[1]Federal Research Centre of Nutrition and Biotechnology, Moscow, Russia,
[2]A.N. Belozersky Research Institute of Physico-Chemical Biology MSU, Moscow, Russia

Comparative proteomic profiling of amygdale and cortex of rats with different behavioral characteristics during metabolic stress

[1]KIRBAEVA N.V., [2]SHARANOVA N.E., [1]MALINKIN A.D., [1]VASIL'EV A.V.

PURPOSE

The brain is the most sensitive structure to stress. It has been shown that stress produces neurochemical and behavioral changes associated with prefrontal cortex function. Limbic system, in particular amygdale, affects the stress-dependent behavior, initiating emotionally motivated responses. A number of data has demonstrated the correlation between rat's physiological ability to adaptation to stress and their behavioral type. To identify proteomic features in rat brain departments caused by metabolic stress we performed comparative proteomic analysis.

EXPERIMENT

Fig.1. "Open field" test

Wistar male rats were divided on 2 groups of behaviorally passive and active animals. Starvation of rats (water *ad libitum*) during 5 days served as a model of acute metabolic stress. There was a 5day recovery period after the starvation, while animals received a standard diet. The protein expression profiles of amygdale and cortex were studied by using two-dimensional electrophoresis and MALDI-TOF.

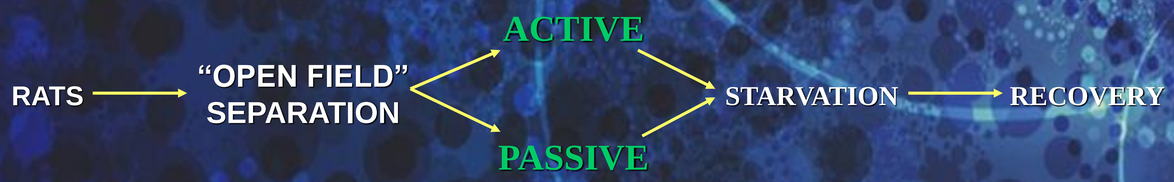

Fig.2. Experiment design

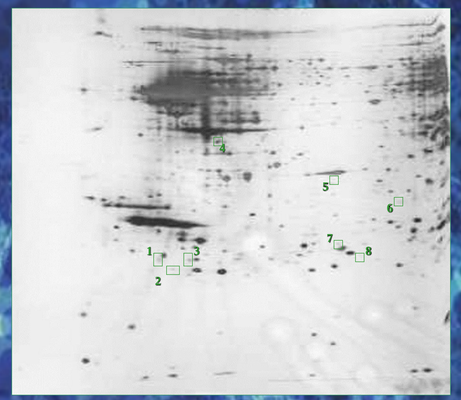

Fig. 3. Rat amygdale electrophoregram

1. Calcineurin B homologous protein 1
2. Peroxiredoxin 2
3. NADH dehydrogenase [ubiquinone] Fe-S protein 8
4. Tropomodulin 2
5. Tcrb protein
6. Glutathione S-transferase omega 1
7. Ras-related protein Rab-14
8. GTP-binding protein SAR1a

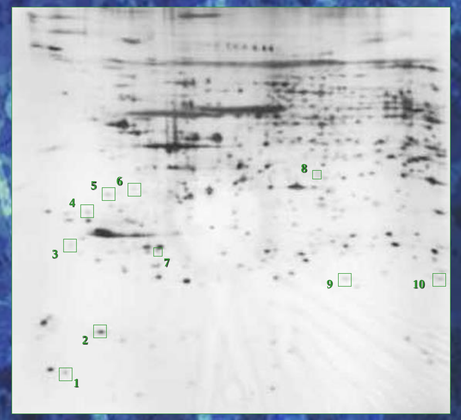

Fig. 4. Rat cerebral cortex electrophoregram

1. Calcineurin subunit B type 1
2. Alpha-synuclein
3. SNAP-25
4. 14-3-3 epsilon
5. Ubiquitin thioesteraseOTUB1
6. WDR61
7. NADH dehydrogenase [ubiquinone] flavoprotein 2
8. Serine/threonine protein phosphatase 1 (PP1)
9. Cell division control protein 42 homolog (CDC42)
10. Proteasome subunit beta type-2 (PSB2)

Group	Behaviour type of rats	Brain departure	
		Amygdale	Cortex
Control	A	↑ Tropomodulin -2 ↓ GTP-binding protein SAR1a	↓ Serine/threonine protein phosphatase 1 PP1 ↑ NADH dehydrogenase [ubiquinone] flavoprotein 2 ↓ Cell division control protein 42 homolog CDC42 ↓ 14-3-3 epsilon
	P	↑ Tropomodulin -2 ↓ GTP-binding protein SAR1a ↓ Ras-related protein Rab-14	↑ NADH dehydrogenase [ubiquinone] flavoprotein 2
Starvation	A	↓ Peroxiredoxin -2 ↓ Glutathione S-transferase omega -1 ↓ Calcineurin B	↓ Serine/threonine protein phosphatase 1 PP1 ↓ ubiquitin thioesterase OTUB1
	P	↓ Peroxiredoxin -2 ↓ NADH dehydrogenase [ubiquinone] Fe-S protein 8 ↑ Tcrb protein ↓ GTP-binding protein SAR1a ↓Gglutathione S-transferase omega -1	↓ ubiquitin thioesterase OTUB1 ↓ Proteasome subunit beta type-2 PSB2
Recovery	A	↑Tcrb protein ↓ Glutathione S-transferase omega -1	↑ NADH dehydrogenase [ubiquinone] flavoprotein 2 ↓ ubiquitin thioesterase OTUB1 ↓ 14-3-3 epsilon ↓ Proteasome subunit beta type-2 PSB2
	P	↓ Calcineurin B	↓ Alpha-synuclein

Tab. 1. Proteins of amygdale and cortex of active (A) and passive (P) rats, identified by mass spectrometry during metabolic stress

(↑-increased expression, ↓-decrease expression)

RESULTS

The proteomic analysis showed the up- and down-regulated expression of some proteins in amygdale and cortex depending on behavioral type of rats and the stage of stress.

CONCLUSIONS

Individual behavioral features affect the specific pathway of organism response to the stress and determine an adaptive potential of the organism.