**Antagonistic Potential of Bio Agents against Causal Organism of Leaf Spot Disease in Cabbage**

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The Mycosphaerella leaf spot has caused great destruction to cabbage cultivation in Nuwara Eliya Districts. The disease has been controlled with chemical fungicides, which caused many negative environmental and health effects. Bio controls of pathogens by antagonistic microbes are considered desirable alternatives owing to their friendly profile for human health and the environment. However, in Sri Lanka so far not any attempt to find potential antagonistic Microorganisms against cabbage leaf spot disease. Therefore, this study was carried out to identify causative agent and potential antagonism to manage leaf spot disease under *in-vitro* conditions. Identification of pathogen was carried out based on macroscopic and microscopic characterization. Potential antimicrobial agents were isolated from healthy cabbage plant samples, and soil samples from different areas of Nuwara Eliya district. All the isolated samples were cultured in potato dextrose agar media and Nutrient agar media and maintain pure cultures for further study. Pathogenicity test was conducted to confirm causal organisms of leaf spot disease. Thirty fungal isolates were isolated from three different areas and dual cultured with causative agent of leaf spot disease were done to screen the antagonism. Based on macroscopic and microscopic characterization that the causative agent of cabbage leaf spot disease is identify as *Mycosphaerella spp*. The pathogen inoculated cabbage plant showed typical leaf spot disease symptoms by confirming their pathogenicity. Out of thirty of fungal isolates 13 showed antagonistic effect in vitro condition. Among those fungus isolates, SE1S was recorded with the highest inhibition against *Mycosphaerella spp*. The microbial isolates, HA2S, SE3H, AG1S, SE4S, SE1S, 2H2S, AG3S, SE2S, HA1S, HA3S, SH1S, showed competition effects against causal organisms of leaf spot of Cabbage. Further study is required to confirm the identity *Mycosphaerella spp* and antagonistic fungal stains by using gene sequencing and to evaluate efficacy of antagonistic fungal stains in field condition.

 **Keywords:** *antagonistic, cabbage, fungal, leaf spot, mycospharella spp*