The diversity of cold stress response mechanism in *Pseudogymnoascus* spp. involved various translation-related processes and metabolic pathways

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In the understanding of stress response mechanism in microorganisms, cold stress has received less attention than heat stress. Various cosmopolitan model organisms such as *Saccharomyces cerevisiae* and *Aspergillus nidulans* have been used as models to understand cold stress response. Nonetheless, psychrophilic and psychrotolerant fungi have also been studied to provide specific details and information particularly in relation to their cold-adapted properties. In this work, *Pseudogymnoascus* spp. isolated from different biogeographic regions were used to represent psychrotolerant species of soil microfungi. The effects of cold stress on their proteome profiles were compared to understand response mechanisms. The term “cold stress” here represents an experimentally lower temperature compared to the optimal growth temperature of *Pseudogymnoascus* spp. This will result in stress-related physiological change such as the reduction of fungal growth rates. Our results showed that the overall mechanism of response towards cold stress varies in the proteins that increased or decreased in relative abundance among isolates of *Pseudogymnoascus* spp. Several metabolic enzymes and ribosomal proteins were among the proteins identified as having changed in relative abundance in all six isolates of *Pseudogymnoascus* spp. when exposed to cold stress. There was however, no significant geographical patterns that contribute to the cold stress response of *Pseudogymnoascus* spp. Although the cold stress response identified in this work does not represent the actual environmental cold stress conditions, information gathered from the proteomic perspective of *Pseudogymnoascus* spp. will provide an initial glimpsed of cold stress response mechanism of various soil microfungi.

Keywords: psychrotolerant fungi, protein abundance ratio, LCMS/MS, biogeographic regions.