Aspergillus species are among the most important filamentous fungi in terms of industrial use and because of their pathogenic or toxin-producing features. The genomes of several *Aspergillus* species have become publicly available in this decade, and genomic analyses have contributed to an integrated understanding of fungal biology. Stress responses and adaptation mechanisms have been intensively investigated using the accessible genome infrastructure. Mitogen-activated protein kinase (MAPK) cascades have been highlighted as being fundamentally important in fungal adaptation to a wide range of stress conditions. Reverse genetics analyses have uncovered the roles of MAPK pathways in osmotic stress, cell wall stress, development, secondary metabolite production, and conidia stress resistance. This review summarizes the current knowledge on the stress biology of *Aspergillus* species, illuminating what we have learned from the genomic data in this "post-genomic era."

Comparison of signaling components in HOG pathway among *Aspergillus nidulans*, *Saccharomyces cerevisiae*, and *Schizosaccharomyces pombe*.