BIOCELL, Vol. 47, Suppl. 1, 2023
ISSN 0327- 9545
ISSN 1667-5746 (online version)

LVIII Annual Meeting of the Argentine Society for Biochemistry and Molecular Biology Research

(SAIB)

ISSN 0327- 9545
ISSN 1667-5746 (online version)

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ISSN 0327- 9545
ISSN 1667-5746 (online version)

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Andean potatoes (*Solanum tuberosum L. ssp. andigena*) are a good source of dietary antioxidant polyphenols. We have previously demonstrated that polyphenol extracts from Andean potato tubers exerted a dose-dependent cytotoxic effect in human neuroblastoma SH-SY5Y cells, being skin extracts more potent than flesh ones. In order to gain insight into the bioactivities of potato phenolics, we investigated the composition and the in vitro cytotoxic activity of total extracts and fractions of skin and flesh tubers of three Andean potato cultivars (Santa María, Waicha, and Moradita). Potato total extracts were subjected to liquid-liquid fractionation using ethyl acetate solvent in organic and aqueous fractions. We analyzed both fractions by HPLC-DAD, HPLC-ESI-MS/MS and HPLC-HRMS to confirm the annotations. Results corroborated the expected composition of each fraction. Organic fractions were rich in hydroxycinnamic acids (principally chlorogenic acid isomers), whereas aqueous fractions contained mainly polyamines conjugated with phenolic acids, glycoalkaloids, and flavonoids. Organic fractions were not cytotoxic against SH-SY5Y cells, and indeed, some increased cellular metabolism compared to controls. Aqueous fractions were cytotoxic and even more potent than their respective total extracts. Treatment with a combination of both fractions showed a similar cytotoxic response to the corresponding extract. According to correlation studies, it is tempting to speculate that polyamines and glycoalkaloids are crucial in inducing cell death. Our findings indicate that the activity of Andean potato extracts is a combination of various compounds and contributes to the revalorization of potato as a functional food.

PL-21

EXPRESSION ANALYSIS OF PROTEASE INHIBITORS IN POTATO PLANTS EXPOSED TO DIFFERENT ENVIRONMENTAL CONDITIONS.

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Analysis of the potato genome (SPUD DB) allowed us to identify 142 protease inhibitors (PIs); 42 PI genes are clustered in tandem in chr.3, position 43 Mbp (3.43): 14 encode Kunitz-type PIs (KTIs), 4 encode trypsin type PIs (TPI) and 1 encodes a cystein PI (CPI), and at position 48 MBp (3.48), 10 genes encode KTIs, 8 encode PIN-II and 5 encode serine type PI (PIN-I). On the other hand, 11 genes encoding 5 KTIs, 3 cystatin B, and 3 PIN-I are grouped in Chr. 6, and 12 PIN-I genes are in chr. 9. This multigene family regulates protein turn-over preventing catabolism of essential proteins during metabolic processes and plays a role in the defense against heterologous proteases from pathogens and pests. PIs have been proposed as an alternative to chemical pesticides for the control of herbivorous insects, and as abiotic stress-protective factors. Degenerate primers were designed against five PIs (Soltu.DM.03G018480, -G018520, -G018580, -G018620, -G018650) of 3.43, seven PIs (Soltu.DM.03G023490, -G023500, -G23510, -G23520, -G23530, -G23540, and -G024110) of 3.48, and seven PIs of Chr. 9 (Soltu.DM.09G025840, -G025850 -G025860 -G025880, -G025900, -G025910, and -G025930) that share at least 83.46, 55,2 and 77,53 % of nucleotide identity. According to RNAseq data these three gene clusters are induced upon drought, salt, mannitol and N2 fertilization, and are downregulated during tuber dormancy release. To confirm the RNAseq data, RT-qPCR assays were performed using RNAs from in-vitro plants cultured under control conditions or a) with different NH4+ and NO3- concentrations, b) exposed during 1 week to continuous darkness, and c) to 150 mM NaCl during 24 and 96 h. In addition, RNA was extracted from greenhouse plants exposed to drought conditions. To analyze, the role of PIs during source-sink processes, RNA was obtained from dormant and sprouting tubers, from etiolated and green sprouts, and from young, fully developed and senescent leaves. In the future we aim to characterize one gene of each cluster in overexpressing or knockdown plants to elucidate their potential as biotechnological tools.

PL-22

S-NITROSATION MODULATES AUXIN SIGNALING DURING THERMOMORPHOGENESIS IN ARABIDOPSIS