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DEVELOPMENT OF AN *IN VIVO* METHOD FOR FUNGUS-SPEROMOSPHERE INTERACTION

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ABSTRACT

The ability of useful fungal rhizoflore to colonize them in the rhizosphere is mainly depend on their early establishment in spermosphere prior to present of other active microbial population. The developing of an *in vivo* system, in which, interacted material (Fungal mycelium and germinated growing seeds) can easily be recovered and separated during different periods is necessary. This research was conducted to set up an *in vivo* system for fungal transcriptome studding during colonization of germinating seeds. Here, *Trichoderma* fungus and tomato-germinating seeds were used as a useful rhizoflore and host spermosphere, respectively. Glass beakers were half-filled with sieved and full-rinsed sandy soil (50-350µm), watered to field capacity, Foil-capped and sterilized. Surface-sterilized tomato seeds were coated with *Trichoderma* spores and alternately added to beakers with separating layers of sterilized sands. This sandy bed free of nutrients was used, in which, seed and rootlet exudates are only nutrient source used by *Trichoderma*. The beakers were incubated in a growth chamber and then removed at desired periods of 12h, 24h, 48 and 72h post-inoculation. Contains of beakers were suspended in larger beakers containing sterilized water. The interacted mycelia and germinated seeds were separately collected by flow of sterilized water and passing through filter papers. Fungal and plant biomass collected in tubes were immediately transferred to -80^{o}C freezer for physiological stop and then freeze-drayed. This high-qualified interacted biomass, which has not noticeable change in mRNA and protein profile, was used in transcriptome studies. This is the first study, to the best of my knowledge, to present new *in vivo* system to set up fungus-speromosphere interaction with easy access to recover interacted biomass.