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Analysis of genetic diversity of cabbage head rot fungus, *Sclerotinia sclerotiorum,* by mycelial compatibility groups

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Cabbage head rot caused by an ascomycete fungus, *Sclerotinia sclerotiorum*, is a severe problem in cabbage growing areas worldwide. The pathogen is well studied in other countries in terms of its etiology and genetic diversity. Genetic diversity is often measured using Mycelial Compatible Grouping (MCG), which is a phenotypic marker controlled by several genes. No research has been done to assess the population variation of the pathogen in Sri Lanka regardless of the fact that the disease is wide spread in cabbage growing areas. The objectives of the current study were to examine genetic diversity of *Sclerotinia* population from upcountry cabbage fields in Sri Lanka using MCGs, and to determine if the disease is spread through clonal infections from the infection foci. It was hypothesized that the pathogen population in Sri Lanka is relatively diverse and when a plant gets infected, nearby infections occur clonally via mycelial infection. If more than one MCG is found in each infection focus it is clear that more than a single infection causes the disease. Isolates were paired in all possible combinations in potato dextrose agar plates amended with red food colouring and barrage formation was observed. Isolates were considered as mycelially compatible if no barrage formation was observed. Nine MCGs were obtained in a population of 42 isolates. The largest MCG consisted of 14 isolates. Many MCGs (56%) had only a single isolate. Based on the results, the Sri Lankan pathogen population was moderately diverse in terms of MCGs. To determine if the disease spreads clonally or not, three infection foci were selected. At least 10 sclerotia from each cabbage head of each infection focus were collected and isolates were obtained. All the isolates within each infection focus were paired in all possible combinations to determine their MCGs. All of the isolates were compatible in all possible combinations in one infection focus. Interestingly, in the second infection focus, two MCGs were found within a single cabbage head. All the other isolates were compatible among themselves. This indicates that multiple infections result in the cabbage head rot. Multiple infections could be due to ascospore infections or introduction of multiple genotypes to the population via seed lots or other means. Relatively high MCG diversity and multiple infections indicate that there is a risk of a *Sclerotinia* epidemic in the Sri Lankan vegetable cultivation system.

Keywords: Cabbage head rot, MCGs, *Sclerotinia sclerotiorum.*

Financial assistance by the National Science Foundation (Research Grant RG/2015/BT/04) is acknowledged.

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