

# Instructions for Abstracts

**Deadline for abstract submission: April 12, 2026**

## Select Session

Please choose the session in which you wish to present:

- **Session 1:** Exploiting Plant-Microbiome molecular crosstalks: diversity, distribution and eco-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<sup>1\*</sup>, Claude Bragard<sup>2</sup>  
and identified as follows, including the e-mail address of the corresponding author:  
<sup>1</sup> Plant Health Institute of Montpellier (PHIM), Univ Montpellier, Cirad, INRAe, Institut Agro, IRD, Montpellier, France (ralf.koebnik@ird.fr)  
<sup>2</sup> 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.**
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It is the authors' responsibility to proofread submitted abstract. Abstracts will be published as submitted.

## SAMPLE ABSTRACT

Please use the format of this example

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

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**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.

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