

cDNA microarray analysis of a non-model organism: pearl millet

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Plants respond to pathogen attack by the activation of biochemical defence responses. We are interested in gene expression underlying these responses. We hypothesize that unique defence mechanisms have evolved in monocots since their divergence from dicots, and have therefore chosen to study pearl millet, an important African cereal. We present a strategy for gene expression profiling on glass slide microarrays that can be generalised for any non-model organism, an important consideration in aligning research with National priorities. cDNA libraries enriched for 2000 transcripts that were differentially expressed in response to pathogen elicitors were constructed using the suppression subtractive hybridisation (SSH) technique. A quantitative method was developed to screen the SSH libraries on microarrays (1) and this indicated that the libraries were of high quality, for example 77% of the clones from the forward library represented up-regulated transcripts, and only 5% of the clones were derived from rRNA. Up-regulation of selected clones was confirmed by inverse Northern analysis, a microarray independent technique. Gene expression profiling of pearl millet plants treated with the defence signalling molecule methyl jasmonate indicated that both defence-homologues and unrelated genes responded differentially.

1. Van den Berg N, Crampton B, Birch P, Hein I, Berger DK (2004) High-throughput screening of SSH cDNA libraries using DNA microarray analysis, *Biotechniques*, 37 (5) 818-824.