Disambiguation of the different types of crossings in a mycelial branching network through complete identification of its spatio-temporal structure.

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From a single spore, fungi can colonize their environment through a very complex interconnected network of hyphae, the mycelium. Yet, the rules governing this growth are simple. Hyphae can only grow from the tip, branch (apically or laterally) [1] creating a new hypha or fuse when meeting another one. However, the local dynamics of growth within the network is not well known such as the inhomogeneity of the density in time and in space. Both types of branching are difficult to analyze spatially and quantitatively, as is the long-distance tracking of apexes. In this work, we characterize the hyphal network expansion and the structure of the model filamentous fungus Podospora anserina under controlled culture conditions [2] [3]. To this end, temporal series of pictures of the network dynamics are produced, starting from germinating ascospores and ending when the network reaches thousands of connections approximately 20 hours later. The completely automated image reconstruction steps allow a postprocessing and a quantitative analysis of the spatio-temporal dynamics using gray level information from the entire image series. Taking advantage of the network's properties we can numerically identify each individual hypha and characterize the nature of the branching it emerges from. Building on spatio-temporal information, we can discriminate hyphal fusion from mere overlapping to get a better understanding of the network topology. Thanks to the identification of each hypha, we analyze the growth of the network at both local and global scale.

Références

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