Identification of the key bitter compounds in our daily diet is a prerequisite for the understanding of the hTAS2R gene polymorphisms affecting food choice.

Abstract:
In order to decode genetic variations affecting food choice and to determine whether to accept or to reject certain food products, it is a necessary prerequisite to deorphanize the hTAS2R/ligand pairs using the key bitter compounds in foods as stimuli rather than doing this either by using artificial molecules, to which the normal consumer had never been exposed, or by using food-born molecules which do not at all contribute to the overall bitterness. Therefore, the chemical structure of the most active bitter molecules in foods needs to be unequivocally determined in order to be sure that hTAS2R polymorphisms are related to the key molecules which really contribute to the overall bitterness perception of food products. As most studies focused primarily on quantitatively predominating compounds, rather than selecting the target compounds to be identified with regard to taste-activity, it seems that yet unknown components play a key role in evoking the bitter taste of food products. Driven by the need to discover the key players inducing the food taste, the research area \textquoteleft{sensomics\textquoteright} made tremendous efforts in recent years to map the sensometabolome and to identify the most intense taste-active metabolites in fresh and processed foods. The present article summarizes recent studies on the identification of orphan key bitter stimuli in fresh, fermented, and thermally processed foods using carrots, cheese, and roasted coffee as examples.