Based on the expression profiles of genes during the day under drought-stress, eight clusters were built, and functional categorization was done based on the known or putative function of the encoded proteins, following the classification established by Yang et al. (2004).

Comparing the ratios of the gene-classes between the induced and repressed genes four groups showed significant difference in favor of the up-regulated genes. The ratio of the genes encoding proteins involved in metabolism, signal transduction and cell growth was higher among the induced genes.

To validate the results of the chip-hybridization, and to find stress-induced and root-specific genes, quantitative real-time PCR experiments were performed. Seven genes were tested, and the chip-hybridization results were confirmed for four of them: an *ABA/WDS induced* gene, a *LEA group 3*, a putative *LEA*, and a gene with unknown function. Furthermore, these genes` expression levels were determined in the shoot samples in all of the three genotypes. The alterations of the expression patterns reflected the differences in the stress-tolerance of the three cultivars. However all of them showed higher induction in roots than in shoots, the *LEA group 3* gene appeared to be the most stress-inducible and root-specific, becoming a candidate to develop expression cassettes including this gene.

Hashimoto M, Kisseleva L, Sawa S, Furukawa T, Komatsu S, Koshiba T (2004) A novel rice PR10 protein, RSOsPR10, specifically induced in roots by biotic and abiotic stresses, possibly via the jasmonic acid signaling pathway. Plant Cell Physiol 45:550-559.

Iwamoto M, Higo H, Higo K (2004) Strong expression of the rice catalase gene *CatB* promoter in protoplasts and roots of both a monocot and dicots. Plant Physiology and Biochemistry 42:241-249.

Yang L, Zheng B, Mao C, Qi X, Liu F, Wu P (2004) Analysis of transcripts that are differentially expressed in three sectors of the rice root system under water deficit. Mol Gen Genomics 272:433-442.

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The study of the Nimrod protein and gene cluster in *Drosophila melanogaster*

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Every multicellular organism has to maintain its homeostasis in masses of invading microbes in its environment. The innate immunity constitutes the first line of defence against this challenge. As the defence mechanism of *Drosophila melanogaster* consists of innate immune processes only, lacking an adaptive immune system, it can be characterised as a less complex homologue of its mammalian counterpart, making the fruit fly a valuable model organism for studying innate immune responses.

The circulating blood cells of the fruit fly are key effectors of its immune defence. These hemocytes can be divided into three characteristic types. In wild type third instar larvae 97% of all circulating hemocytes are plasmatocytes, but even though it is the most abundant cell type in circulation, previously it could only be characterised based on its phagocytic capacity.

Our group identified the first plasmatocyte-specific immunological marker. After screening thousands of candidate hibridoma clones, we found two specific monoclonal antibodies, recognising different epitopes on the same molecule. We purified the antigenic protein, and analysed it with MALDI-TOF. A protein was identified with characteristic domain structure, containing a signal peptide, a CCxGY motif, EGF repeats, one transmembrane and an intracellular domain.

We have shown that the protein functions as a putative phagocytosis receptor of the plasmatocytes. As this protein helps the major sentinel cells catching bacteria we decided to name it after the big hunter Nimrod (*nimC1*; Kurucz et al. 2007b). The RNAi induced loss of function *nimC1* mutant plasmatocytes phagocytose *S. aureus* bacteria at significantly lower levels than the wild type, but *E. coli* phagocytic capacity was not compromised. On the other hand ectopic expression of the *nimC1* gene in S2 *Drosophila* cell line significantly enhanced the phagocytic capacity of cultured cells.

As it seemed that NimC1 is not the only phagocytosis receptor in *Drosophila*, we did in silico analysis searching for similar proteins in the fruit fly genome. Nimrod belongs to the superfamily of EGF repeat containing proteins, from which only 12 contain the characteristic CCxGY motif. In these proteins one or more EGF domains can be found, which fit a specific, more stringent consensus sequence, which we named NIM repeat. Nine of these genes, including *nimC1* can be found in a genomic region spanning 88 kilobase on the second chromosome. (Kurucz et al. 2007a; Somogyi et al.)

To prove, that these predicted genes are really transcribed, and to characterise their expression pattern we performed reverse transcription polymerase chain reactions using samples from whole third instar larvae, isolated hemocytes in wild type and hemocyte overproducing *l(3)mbn-1* mutant, and wild type adults.

All of the predicted genes were transcribed in every studied condition; the only exception was *nimA* which did not show any transcription activity in hemocytes.

In order to study the expression pattern of the *nimC1* homologues in more detail, we intend to produce new specific antibodies recognising the NimC1 homologue proteins. In order to acquire suitable amount of isolated protein for immunization, we have cloned the non-homologues regions of four different *nim* genes into prokaryotic expression vectors containing a HIS affinity tag, allowing isolation of the produced protein. In order to allow possible post-translational modifications of the expressed proteins, two of them are already cloned into affinity tagged eukaryotic expression vectors.

Kurucz É, Márkus R, Zsámboki J, Folkl-Medzihradszky K, Darula Zs, Vilmos P, Udvardy A, Krausz I, Lukacsovich T, Gateff E, Zettervall C-J, Hultmark D, Andó I (2007a): Nimrod, a putative phagocytosis receptor with EGF repeats in *Drosophila melanogaster*. Curr Biol 17:1-6.

Kurucz É, Váczi B, Márkus R, Laurinyecz B, Vilmos P, Zsámboki J, Csorba K, Gateff E, Hultmark D, Ando I (2007b) Definition of Drosophila hemocyte subsets by cell-type specific antigens. Acta Biol Hung 58:95-111.

Somogyi K, Sipos B, Pénzes Zs, Kurucz É, Zsámboki J, Hultmark D, Andó I. Evolution of genes and repeats in the Nimrod superfamily. (Submitted manuscript).

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