Anti-ageing natural products: Fluorescence-based screening and identification in complex mixtures using 13C-NMR

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Abstract

Advanced glycation end-products (AGEs) are formed during non-enzymatic reactions involving proteins and sugars, *i.e.* the Maillard or browning reaction. The early glycation is reversible and involves the production of a Schiff base from the carbonyl group of a reducing sugar and the primary amino groups of a protein (lysine, arginine). The imine adduct undergoes a rearrangement yielding Amadori products. During the late stage, complex irreversible oxidation, condensation and cyclisation reactions lead to AGEs via intra- and inter-molecular protein crosslinkage (Fig 1). Depending on the protein involved, such reactions may lead to diabetes complications but also to skin ageing. Thus, antioxidant natural products (NPs) acting by radical scavenging or metal chelation as well as compounds capable of trapping dicarbonyl species or breaking AGEs may also reduce the amount of AGEs and ageing processes [1]. With this in mind, our research has focused for about 10 years on the investigation of anti-AGE NPs and extracts.

In the process we have developed a simple, cheap and high-throughput screening (HTS) assay based on AGE fluorescence, which is highly suitable for the analysis of NPs and extracts [2,3] By now one ongoing project is to identify promising NPs and plants for future applications as cosmetics. First, this assay was thus adapted and patented for the identification of active anti-AGE compounds designated for cosmetic purposes [4]

Then, to assist the identification of NPs in complex anti-AGE mixtures, a new dereplication method using 13C-NMR was developed in the form of a freely distributed software. The MixONat algorithm compares chemical shifts in the extract with the ones of all NPs in a given database and gives them a score depending on the percentage of matched signals. The matching process can be improved if additional information is added, like DEPT experiments or mass spectrometry data. As a proof of concept, the program was tested on a series of various vegetal extracts. In each case, the program managed to identify correctly the major NPs, showing that the functionalities implemented in the algorithm provides confident results [5].

References

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