Belgium
* Ralf Koebnik@ird.fr
6. Authors may add up to five **keywords** before the abstract
7. Optional: **References** (max. three) may be included in the abstract and bibliography must be formatted as indicated on the template (authors, year, paper title, journal, volume, pages)
8. Optional: **Funding** can be added at the end of the abstract.
9. **Format:** Abstracts must be Word documents (DOC or DOCX formatted, **not** ODT format) on A4 (21 cm x 29.7 cm), with all margins (Top, Bottom, Left, Right) set to 2.5 cm.
PDF files won't be accepted.
10. **Font:** Calibri, 11 points, single space.
11. **Name your file** as follows: Session-Number_O/P_SURNAME of corresponding author (O for *Oral presentation*, P for *Poster*), e.g., 2_O_KOEBNIK.docx

It is the authors' responsibility to proofread submitted abstract. Abstracts will be published as submitted.

SAMPLE ABSTRACT

Please use the format of this example

First description of the genetic determinants for a lateral flagellin and biosynthesis of coronatine-like molecules in *Xanthomonas*

Chloé Peduzzi¹, Angeliki Sagia^{1,2}, Daiva Burokienė³, Ildikó K. Nagy⁴, Marion Fischer-Le Saux⁵, Perrine Portier⁵, Veronica Roman-Reyna^{6,7}, Jonathan M. Jacobs^{6,7}, Claude Bragard¹ and Ralf Koebnik^{2*}

¹ Earth & Life Institute, UCLouvain, Louvain-la-Neuve, Belgium

² Plant Health Institute of Montpellier, Univ Montpellier, Cirad, INRAE, Institut Agro, IRD, Montpellier, France

³ Nature Research Centre, Institute of Botany, Laboratory of Plant Pathology, Vilnius, Lithuania

⁴ Enviroinvest Corp., Pécs, Hungary

⁵ Univ Angers, Institut Agro, INRAE, IRHS, SFR QUASAV, CIRM-CFBP, Angers, France

⁶ Department of Plant Pathology, The Ohio State University, Columbus, OH, U.S.A.

⁷ Infectious Diseases Institute, The Ohio State University, Columbus, OH, U.S.A.

*Ralf Koebnik@ird.fr

Keywords: Comparative genomics; Flagella; Hormone; Protein secretion; *Xanthomonas*

Evolutionarily early-branching xanthomonads, also referred to as clade-1 xanthomonads, include major plant pathogens, most of which colonize monocotyledonous plants (1). Seven species have been validly described, among them the two sugarcane pathogens *Xanthomonas albilineans* and *Xanthomonas sacchari*, as well as *Xanthomonas translucens*, which infects small grain cereals, diverse grasses, but also asparagus and pistachio trees. In an effort to systematically sequence understudied non-model xanthomonads, we used long-read sequencing technology to obtain complete, circular chromosomal sequences for representative strains of three novel species, all belonging to clade 1: (i) strain CFBP 8444, the causal agent of bacterial streak on New Zealand flax, (ii) strain CFBP 8443, isolated from common bean, and (iii) strain CFBP 8445, originating from a banana plant. Genome mining revealed novel genetic traits, hitherto undescribed in the *Xanthomonas* genus. In strain CFBP 8444, we identified genes related to the synthesis of coronatine-like compounds, a phytotoxin produced by several pseudomonads, but also in some plant-pathogenic enterobacteria and streptomycetes. In addition, strain CFBP 8444 was found to encode a second, atypical flagellar gene cluster in addition to the canonical flagellar gene cluster, including a homolog of lateral flagellins. Overall, this research represents an important step towards better understanding the evolutionary history and biology of early-branching xanthomonads.

References

1. Parkinson N, Aritua V, Heeney J, Cowie C, Bew J, Stead D (2007). Phylogenetic analysis of *Xanthomonas* species by comparison of partial gyrase B gene sequences. *Int. J. Syst. Evol. Microbiol.* 57: 2881-2887.

Funding: Support was provided by the Fonds pour la Formation à la Recherche dans l'Industrie et l'Agriculture (FRIA grantee 1st grant 40009043) and the European Commission and the Athens University of Economics and Business for providing an Erasmus+ higher education study and training grant (grant number 7009/2019). This presentation is based upon work from COST Action CA16107 EuroXanth, supported by COST (European Cooperation in Science and Technology).