Introduction: Aloe vera leaf gel has been reported to possess a wide range of pharmacological properties. It has been extensively used to treat gastric symptoms. However, the pharmacological evaluation of major Aloe vera leaf gel compounds for the treatment of chronic gastritis remains vague to date. Potential drug targets of aloeresin D, aloesaponarin I, aloesin, aloin, azelaic acid, chrysophanol, erucic acid, esculetin, helminthosporin, rhein and umbelliferone, major Aloe vera leaf gel compounds, were analyzed using a network pharmacology approach.

Methods: First, chronic gastritis related gene targets were acquired using DisGeNETand Kyoto Encyclopedia of Genes and Genomes (KEGG) data bases. Second, predicted drug targets of above compounds were extracted using Pharmmapper, SwissTarget Prediction and Similarity ensemble approach (SEA) databases individually. A network for active ingredients-candidate targets-proteins"was constructed and visualized using Cytoscape software. Finally, compound targets and enriched pathways were observed by Gene Ontology (GO) and KEGG pathway enrichment analysis.

Results: A total of 267 genes were identified to associate with chronic gastritis. Following analysis, 33 predicted targets of all major Aloe vera compounds mentioned above were found to intersect with genes associated with chronic gastritis. Predicted targets were validated using KEGG pathway analysis. The results of the pathway enrichment analysis indicated that putative targets of major Aloe vera gel compounds mostly participated in signaling pathways associated with anti-inflammation response. Among the putative targets of Aloe vera gel compounds, NOS2 (Nitric Oxide Synthase 2), amajor mediator of gastritis related inflammations, was identified.

Conclusion: This analysis provides a rationale for researchers to explore molecular mechanisms implicated in Aloe vera gel compounds for chronic gastritis in-vitro and in-vivo.