

Assessment of the combined effect of temperature and relative humidity on fungal growth

L. De Ligne^{1,2}, G. Vidal Diez de Ulzurrun¹, J.M. Baetens¹, J. Van den Bulcke², J. Van Acker², and B. De Baets¹

¹ KERMIT, Department of Mathematical Modelling, Statistics and Bioinformatics, Ghent University, Belgium

² Laboratory of Wood Technology, Department of Forest and Water Management, Ghent University, Belgium

Biological background and motivation

Fungi are resilient organisms that are able to grow in almost any environment. They generally form a **mycelium** (Fig. 1 a-b), a wide-spread network of narrow, thread-like structures called **hyphae** (Fig. 1 c). Growth occurs at the hyphal tips, known as **apices**. New biomass is generated either by the extension of existing hyphae or by the creation of new apices, a process called **branching** (Schmidt, 2006).

Fungal growth is determined by the **environmental conditions** when nutrients are not limiting. Each fungal species grows under a certain range of environmental conditions and most species achieve their maximum growth rate under very specific circumstances only, referred to as the **optimal growth conditions**. Of those environmental conditions, **temperature** and **relative humidity** are the most influential (Vereecken & Roels, 2012).

Defining the optimal growth conditions has been frequently done, since they allow to optimize **industrial processes** and provide information about fungal species that cause **damage to crops** (e.g. *Rhizoctonia solani*) and in **construction** (e.g. *Coniophora puteana*) (Fig. 1 d-e).

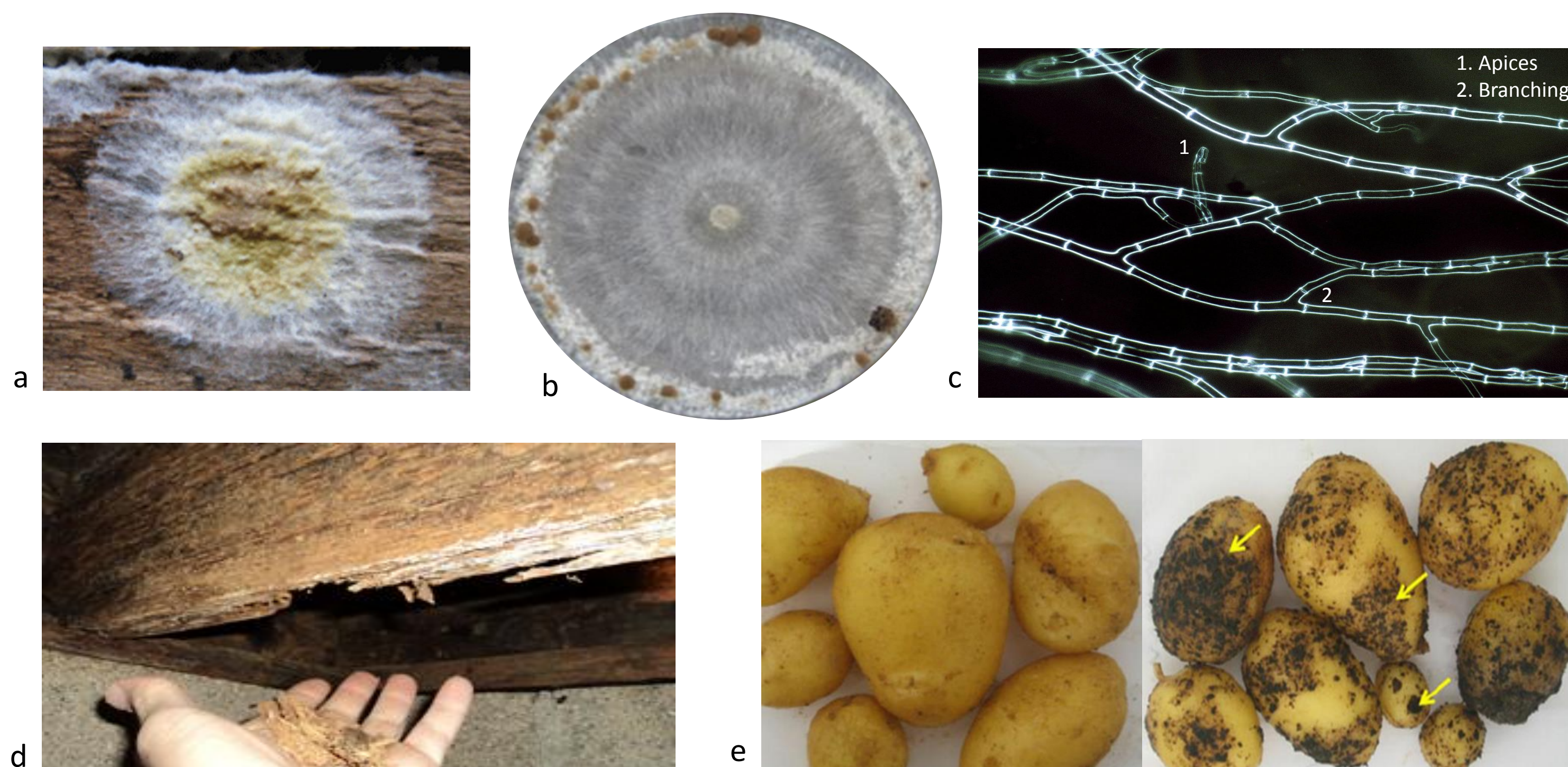


Fig. 1 *Coniophora puteana* mycelium (a) and wood damage (d); *Rhizoctonia solani* mycelium (b) and potato crop damage (e); Fungal hyphae (c)
Sources: (a) and (b) Sachverständigenbüro für Holzschutz, 2016; (d) Lu et al., 2016; (e) Bernon, 2013; (c) Djebali et al., 2014

Material and methods

The optimal growth conditions of two frequently studied fungal species are examined, the brown rot fungus *Coniophora puteana* and the plant pathogen *Rhizoctonia solani*.

Mother cultures of these fungi were used to extract a **disk-shaped inoculum** of about 1 cm diameter. Then, the inoculum was placed at the centre of the bottom lid of a Petri dish, surrounded by 12 small substrate disks (Fig. 2). The top lid of the Petri dish was placed on top of the bottom lid, as such **restricting the height** between the lids to 0.6 mm and enforcing **growth in two dimensions** only.

Images of the growing fungi were captured using a **flatbed scanner** on top of which the Petri dishes were mounted. **Growth was tracked for 72 hours**. In order to assess the effects of the environmental conditions on fungal growth, we placed the flatbed scanner in a **climate chamber** where temperature and relative humidity could be adjusted. **Temperature** was varied from **15 to 30 °C** in steps of 5 °C, while **relative humidity** was varied from **65% to 80%**, in steps of 5%.

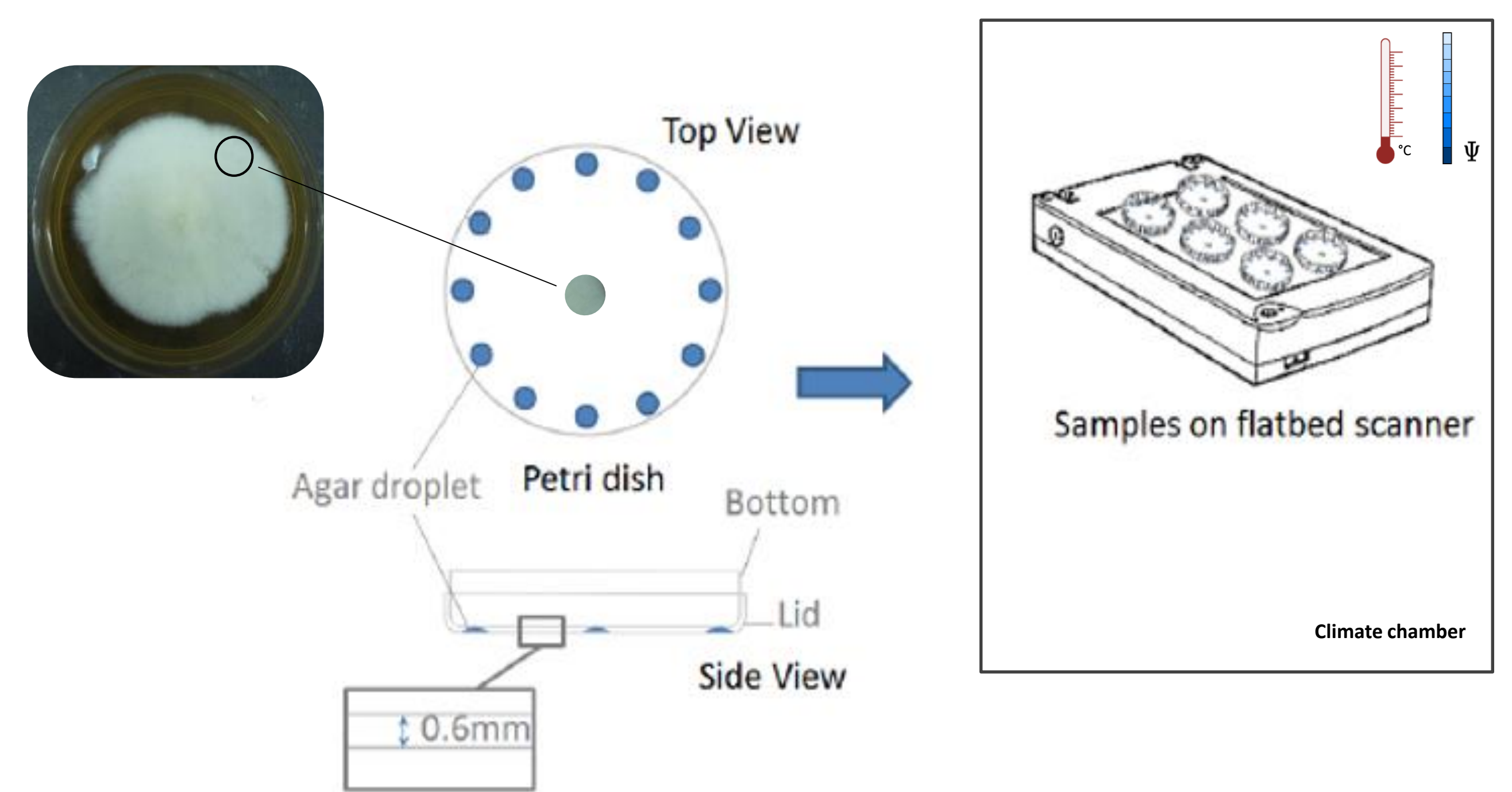


Fig. 2 Scheme of the experimental set-up.

Image Analysis

In order to extract fungal growth features from the initial image (Fig. 3 a), four steps need to be taken.

Step 1: Removing noise in the images, such as droplets of agar and the initial inoculum (Fig. 3 b)

Step 2: Extracting the fungal network. A **line detection algorithm** (Lopez-Molina et al., 2015) is used to extract a thin **binary ridge map** from each image, which represents the fungal network (Fig. 3 c). Binary ridge maps for *Rhizoctonia solani* growing in vitro are represented in Fig. 4.

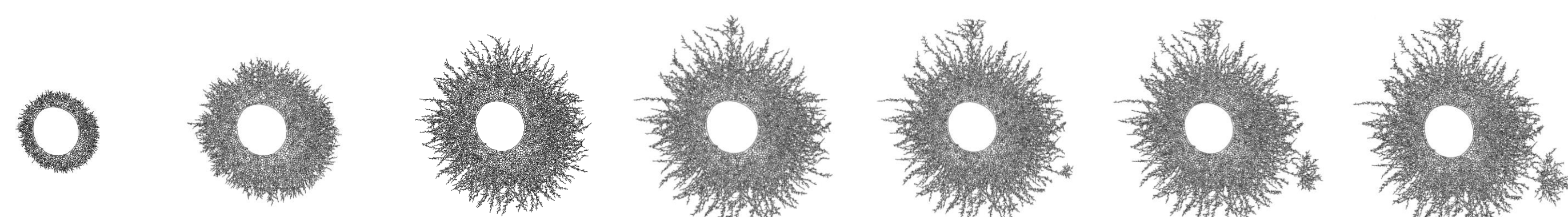


Fig. 4 Evolution of the fungal network of *Rhizoctonia solani*, extracted using a line detection algorithm (Lopez-Molina et al., 2015). The pictures represent the growth from 10 to 72 hours at intervals of 10 hours.

Step 3: Converting the ridge map into a mathematical graph. The MorphologicalGraph function of Mathematica converts images into **mathematical graphs** (Fig. 3.d), where the intersections represent junctions of hyphae and apices of the mycelium and the line segments represent the hyphal segments connecting them.

Step 4: Extracting fungal features. Using the information contained in the graphs we can compute some of the most important fungal kinetic parameters: **total length of the mycelium**, **total number of tips**, **area of the mycelium**, etc.

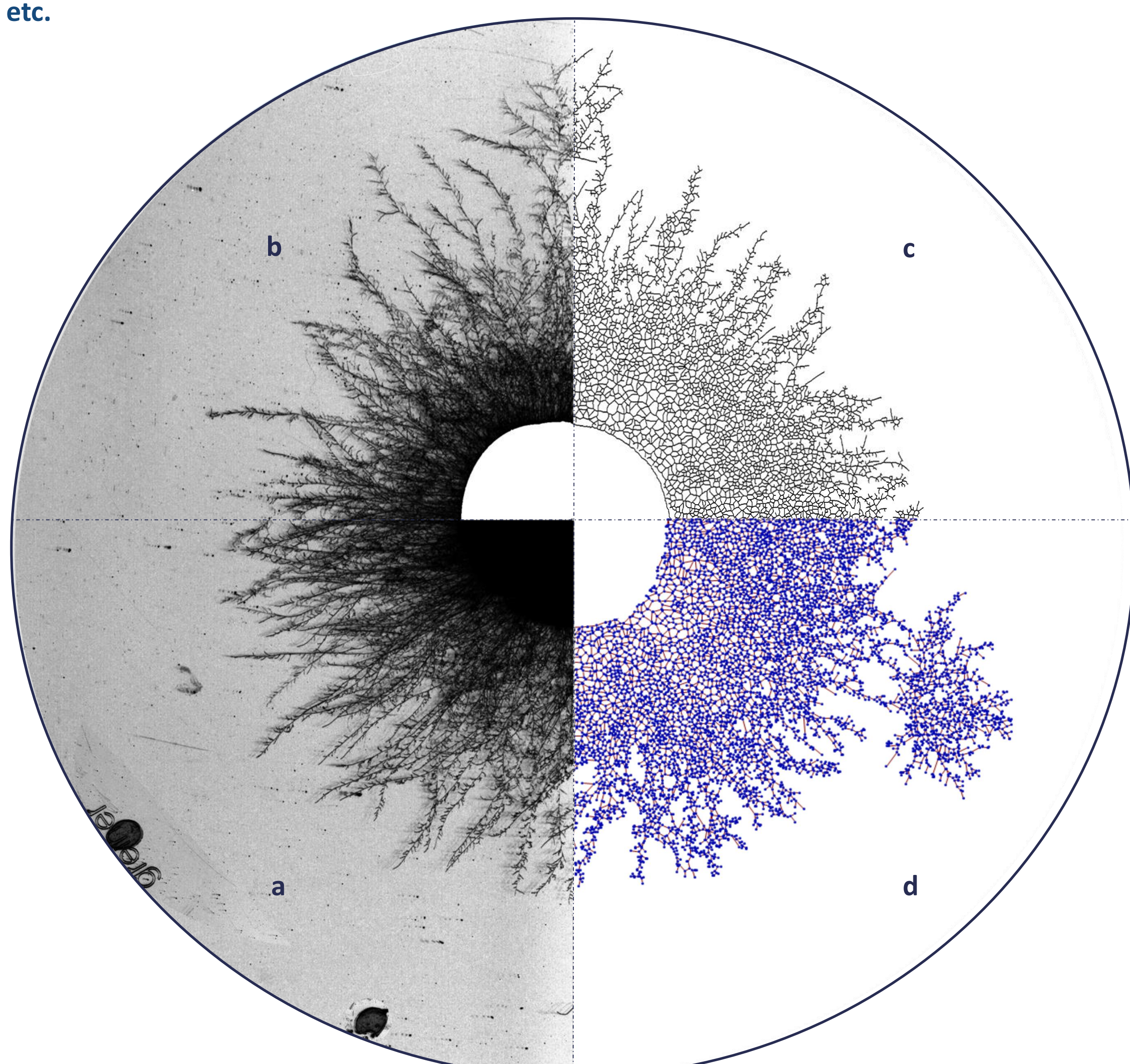


Fig. 3 Summary of the complete process of fungal growth feature extraction from an image of *Rhizoctonia solani*.
a) Initial image; b) Cleaned image; c) Binary ridge map; d) Mathematical graph.

Results

The evolution of the total length of the mycelium and the number of tips, as a function of temperature and relative humidity, can be found in Fig. 5 for *Rhizoctonia solani*.

Some of the main findings:

- Maximal mycelial length and number of tips at 20°C and 65% relative humidity
- At the highest temperature (30°C) there is rapid growth only at the beginning, after which a plateau is reached and growth stabilizes

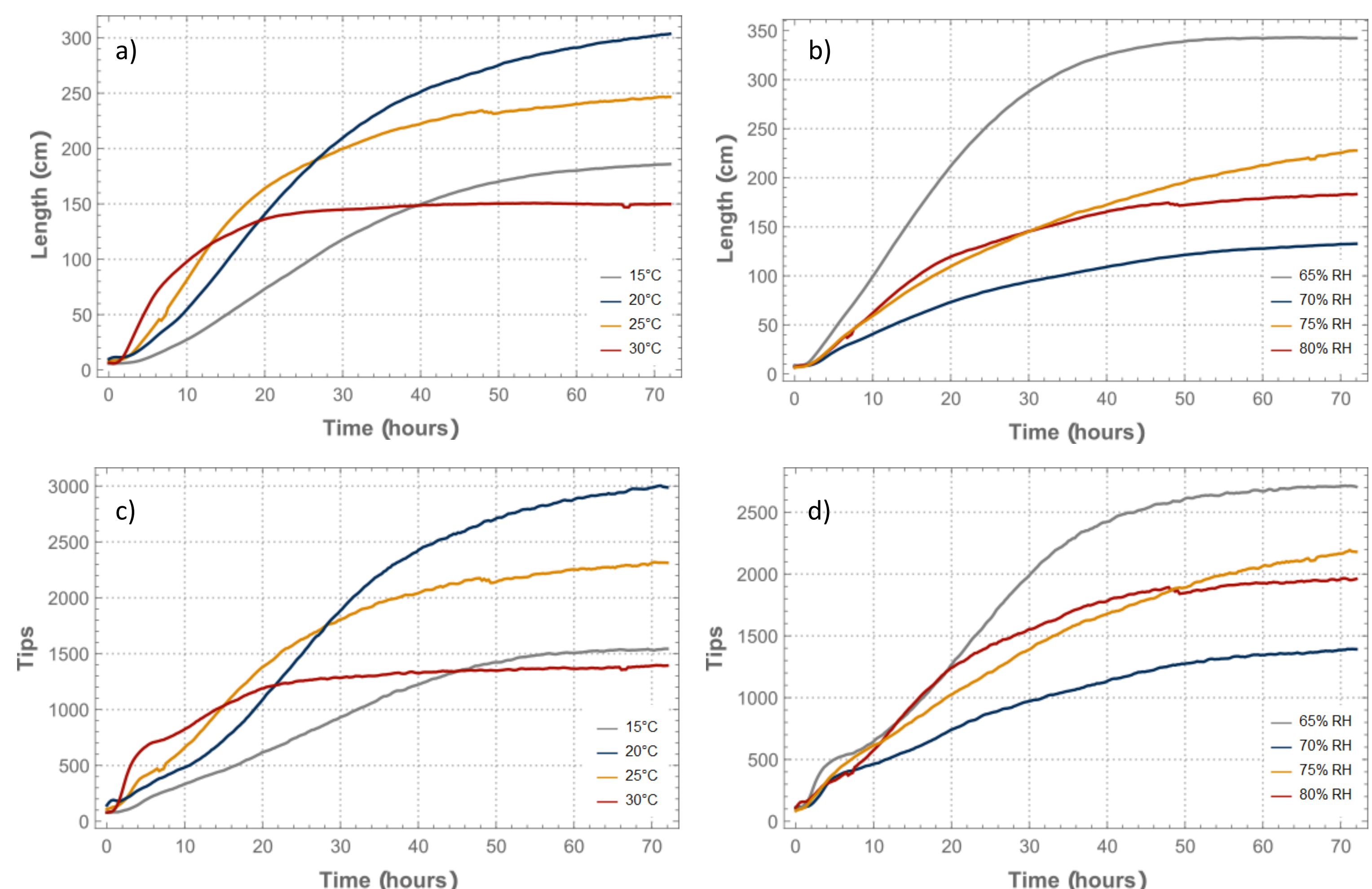


Fig. 5 Topological measures for *Rhizoctonia solani* averaged over temperature (°C) or relative humidity (%RH). The graphs show the evolution over time of the total length of the mycelium (a-b) and the number of tips (c-d) grouped by temperature and relative humidity, respectively.

References

- Lopez-Molina, C., Vidal-Diez de Ulzurrun, G., Baetens, J., Van den Bulcke, J., De Baets, B., 2015. Unsupervised ridge detection using second order anisotropic Gaussian kernels. *Signal Process.* 116 (0), 55–67.
- Schmidt, O., 2006. *Wood and Tree Fungi: Biology, Damage, Protection, and Use.* Springer-Verlag Berlin Heidelberg.
- Vereecken, E., Roels, S., 2011. Review of mould prediction models and their influence on mould risk evaluation. *Building and Environment* 51, 296-310.
- Vidal-Diez de Ulzurrun, G., Baetens, J. M., Van den Bulcke, J., Lopez-Molina, C., De Windt, I., De Baets, B., 2015. Automated image-based analysis of spatiotemporal fungal dynamics. *Fungal Genetics and Biology* 84 (2), 12–25.
- Vidal-Diez de Ulzurrun, G., 2016. *Fungal growth modelling and assessment: Towards a lattice-free three-dimensional fungal growth model.* PhD Thesis, Department of Mathematical Modelling, Statistics and Bioinformatics, Ghent University, Ghent, Belgium.

Acknowledgements

FWO Research Foundation Flanders (Fonds Wetenschappelijk Onderzoek – Vlaanderen).

