Colorectal cancer (CRC) is the most common malignancy affecting the gastrointestinal tract. CRC is currently ranked as the third most commonly diagnosed cancer, and a leading cause of cancer-related deaths worldwide [1]. The involvement of microRNAs in cancers plays a significant role in their pathogenesis [2]. Present estimates suggest that nearly one third of all cellular transcripts may be regulated by the few hundred human microRNAs currently known to exist. Specific expressions of these microRNAs also serve as biomarkers for early CRC diagnosis but their laboratory/molecular identification is challenging and expensive [3]. Current diagnostic methods are invasive, more expensive, and lack specificity and sensitivity. Therefore, there is a need for a less invasive, more sensitive and disease-specific biomarkers for development of diagnostic tools to detect CRC in early stages.

Diagnosis of CRC often occurs when the disease is already in its advanced stage, and difficult to treat as it has metastasized to other organs. Moreover, conventional CRC detection strategies are invasive and cannot be used to detect benign tumors. Therefore, developing a standardized diagnostic approach that is less-invasive, sensitive, disease-specific and able to classify different CRC stages could increase patient’s survival rate.

The aim of the study was to identify microRNAs that are involved in the onset and progression of CRC and their target genes using in silico approach for CRC diagnosis.

3. Experimental design and Results

3.1. Identification of CRC microRNAs

<table>
<thead>
<tr>
<th>Total microRNAs (miRBase)</th>
<th>Reference microRNAs (Datasets for CRC microRNAs)</th>
<th>Query microRNAs</th>
<th>Redundancies removal (CH-HIT-EST)</th>
<th>Sequence similarity search (BlastN and CD-HIT-EST-2D)</th>
<th>Unique sequences (Text mining)</th>
<th>Candidate microRNAs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Candidate microRNA</td>
<td>Valued Fasta sequences</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td>miR-1</td>
<td>hsa-mir-195-5p: MIMAT0004414</td>
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<td>miR-5</td>
<td>hsa-mir-512c-3p: MIMAT0094771</td>
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</tr>
</tbody>
</table>

**Table 1:** Candidate microRNAs and their clusters.

3.2. Identification of targets and downstream analysis

**TARGET PREDICTION**

(TargetScan, miRDB, miRDiP)

- Unique microRNAs genes
- Unique CRC genes (ghCRC, CoReCG)
- Gene interaction analysis
- Genes with clear link to CRC

**ANALYSIS**

- Gene Prioritization: cBioPortal

**Phase 1 Analysis** (DAVID and KEGG pathway, and Interaction analysis)

**Phase 2 Analysis** (GO, prognostic, predictive, gene expression analysis)

3.3. MicroRNA target prediction: in silico approach

4. Discussion and Conclusion

Using in silico approaches, this study identified five candidate microRNAs with seven significant target genes. The patterns of expression obtained in their target genes relative to their microRNAs and their prognostic values could be inferred that patients with alterations in the microRNA prioritized target genes have significantly better overall survival than patients without these alterations. These could be further exploited and could potentially serve as a resource for explicitly selecting targets for diagnosis, drug development, and management of CRC. Although the study awaits molecular validation to conclude the biological fitness of these findings, the study indicated that the identified microRNAs and the hub genes (CTNNB1 and EGFR) stimulate better understanding of the molecular mechanisms underlying the development of CRC, and might be used as molecular targets and potential diagnostic biomarkers CRC treatment.

5. References