

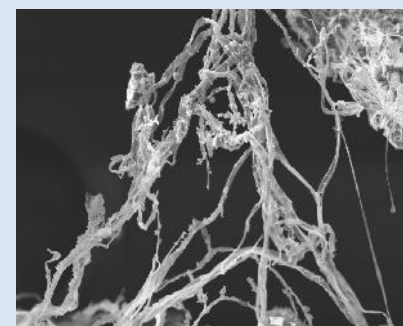


Genome Information for Representative Genome

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We are pioneer in the world to report *Sclerotium rolfsii* (*Athelia rolfsii*) Genome. If we want to understand molecular basis of pathogen and host interaction, it's essential to know the genome structure of plant pathogen. This research will spread light on hidden killing mechanism of *S. rolfsii* viz. Identification of PR genes, Toxin producing protein, Control mechanism, as well up and down regulations of genes which are part of host pathogen interaction. These tools can become an integral part of future research to develop resistant Groundnut varieties and other crops.

- Dr. B. A. Golakiya
Professor and Head
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Electron micrograph shows mycelia of *S. rolfsii*.

WHOLE GENOME SEQUENCING of *Sclerotium rolfsii*

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Genomic approaches are beginning to revolutionize our understanding of plant disease resistance. With the advantage of genomics, the entire blueprint of an organism can be determined, and a deep transition into genome-enabled biology can be revealed. This new era of research allows a comprehensive study of gene function that has already delivered tremendous insights into the basic biology of living organisms.

First completed genome of plant-associated fungi, that of the peanut pathogen *Sclerotium rolfsii*, has been reported by team of Department of Biotechnology. This information generated will reveal the detailed organization of virulent-gene clusters and the genetic mechanisms involved in generating disease by the pathogen. *S. rolfsii*, an omnivorous, soil borne fungal pathogen, causes disease on a wide range of agricultural and horticultural crops. Agricultural hosts include peanut (*Arachis hypogea*), pumpkin (*Cucurbita pepo* L.), corn (*Zea mays*), wheat (*Triticum vulgare*) and sweet potato (*Ipomea batatas*). Horticultural crops affected by the fungus are included in the genera Narcissus, Iris, Lilium, Zinnia, and Chrysanthemum.

In peanuts, early symptoms of infection are manifest in yellowing and wilting

of the lateral branches, main stem, or the entire plant. Peanuts also sustain brown lesions at the stem base and developing pegs. Infected pods rot, becoming wet, tan, and spongy.

Through the tool of whole genome sequencing in plant pathogen all inversions, rearrangements, and insertions in fungal genome would be viewable, giving rise to all sorts of questions: What does the arrangement of genes in a pathogen tell us about evolution of host specificity or pathogenicity? Which sequences indicate gene transfer between related or unrelated organisms? The range of exciting research questions being limited only by the imagination. It will also pinpoint functional variants from association studies and improve the knowledge available to researchers interested in evolutionary biology, and hence may lay the foundation for predicting host response and disease resistance.

Photos, clock wise from top left : Dr. Tomar working on fungal genome project; Light microscopy of *A. Rolfsii*; Electron Micrograph of plant pathogen interaction; Field infection of *S. rolfsii* in peanut. (Photo courtesy : R. L. Bhalara)