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Proteomic analysis of protein composition of rat forebrain cortex exposed to morphine for 10 days: Comparison with animals exposed to morphine and subsequently nurtured for 20 days in the absence of this drug

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Proteomic analysis was performed in post-nuclear supernatant fraction (PNS) prepared from forebrain cortex of rats exposed to increasing doses of morphine (10-50 mg/kg) for 10 days and sacrificed 24 h (group+M10) or 20 days (group +M10/-M20) after the last dose of morphine. PNS fraction was resolved by 2D-ELFO and stained by CBB. Analysis of the difference between (+M10) and (-M10) samples of PNS by PDQuest accompanied by MALDI-TOF MS/MS indicated the significant change of 28 proteins. Importantly, the number of altered proteins was decreased to 14 after 20 days of nurturing the animals in the absence of this drug. This new and important finding was verified by an independent methodology: Gel-free & label-free quantification and normalization procedure denominated as MaxLFQ. The 113 proteins were identified as altered by morphine in (+M10) samples when compared with (-M10) samples of PNS and this number was decreased to 19 after 20 days since the last dose of morphine. To conclude, depending on the method used for protein detection and quantification, 28 (MALDI-TOF MS/MS) or 113 (MaxLFQ) altered proteins were identified. Importantly, in rats sacrificed 20 days after the last dose of morphine, the number of altered proteins were identified. Importantly, in rats sacrificed 20 days after the last dose of morphine, the number of altered proteins was decreased to 14 (MALDI-TOF MS/MS) and 19 (MaxLFQ), respectively. Our data indicate the high ability of living organism to oppose the drastic, morphine-induced change of the target tissue protein composition with the aim to return to the physiological norm after 20 days of drug withdrawal.

Biography

Hana Ujcikova has completed her PhD from Charles University in Prague. She is a Junior Researcher at the Institute of Physiology of the Czech Academy of Sciences. She has published in reputed journals, such as BBA General Subjects and Journal of Proteomics.

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