ESPS Peer-review Report

Name of Journal: World Journal of Gastroenterology

Ms: 3677

Title: Epigenetics of Hepatocellular Carcinoma: Role of MicroRNA

Reviewer code: 01560071

Science editor: s.x.gou@wjgnet.com

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CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
[ ] Grade A (Excellent)	[ ] Grade A: Priority Publishing	Google Search:	[ ] Accept
[ ] Grade B (Very good)	[ ] Grade B: minor language polishing	[ ] Existed	[ ] High priority for publication
[ ] Grade C (Good)	[ ] Grade C: a great deal of	[ ] No records	
[ ] Grade D (Fair)	language polishing	BPG Search:	[Y]Rejection
[Y] Grade E (Poor)	[Y] Grade D: rejected	[ ] Existed	[ ] Minor revision
		[ ] No records	[ ] Major revision

COMMENTS

COMMENTS TO AUTHORS:
The authors discuss the role of microRNA in diagnosis and treatment of HCC. I think this is a review article. If so, the authors should clarify it in the title, abstract, and text.

ESPS Peer-review Report

Name of Journal: World Journal of Gastroenterology

Ms: 3677

Title: Epigenetics of Hepatocellular Carcinoma: Role of MicroRNA

Reviewer code: 00007404

Science editor: s.x.gou@wjgnet.com

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CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
[ ] Grade A (Excellent)	[ ] Grade A: Priority Publishing	Google Search:	[Y] Accept
[Y] Grade B (Very good)	[Y] Grade B: minor language polishing	[ ] Existed	[ ] High priority for publication
[ ] Grade C (Good)	[ ] Grade C: a great deal of	[ ] No records	
[ ] Grade D (Fair)	language polishing	BPG Search:	[ ]Rejection
[ ] Grade E (Poor)	[ ] Grade D: rejected	[ ] Existed	[ ] Minor revision
		[ ] No records	[ ] Major revision

COMMENTS

COMMENTS TO AUTHORS:
study well conducted

ESPS Peer-review Report

Name of Journal: World Journal of Gastroenterology

Ms: 3677

Title: Epigenetics of Hepatocellular Carcinoma: Role of MicroRNA

Reviewer code: 02461868

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CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
[ ] Grade A (Excellent)	[ ] Grade A: Priority Publishing	Google Search:	[ ] Accept
[ ] Grade B (Very good)	[ ] Grade B: minor language polishing	[ ] Existed	[ ] High priority for
[Y] Grade C (Good)	[Y] Grade C: a great deal of	[ ] No records	publication
[ ] Grade D (Fair)	language polishing	BPG Search:	[ ]Rejection
[ ] Grade E (Poor)	[ ] Grade D: rejected	[ ] Existed	[Y] Minor revision
		[ ] No records	[ ] Major revision

COMMENTS

COMMENTS TO AUTHORS:

Article Title Epigenetics of Hepatocellular Carcinoma: Role of MicroRNA   Authors Sharad Khare, Qiong Zhang, and Jamal A. Ibdah   Article Summary   Sharad Khare et al. have studied and reported the role of microRNAs (miRs) in the progression of a frequently diagnosed and lethal liver cancer, hepatocellular carcinoma (HCC). The researchers elaborate on miRs, explaining that they function to repress gene expression by the mechanisms of mRNA degradation, or translational repression. Here the proto-oncogene c-myc and tumor suppressor gene p53 are mentioned, which activate miRs in HCC. The synthesis of miRs is also explained in the introduction, including the repressive effects at the 3' UTR region of mRNA, and conversely, the activation of genes at the 5' UTR.   Following the introduction, Khare et al. explain the deleterious expression of miRs, and their role in the progression of HCC. MiRs which are down-regulated act as tumor suppressor genes, and those miRs (onco-miRs) which are up-regulated target tumor suppressor genes. These up-regulated and down-regulated miRs can be found in tables 1 and 2 of the article. Next, single nucleotide polymorphisms (SNPs) in miRs have been found to influence the onset of cancer due to the great specificity required in the binding of miRs and the target gene. In section 3.2, Khare et al. explain that miRs act as biomarkers in HCC. For example, down-regulation of miR-let-7g causes a poor HCC prognosis, whereas up-regulation of miR-10b also leads to poor prognosis. Finally, the researchers explain that miRs can act as therapeutic targets in HCC, since one miR can have an effect on several genes involved in HCC. Also, since miRs do not have toxic effects like those of chemotherapy, they could be used successfully, and harmlessly to treat HCC.   In the concluding remarks, Khare et al. suggest that miR profiling of

high-risk populations could be helpful in finding SNPs which would be determinants of the onset of HCC. In future research, they hope to gain a better understanding of "regulatory networks" of miRs, and how they contribute to HCC.   Major Adjustments   The sentence in the introduction "The expression of miRs is also controlled at the post-transcriptional level…" seems unnecessary as that idea had just been mentioned a couple sentences above. Also, that sentence and the one following seem to be a smaller font than the rest of the paragraph.   In the third paragraph of the introduction, there are another couple of sentences that are of a smaller font than the rest of the words.   The last part of section two, where the authors describe "numerous reported studies…", there needs to be some sort of reference. It does not seem reasonable that the authors would explain other research methods without citing these.   In section 3.3, Khare et al. mention that "Tumor suppressive miRs… are lost in tumor tissues…". The idea of the miRs being "lost" is rather vague, it would be helpful to mention the mechanism or give an explanation of this phenomena.   The overall conclusion of the article mentions that with miR profiling in high-risk populations, specific miRs (and polymorphisms) and traits can be recognized, which "might be the first step toward preventing HCC". However, in the introduction it is mentioned that 90% of cases of HCC arise from cirrhosis and other risk factors. It does not seem logical to perform genetic high-throughput sequencing in order to profile miRs unless the researchers profile those with cirrhosis already, or those that have the specified risk factors. Testing "geologically dispersed populations" as the article suggests is very vague. The researchers need to be much more specific on which populations they hope to profile, otherwise it might just be assumed that random populations would be profiled.   Minor Adjustments   The abstract would benefit with a little more information, just more detail on the paper as a whole to entice the reader. For example, where