

## Emerging Research for Fungal Genomics and Biology

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The precursor to all mammalian genomics resides within the study of simple life forms, such as Fungi. Since the first DNA (Sanger) Sequencing of the first fungal genome was sequenced in 1996, sequencing technologies have advanced dramatically. Since then, quantum leaps in technology and even the sources of template (lysates) for these studies have changed. This has been paralleled by an increase in computational power and resources, to process and translate raw sequence data into meaningful information.

But, always at the forefront are fungal organisms used as the backbone for many types of analyses, ranging from evolution to development to MicroRNAs.

Synthesis of the AAP rapidly reduces gene expression in response to Arg. AAP-mediated regulation is observed in vivo, in both *Neurospora crassa* and *Saccharomyces cerevisiae*, and in vitro, using fungal, plant

and animal extracts. Investigators at the Broad Institute and others have examined the functions of these upstream ORFs (uORFs) that were observed to be evolutionarily conserved in three *Aspergillus* species. In silico experimental study and validation of such conserved elements will only be found by performing large scale analyses of the *N. crassa* genome, and understanding the functions of *N. crassa* genes with the mechanisms that regulate them.

Data-housing of fungal genomic data for gene models and proposed functions, as well as data mining, is important for all functional fungi genomic efforts, particularly in intron-rich organisms, such as *N. crassa*.

Next Generation Sequencing (NGS) may prove to be a new platform for unlocking nature's truths.

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