

[P7] Getting better at predicting bitter

Ayana Dagan-Wiener and Masha Y. Niv

Institute for Biochemistry, Food Science and Nutrition, The Robert H. Smith Faculty of Agriculture, Food and Environment, and Fritz Haber Center for Molecular Dynamics, The Hebrew University of Jerusalem, Israel.

Bitter taste is a significant factor in animal's choice of food. Animals avoid eating bitter food components, many of which are toxic. Nevertheless, it is known today that bitterness is not always noxious, and that some of the bitter compounds have beneficial effects on health. These days we are in the middle of a "revolution" in bitter taste research following the finding that bitter receptors (a subfamily of GPCRs) are not only present on the tongue but also in many other organs such as the stomach, intestine, nasal and sinus cavities. Recent studies suggest that bitter receptors aid the digestive process, have an impact on respiration and are involved in activating the immune system. Therefore, the bitter taste receptors now emerge as novel drug targets.

We aim to identify common properties of bitter compounds and to predict additional ones. To this end we established BitterDB¹ a database of bitter compounds, available at <http://bitterdb.agri.huji.ac.il/bitterdb/>, which currently includes over 600 compounds that were reported to be bitter for humans.

Recently we gathered structures of over 1500 compounds that are likely to be non-bitter. Chemoinformatic analysis of these sets suggests a chemical sub-spaces that bitter and non-bitter compounds occupy compared to random set of molecules (represented by the ChEBI dataset). We found sets of topological and ADME (absorption, distribution, metabolism, and excretion)/TOX descriptors that can partially distinguish between bitter and non-bitter compounds. Predictions of bitterness based on chemical structure and molecular descriptors are currently underway. In parallel, co-occurrence of compound name with the word "bitter" in PubMed publications was analyzed and resulted in a set of over 500 likely bitter compounds within clinically approved drugs and ChEBI molecules. These findings indicate the feasibility of predicting bitterness despite extreme variability among known bitter compounds and may facilitate potential repurposing of existing drugs for novel indications via their action on bitter taste receptors².

[1] Wiener, A., Shudler, M., Levit, A. & Niv, M. Y. Nucleic Acids Res, 40 (2012), D413-419, doi:gkr755 [pii]10.1093/nar/gkr755.

[2] Levit, A. et al. The FASEB Journal, doi:10.1096/fj.13-242594 (2013).