

ABSTRACT BOOK

**hgm**  
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**SINGAPORE**

Human Genome Meeting / International Congress of Genetics

## The Convergence of Two Major Meetings

Joint Conference of HGM 2013 and 21<sup>st</sup> International Congress of Genetics

# Genetics & Genomics OF GLOBAL HEALTH AND SUSTAINABILITY

13 - 18 April 2013 | The Sands Expo and Convention Center, Marina Bay Sands

[www.hgm2013-icg.org](http://www.hgm2013-icg.org)

Host



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**Results:** We provide evidence of miR-371, miR-372 and miR-373 upregulation significantly in esophageal squamous cells compared with their adjacent normal cells (P <0.05).

**Conclusion:** As the first report for all members of these microRNA cluster in ESCC, our findings support the hypothesis that these microRNAs might play an oncogenic role or in the antiapoptotic and tumor suppressor processes of ESCC.

**Disclosure of Interest:** None Declared

HGM2013-ICG-1339

### **Mir-338-3p is aberrantly expressed in iranian patients with esophageal squamous cell carcinoma**

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**Objectives:** Esophageal cancer is one of the most lethal cancers that its mortality: incidence ratio is about 91% and at the time of diagnosis, nearly 50% of patients have metastasis. northeast of Iran has one of the highest incidence rates of esophageal cancer worldwide. microRNAs are a new-identified class of non-coding RNAs that their miss-regulated expression has been observed in many diseases such as cancers. miR-338-3p has an important role in cancer-related processes regarding to its validated targets such as Mmp9 (matrix metalloproteinase 9), SMO (smoothend protein), neuroblastoma RAS viral (v-ras) oncogene homolog (N-ras) and MYC. Mmp9 is a matrix metalloproteinase involved in normal and disease processes, such as metastasis. SMO can function as an oncogene and its mutations can lead to unregulated activation of the hedgehog pathway that has been implicated in the development of cancer.

**Methods:** Our aim in this study has been to evaluate miR-338-3p expression levels in esophageal squamous cell carcinoma (ESCC) tumor samples in comparison with non-tumor marginal area. So after preparation of

37 FFPE (formalin-fixed paraffin-embedded) clinical samples (tumor cells and their adjacent normal cells), extraction of microRNAs in total RNA, specific cDNA synthesis and real-time PCR amplification of miR-338-3p was performed.

**Results:** According to statistical analysis, our data indicates that the expression level of miR-338-3p in tumor cells is significantly lower than adjacent normal esophageal tissues. miR-338-3p down-regulation has been reported in some other cancers such as HCC and liver cancer.

**Conclusion:** In our data, as the first aberrant miR-338-3p report in an area with high incidence of ESCC (hot region), this microRNA may play as a tumor suppressor in ESCC. Since microRNA-based tumor-markers have advantages vs. other types of biomarkers, such as stability in FFPE tissues and availability in body liquid, this microRNA might be a novel tumor marker for early diagnosis of ESCC.

**Disclosure of Interest:** None Declared

HGM2013-ICG-1337

### **Upregulation of mir-196a in esophageal squamous cell carcinoma**

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**Objectives:** Esophageal cancer (EC) is one of the most aggressive cancers in the world. Patients with EC generally present with advanced stages and despite of invasive treatment, the overall 5-year survival is 25 percent. The incidence rate of EC is high in some regions such as Iran, thus finding new biomarkers for screening of disposed people in high-risk areas is important. MicroRNAs are small non-coding RNAs that regulate gene expression at the post-transcriptional level. MicroRNA studies have shifted the focus to