cancer, according to Cancer Research UK. Probiotics have also been shown to attenuate hepatotoxic effects of aflatoxin, a well known liver carcinogen, in rats and to reduce biomarkers of liver cancer risk in a human intervention trial. Probiotic bacteria could block the intestinal absorption of aflatoxin B1 and thereby lead to reduced urinary excretion of aflatoxin B1-N7-guanine (AFB1-N7-guanine), a marker for a biologically effective dose of aflatoxin exposure. Elevated urinary excretion of this aflatoxin-DNA adduct is associated with an increased risk of liver cancer.

**Conclusion:** The probiotic theory offers an intriguing approach to controlling negative metabolic or pathogenic activities of microbes to which we are exposed on a daily basis. Results suggest that consumption of a high amount of fermented milk products may have a protective effect on the risk of cancer.

**Keywords:** Probiotic, Anticancer, *Bifidobacterium*, *Lactobacillus*, Receptor.

**Computational approach for evaluation of possible role of miR-342-3p in patients with gastric carcinoma**

Ameneh Shahrokhi a, Hamzeh Mersian Tanha b, Kamran Ghaedi b,c, Mansoureh Azadeh c,d

a Division of Cellular and Molecular Biology, Department of Biology, Nourdanshe University of Meymeh, Meymeh, Isfahan, Iran
b Division of Cellular and Molecular Biology, Department of Biology, Faculty of Science, University of Isfahan, Isfahan, Iran
c Zistfanavari Novin Biotechnology Institute, Isfahan, Iran

e-mail address: kamranghaedi@yahoo.com

Extended Abstract

**Introduction:** Gastric cancer (GC) is the most common malignancy and the second cause of cancer death worldwide which is often diagnosed in advanced stages. GC is a highly heterogeneous and multistep disease due to deregulation of common oncogenic pathways. *Helicobacter pylori* infection, diet, alcohol consumption, and smoking are main environmental risk factors for GC. The World Health Organization International Agency for Research on Cancer (WHO/IARC, 69372 Lyon CEDEX 08, France) has introduced *Helicobacter pylori* as the first group of carcinogens. It is reported that *Helicobacter pylori* infection is associated with chronic inflammation and can induce chronic gastritis, intestinal metaplasia, intestinal dysphasia, and also GC. MicroRNAs (miRNAs) are a large class of short non-coding RNAs (containing about 22 nucleotides) which have critical role in regulation of oncogenes, tumor suppressors, and cancer-related genes controlling cell cycle, apoptosis, cell migration, and angiogenesis. Therefore, miRNAs can be utilized as a prognostic biomarker and also therapeutic targets for treatment strategy. The role of miR-342-3p has been defined in cervical, colorectal, breast cancers, and hepatocellular carcinoma (HCC). It significantly inhibits HCC cell proliferation via NF-κB pathway. Moreover, miR-342-3p inhibits cell proliferation, migration, and invasion in cervical cancer cell lines. In addition, it may act as a tumor suppressor gene in colorectal cancer development. However, the probable role of miR-342-3p in gastric carcinogenesis is unknown. This study aimed to expand current knowledge of probable molecular function of miR-342-3p in patients with GC by using bioinformatics tools.

**Methods:** Predicted and validated targets of miR-342-3p were obtained from miRwalk (a comprehensive atlas of microRNA-target interactions, http://zmf.umm.uni-heidelberg.de/apps/zmf/mirwalk2/) and miRTarBase (experimentally validated microRNA-target interactions database, http://mirtarbase.mbc.nctu.edu.tw/) databases respectively. The expression patterns of targetable genes in normal stomach and gastrointestinal tumor were investigated by UniGene (http://www.ncbi.nlm.nih.gov/unigene/term) database. Finally, GC specific targetome were classified into molecular pathways by DAVID (database for annotation, visualization and integrated discovery, https://david.ncifcrf.gov/home.jsp) database.

**Results:** MiR-342-3p targetome manifested “pathway in cancer” as the most statistical relevant pathway (Table 1). It is predicted that critical mRNAs in angiogenesis pathway including, TGFα, EGF, Grb2, SOS, Raf, MEK, ERK, cJun, Ets1, VEGF, and MMPs are targeted by miR-342-3p. Interestingly, our data showed that miR-342-3p inhibits some well-known oncogenes such as JAK, SHP2, STAT, GRB, SOS, and BclXL in “JAK-STAT pathway” which is one of the inflammation-related signaling pathways.

**Conclusion:** Chronic inflammation is an important risk factor for GC with approximately 25% of all gastric carcinoma worldwide. Adherence of *Helicobacter pylori* to gastric epithelial cells has been shown to trigger several signaling pathways. NF-κB and JAK/STAT are the two most remarkable inflammation-related signaling pathway. NF-κB is one of the major transcription factors that regulate the expression of genes involved in inflammation, cell proliferation, differentiation, and apoptosis. The Janus kinase/signal transducers and activators of transcription (JAK/STAT) has critical role in inflammation signaling immune system, and cytokine-cytokine interaction pathways in various kind of cells. Boram Cha et al. showed that JAK1/STAT3 is upstream signaling effectors of NF-κB in *Helicobacter pylori*-infected gastric epithelial cells. Moreover, some studies have suggested that JAK/STAT may play an important role in expansion of gastric carcinoma. In addition, Boram Cha et al. found that inhibition of Jak1/Stat3 may be beneficial for the treatment of *Helicobacter pylori*-induced gastric inflammation. According to our data, miR-342-3p acts as a tumor suppressor molecule and may be involved in GC carcinogenesis by altering regulation of angiogenesis and some GC-related pathways. More specifically, our data proposed a probable strong correlation between miR-342-3p and NF-κB and JAK/STAT signaling pathways based on in-depth in silico investigation. However, clarification on the exact function of miR-342-3p needs real laboratory procedure. To sum it up, miR-342-3p might be a useful prognostic biomarker in GC patients.

**Table 1 Enrichment analysis of miR342-3p targetome.**

<table>
<thead>
<tr>
<th>Pathway</th>
<th>Count (Gene no.)</th>
<th>Enrichment p value</th>
<th>Target gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathway in cancer</td>
<td>11</td>
<td>3.9E-5</td>
<td>TGFα, EGF, Grb2, SOS, Raf, MEK, ERK, cJun, Ets1, VEGF and MMPs</td>
</tr>
<tr>
<td>JAK-STAT</td>
<td>6</td>
<td>4.6E-2</td>
<td>JAK, SHP2, STAT, GRB, SOS, BclXL</td>
</tr>
</tbody>
</table>