



SDI Review Form 1.6

Journal Name:	Journal of Advances in Microbiology
Manuscript Number:	Ms_JAMB_40780
Title of the Manuscript:	Screening and Characterization of Putative Probiotic Lactobacillus Strains from Honey Bee Gut (Apis mellifera)
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	<p>Please explain why only few genes (and how they were selected) (line 144....The genes involved in pH and bile salt tolerances that were screened are shown in Table 1.) potentially involved in pH and bile salt tolerance were investigated. HSP (even sHsp), CtsR, FtsH.....are all stress responsive genes even involved in bile salt tolerance. Furthermore, it not clear why only the Histidine decarboxylase gene (ref. 19) was analysed. The hdc gene is involved in histamine production.....other BA producing genes could be used as well as BA production (not only histamine) is associated to pH tolerance. The CpL gene as well, is only a piece of the Clp genes in LAB involved in stress tolerance.</p> <p>Table 7 and 16S LAB identification. Please, consider that the differences in 16S within the L. plantarum group are really few. To distinguish between L. plantarum and L. paraplantarum a recA analysis should be performed. Otherwise the strains are suppose to be putative species identification.</p>	<p>This part was aimed part to detect the genes involved in survival in the gastrointestinal tract. At this stage of our work, isolates were not yet identified. Then, literature review allowed us to easily have primers for the chosen genes. <i>The gtf and hdc</i> genes were chosen with a double purpose. At the same time as they involved in the survival in the gastrointestinal tract, they are also physiologically endowed with certain properties. The <i>gtf</i> gene codes for Glucan synthase, an enzyme that, in addition to its function in survival, is moreover implicated in beta-glucan production. This exopolysaccharide may modify the organoleptic properties of the food. It has also been acknowledged to have numerous health-promoting properties. However, none expression of <i>hdc</i> gene would be considered as a positive characteristic. In fact, ingestion of a large amount of histamine can cause serious health problems as we mention it in our discussion. Histamine is known as the most toxic biogenic amine that may be formed after decarboxylation of histidine by the enzyme histidine decarboxylase encoded by the <i>hdc</i> gene of certain bacteria. <i>clpL</i> because it was involved in gastrointestinal survival in several probiotic strains whose genomes have already been sequenced.</p> <p>Indeed, genetic heterogeneity in the <i>L. plantarum</i> group exists. We intend in our future studies, to perform among our <i>L. plantarum</i> strains to see if they are really dissimilar, DNA-DNA hybridization or <i>recA</i> gene sequencing comparison. Further study based on these assays could be performed in order to raise the existence or not of a genetic polymorphism between our identified isolates.</p>
Minor REVISION comments		
Optional/General comments	<p>Paper is, in general, well written (apart some physiological mistakes/grammatical errors). Experimental parts competently done, although authors should specify some choice.</p>	