Abstract No: PO-15

Selection of the best fitting mathematical models to investigate the growth inhibition of selected plant pathogenic fungi by *Trichoderma harzianum*

V. A. Poornima[1*], J. Munasinghe[1] and S. D. Kannangara[2]

[1] Department of Mathematics, Faculty of Science, University of Kelaniya, Sri Lanka
[2] Department of Plant and Molecular Biology, Faculty of Science, University of Kelaniya, Sri Lanka
poornima_ps16172@stu.kln.ac.lk*

Plant diseases can cause a significant impact on agricultural productivity. One of the main causative factors for plant diseases is pathogens. Plant pathogens can be fungi, bacteria, viruses, or nematodes. Plant diseases can be prevented, mitigated, or controlled by using a variety of methods. Among these methods, bio-controlling is more effective and environmentally friendly. *Trichoderema* species are the most commonly used fungal biocontrol agents against various plant pathogens. Many researchers observed that the potential of *Trichoderma harzianum* in controlling various pathogens, but there were no proper mathematical models to understand how this fungus inhibits those pathogens. This research is focused on selecting the most suitable mathematical models to investigate the growth inhibition of pathogenic fungi; *Fusarium oxysporum, Colletotrichum gloeosporioides, Lasiodiplodia theobromae,* and *Xylaria spp.* by *Trichoderma harzianum*. For this purpose, five existing growth models, namely Exponential, Logistic, Brody, Von Bertalanffy, and Gompertz were used to investigate the growth inhibition. The data had been collected using the dual culture method to test the antagonistic properties of *Trichoderma* against the fungal pathogens. The data set consisted of 50 data points for six consecutive days. First, statistical analysis was performed to identify the distribution and characteristics of the data and detect outliers. Then one-way Analysis if Variance (ANOVA) test was done under the 95% confidence level. The results revealed that all the mean values are statistically significant. Tukey test was then conducted to check which specific group means were different. Then the most suitable growth models were identified for each fungus separately under two conditions: in the absence of *T. harzianum* and in the presence of *T. harzianum.* In the absence of *T. harzianum,* for the fungi; *F. oxysporum, C. gloeosporioides, L. theobromae,* and *Xylaria spp.* the best fitted models were given by Exponential, Gompertz, Exponential, and Exponential, respectively. In the presence of *T. harzianum* for the fungi; *F. oxysporum, C. gloeosporioides, L. theobromae,* and *Xylaria spp.* the best fitted models were given by Brody, Exponential, Brody, and Von Bertalanffy respectively. The goodness of fit was tested using the Coefficient of Determination (R^2), Root Mean Square Error (RMSE), Sum Squared Error (SSE), and residual plots. Then the comparison of the growth in the absence of *T. harzianum* and the presence of *T. harzianum* was made graphically using the above best fitted models. Hence the simulation results indicated significant growth controls of all the pathogenic fungi tested by *T. harzianum.*

Keywords: Fungi, Mathematical model, *Trichoderma harzianum*