# How do climate warming affect Sphagnum secondary metabolites?

Guillaume Foursov*[1], Coralie Bertheau-Rossel[1], Philippe Binet[1], Soraya Rouifed[2], Guillaume Meiffren[3], Clément Bardon[3], Gille Comte[3], Steven Criquet[4], Pierrick Priault[5], and Geneviève Chiapusio[6,1]

[1]Chrono-Environnement, Université de Franche-Comté UMR UFC/CNRS 6249, Montbéliard – Université de Bourgogne-Franche-Comté – France

[2]UMR 5023 LEHNA, CNRS, Université Claude Bernard Lyon 1 69622 Villeurbanne Cedex, France – Université Claude Bernard - Lyon I – France

[3]UMR 5557 CNRS-Université Claude Bernard Lyon 1, Ecologie Microbienne, USC INRA 1193-VetAgroSup, 69622 Villeurbanne Cedex, France – Université Claude Bernard - Lyon I – France

[4]IMBE, Aix-Marseille Université, UMR CNRS/IRD 7263/237, Marseille, France – Aix Marseille Univ, Univ Avignon, CNRS, IRD, IMBE, Marseille, France – France

[5]Université de Lorraine, AgroParisTech, INRA, UMR SILVA, FR-54000 Nancy, France – Université de Lorraine, INRA, AgroParisTech : UMRSILVA – France

[6]CARRTEL UMR INRA 042 Université de Savoie Mont-Blanc Domaine Universitaire FR- 73376 Le Bourget du lac – Université de Savoie – France

**Abstract**

*Sphagnum* genus have a key role in peatland functioning by creating the conditions for the accumulation of one third of the world's soil carbon. However, *Sphagnum* secondary metabolites are poorly quantified compared with vascular plants. Recent works has shown that total phenolic compounds produced by living *Sphagnum* influence microbial communities, fungal enzymatic activities and vascular plant mycorrhizae. They also vary according to the season and are reduced by global warming. It is then timely to better understand how *Sphagnum* secondary metabolism responds to global change.

We investigated how climate warming affect Sphagnum specific phenolics (Sphagnum acids) using a metabolic profiling approach. Two *sphagnum* species (*S. magellanicum* and *S. fallax*) were collected along an experimental site in a peatland of Jura (Frasne, 25) within two microhabitats (wet lawn versus dry hummock) submitted to an increase of +1∘C thanks to the installation of Open top chamber since 2008. *Sphagnum* acids of ethanolic extracts (v/v20/80%) were evaluated by UHPLC MS-Qtof.

Our results identified four sphagnum acid forms (i.e. a simple sphagnum acid, a glycosylated form, a conjugated form with uronic acids and an ethylester form). Their production was majoritary in the capitulum and varied between months and species. Global warming had little effect on the production of sphagnum acids for both species. Interestingly, the microhabitat influenced only the production of glycosylated and conjugated with uronic acids forms in *S. fallax*. For this species, the sphagnum acids production was positively correlated to the air temperature and mire water pH. For *S. magellanicum*, they were negatively correlated to

*Speaker

air temperature and water level but positively to the *Sphagnum* pH. These results underline the importance to study the production and regulation of sphagnum acids among *Sphagnum* species. Allelopathic roles of these metabolites between *Sphagnum* species, vascular plants and microbial communities offer interesting perspectives.