Walnut-derived peptide in a model of low-grade inflammation: any nutrigenomic effect?

Fanrui Zhao[1,2], Laura Bordoni[3], Weihong Min[2], Rosita Gabbianelli[3]

[1]School of Advanced Studies, University of Camerino, Italy.

[2]College of Food Science and Engineering, Jilin Agricultural University, Changchun, P.R. China.

[3]Unit of Molecular Biology and Nutrigenomics, University of Camerino, Italy.

INTRODUCTION

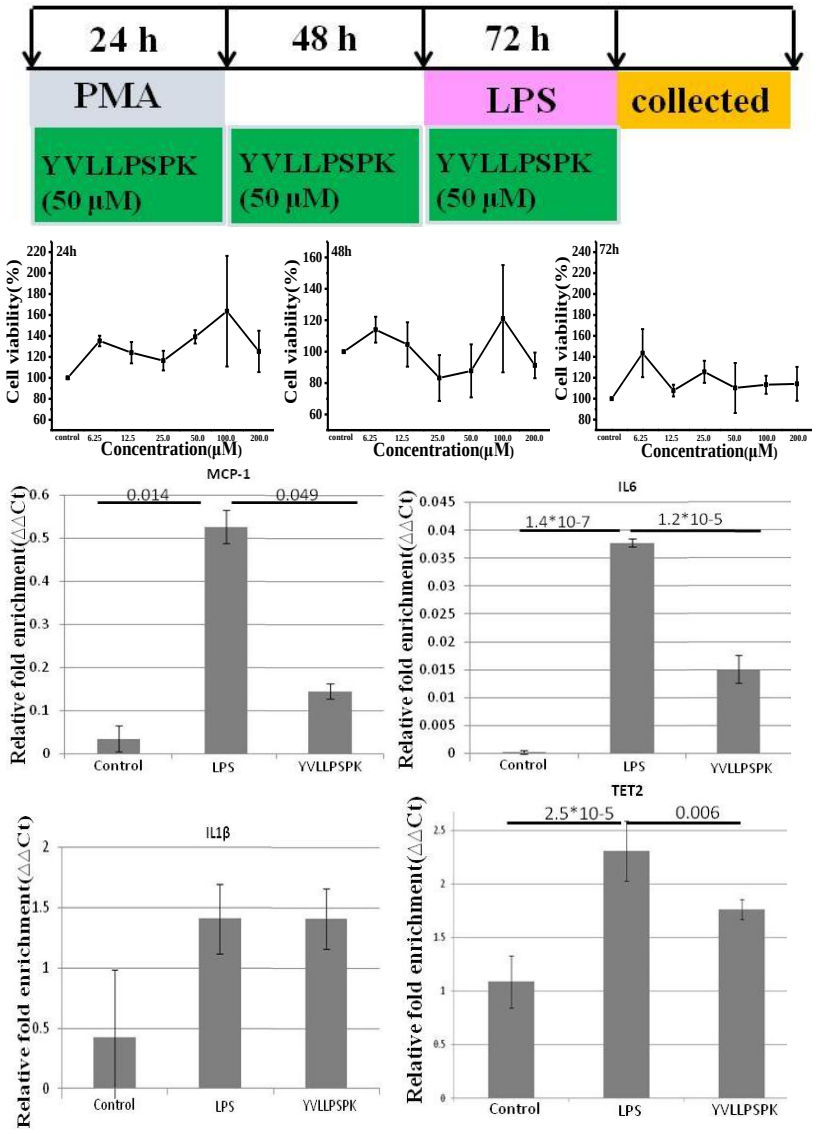
Epigenetic plays a major role in inflammation, which promotes the onset of chronic complex diseases. Bioactive components and nutrients contained in foods can modulate epigenetic pathways. Walnut dregs are by-products of the deep processing of walnut oil and are hydrolyzed by enzymes to obtain walnut hydrolysate proteins (WHPs) with different molecular weights. Subsequently, WHPs are isolated and purified by SEC, RP-HPLC and HPLC-MS/MS into walnut peptides[1].

AIM OF THE STUDY

This study investigates the nutrigenomic effects of walnut-derived peptide with high antioxidant activity, YVLLPSPK, against LPS-induced low-grade inflammation in THP-1 cells.

REFERENCES

[1] Liu C, Guo Y, Zhao F, et al. Food & function, 2019, 1(6):3351-3491.



EXPERIMENTAL

Cell viability for THP-1 cells was measured by the MTT assay. The YVLLPSPK was added before the exposure to LPS, as a pre-treatment with PMA for 72 h. The expression of genes involved in the control of inflammation and the epigenetic homeostasis was tested by qPCR.

RESULTS

The results on cell viability showed that the concentrations and time of YVLLPSPK had no significant impact on cell viability compared with the control. Analysis of the expression of inflammatory genes revealed that pre-treatment with YVLLPSPK significantly suppresses IL6 and MCP-1in LPS-induced low-grade inflammation. However, no significant modulation of IL1β gene was detected. Among genes involved in the regulation of epigenetic homeostasis, only TET2 was significantly modulated by the peptide.