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Plant micro RNAs can control cancer genes expression through a sequence-specific targeting mechanism: the case of MALAT1 and NEAT1

Flaviana Marzano[1]✉, Mariano Francesco Caratozzolo[1], Arianna Consiglio[2], Flavio Licciulli[2], Sabino Liuni[2], Elisabetta Sbisà[2], Domenica D'Elia[2], Apollonia Tullo[1], Domenico Catalano[2]

[1] Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies, National Research Council, Bari, Italy
[2] Institute for Biomedical Technologies, National Research Council, Bari, Italy

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It is well known that some plant compounds, or phytochemicals, can positively affect human health by reducing inflammation and oxidative stress (Issa *et al.*, 2006; Dell'Agli *et al.*, 2013). Although the large number of works published, the molecular mechanisms through which plants can impact human health are still unclear. Recent studies suggest that plant nutrients control the expression of human genes by DNA methylation and histone modifications (Choi and Friso, 2010; Tollefsbol 2014). Moreover, some plant/food-derived microRNAs (miRNAs) accumulate in the sera and tissues of various animals and regulate their gene expression in a sequence-specific manner (Zhang *et al.*, 2012; García-Segura *et al.*, 2013).

We performed a study using a combined in silico and experimental approach to investigate the potential effects and elucidate the molecular mechanisms of edible plant miRNAs on the expression of human genes involved in cancer onset and progression (Marzano *et al.*, 2020). This study demonstrates that plant miRNAs can bind human transcripts in a sequence-specific manner and that their binding is functional. In particular, we have shown that the plant mtr-miR-5754 and gma-miR-4995 directly target the tumour-associated long non-coding RNAs MALAT1 and NEAT1, respectively, in a sequence-specific manner, thus reducing cancer cell proliferation. For the first time, we provide evidence that plant miRNAs can also target human regulatory ncRNAs. These findings open the way to new biotechnological applications in human nutrition and chronic diseases prevention.

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