

## **Researchers study the warming effect of consumed ginger**

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Ginger is a widely used spice, particularly in the cuisine of East and South Asia. It is known to have some physiological effects and is commonly used in Traditional Chinese Medicine (TCM). Writing in the *International Journal of Computational Biology and Drug Design*, Guang Zheng, Fei Hou, Jinghu Wang, and Nannan Wang of Lanzhou University, China, focus on one of the spice's most well-known



properties: its warming effect on the body.

The spice we know as ginger is derived from the root of the flowering plant Zingiber officinale. It feels hot to the mouth when you eat something containing this spice, but it also has an apparent warming effect on the stomach and the small intestine. However, a mechanism for this purported activity noted in TCM, specifically at the leve of protein regulating networks remains obscure, the team writes.

The researchers have now used literature and protein database searching of the two main active natural products in ginger, 6-gingerol and 6-shaogaol, and identified proteins targeted/regulated by these compounds. They were then able to piece together likely compoundprotein and functional protein-protein interactions to build up a picture of the underlying regulating networks within the stomach and the <u>small</u> <u>intestine</u> that might respond to these ginger compounds.

The team has found through enrichment analysis of functional proteinprotein interactions that in participating proteins there are five key metabolic processes that seem to be linked to the warming effect of ginger. The two main bio-active compounds present in ginger having a regulator effect on <u>adenosine triphosphate</u> (ATP), glycogen, glycerolipid, fatty acid, and coenzyme. The team suggests that such insights might add to the <u>evidence base</u> that supports the modernisation of TCM.

**More information:** Guang Zheng et al. Networks regulated by ginger towards stomach and small intestine for its warming interior function, *International Journal of Computational Biology and Drug Design* (2019). DOI: 10.1504/IJCBDD.2019.099763



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