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Journal Name:	**Journal of Pharmaceutical Research International**
Manuscript Number:	**Ms_JPRI_76241**
Title of the Manuscript:	**Comprehensive Analysis and Assessment on Codon Usage Pattern of hemolytic genes from different strains of Leptospira interrogans**
Type of the Article	**Original Research Article**

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty'**, provided the manuscript is scientifically robust and technically sound.
To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

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PART 1: Review Comments

	Reviewer's comment	**Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)*
Compulsory REVISION comments	Authors should check spelling throughout the text, there are misspelled words or they have no space between words (for example: in the Background: Leptospira interroganswirulency) Tables and figures are not cited in the text There is no mention of where the 49 strains were obtained or what serovar are they? The discussion does not have citations to support its results The Conclusions are incomplete. The section should briefly include the following: • State major result or results. • State whether your hypothesis was supported. • Say why the outcome is interesting. • Indicate the relevance of your findings to other published work. • Suggest future directions.	
Minor REVISION comments	This text should not be included in the introduction The codon usage bias for leptospiral gene SphH has been conducted in this paper with the help of statistical analysis. CUB analyses include RSCU (Relative Synonymous Codon Usage analysis) done to analyze the frequency with which codons in a particular gene occurs, ENC (Effective number of codon analysis) to examine to what extent codon usage in the gene is biased [10], Parity rule2 and Neutrality plot to understand if the driving evolutionary force of the gene SphHis mutational bias or natural selection [11]. R is a statistical software that was developed by Bell laboratories was used to aid the statistical analysis. R language along with R-studio, have good graphical user interface. It can be also used to generate statistically aesthetic plots. MEGA X is a phylogenetic analysis software, was used to edit and align the sequences of leptospirainterrogans. What is written in the abstract is not a conclusion, it seems material and methods **Conclusion**: In the dinucleotide frequency there was more abundance of GpG with frequency of 1.43. Out of seven ApG-containing codons five had RSCU values less than 0.6 suggesting that dinucleotide ApG were inhibited. The pearsons coefficient (R^2) was a positive 0.13 indicating that natural selection may have been the dominant factor, although mutation pressure had a small effect in determining the CUB of the SpHh gene.	
Optional/General comments		

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PART 2:

	Reviewer's comment	**Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)*
Are there ethical issues in this manuscript?	*(If yes, Kindly please write down the ethical issues here in details)*	

Reviewer Details:

Name:	**Erika Palomares Resendiz**
Department, University & Country	**Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico**