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Micronome revealed key microRNAs regulating cell proliferation in oral squamous cell carcinoma

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Introduction & Aim: Although substantial advancement has been achieved in the techniques and therapies related to oral squamous cell carcinoma (OSCC). Still, there is requisite for the novel approaches to reveal the various pathways and their regulators to treat the disease. We aim to find out key genes and miRNAs involved in cell proliferation and its positive regulation.

Method: To analyze the genes, differentially expressed OSCC genes were obtained from various published papers and databases. Gene ontology (GO) was done using STRING v.10 to obtain genes involved in cell proliferation (CP) and its positive (+ve) regulation. Top ten genes showing >80 interactions in the database were selected for further analysis. Experimentally validated miRNA-target interactions (MTIs) were retrieved from miRTarBase. The target genes of miRNAs were predicted by TargetScan. The key miRNAs and genes of cell proliferation and of positive regulation cell proliferation were identified using Cytoscape 3.3.0.

Results: Seventy-one (71) genes regulated cell proliferation in OSCC whereas 90 genes were found to be involved in positive regulation of cell proliferation. Micronome of CP and its +ve regulation revealed 306 common miRNAs. Gene ontology based network by STRING v.10 revealed *AKT1, MYC, EGFR, JUN, STAT3, BCL2, CCND1, TGFB1, PTEN, FGF2* and *VEGFA* as the important genes of CP and its +ve regulation. Finally, micronome of these eleven genes revealed mir-20a/b, mir-17, mir-106a/b, mir-195, mir-15a/b and mir-16 as the key regulation of cell proliferation in OSCC.

Conclusion: mir-20a/b, mir-17, mir-106a/b, mir-195, mir-15a/b and mir-16 are the key regulators of cell proliferation and could be the potential candidates for drug targets in OSCC.

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