Date: October 29, 2019

To Whom It May Concern:

As a major advisor of his PhD dissertation advisory committee, I know Achal very well in terms of his research and academic potential. Achal has been working in my lab as a PhD student since August 2017. Prior to joining my lab, Achal earned his BS in Biological Science from University of DC (Washington DC, USA) in 2009 and an MS degree in Biology (Bioinformatics) from South Dakota State University in 2013.

Achal has been working on his dissertation titled Dissecting RNA Silencing Pathways in the White Mold Fungus*, Sclerotinia sclerotiorum*, including on several other bioinformatics projects. Specifically, in my lab, Achal has been using gene disruption mutants to identify the roles of dicers (dcl-1 and dcl-2) and argonaute enzymes (agl-2 and agl-4) in the small RNA (sRNA) metabolism of the plant pathogenic fungus, *Sclerotinia sclerotiorum*. Achal studied the characteristic changes in mRNA and small RNA accumulation in *Sclerotinia sclerotiorum* infected by Sclerotinia sclerotiorum hypovirus 2-L (SsHV2-L), and predicted the classes of endogenous smallRNAs, including tRNA-derived small RNAs. He also studied the effectiveness of ds-RNA based pesticides that target the *S*. *sclerotiorum* RNA silencing pathway. Achal also studied the diversity and evolution of mycoviruses identified from the whole root metatranscriptomes of various plant host species infected by arbuscular mycorrhizal fungi. He has been able to publish the outcomes of these research in peer-reviewed journals.

Currently, Achal is working on a manuscript in which he is profiling the classes of the RNA editing in virus-derived small RNAs in white mold *Sclerotinia sclerotiorum* looking at distinct patterns of internal and terminal nucleotide mismatches using dicer and argonaute gene mutants infected by Sclerotinia sclerotiorum hypovirulence-associated DNA virus 1 (SsHADV-1).Additionally, Achal has been working on two microbiome projects looking at the effects of- i) crop rotation in soil microbiome diversity affecting the overall yield from Illinois-Urbana; and ii) soil salinity in microbiome diversity by analyzing 16S and ITS data from South Dakota.

Achal has demonstrated a well-rounded academic background as a bioinformatics researcher with extensive experience and research skills. Achal has gained extensive experience in the analyses of next generation sequencing (NGS) data (such as, small RNA/RNA-seq, degradome-seq, microbiome, genotype by sequencing). Achal also exhibits sound knowledge of statistical analyses in interpreting these results. He has been writing computer programs in R, Python and Perl to analyze next generation sequencing data generated in our lab. He is also highly skilled in building bioinformatics pipelines with extensive knowledge of Linux/Unix systems, HPC clusters, including command line tools and shell programming for bioinformatics research.

Additionally, during his graduate program, Achal has taken several courses in Molecular Biology, Statistics and Computer programming that also helped him gain well-rounded academic experience as a PhD student in a highly inter-disciplinary field of bioinformatics.

I also found Achal extremely hardworking, result-oriented, highly motivated and a critical thinker. He is also very articulate and communicates very effectively. I strongly recommend Achal for a bioinformatics research position at your institution. Achal is anticipated to graduate in May 2020 with a PhD in Biology (bioinformatics).

Please feel free to contact me if you need any further information.