Conclusion

An unbiased quantitative proteomics approach was employed to identify proteins secreted from HNSCC cells compared to normal oral keratinocyte. To my knowledge the current study reports the largest catalog of secreted proteins from HNSCC cells using iTRAQ-based quantitative proteomics approach. Through this study I was able to identify a number of novel proteins which were not studied in context of HNSCC. Few of the candidates were validated using immunohistochemistry and western blot. These markers can be tested in the sera of HNSCC patients using assays such as multiple reactions monitoring (MRM) or enzyme-linked immunosorbent assay (ELISA) to determine the diagnostic potential of these proteins for the early detection of HNSCC leading to improved patient outcome. Quantitative proteomics is also helpful for identification of differentially expressed proteins from cell lines which could crucial for discovery of biomarkers for prognosis, prediction to drug response and therapeutic interventions. HMGB2 may serve as a predictive biomarker between responders and non-responders to chemotherapy in HNSCC. Further studies can be done to understand the exact mechanism of modulated sensitivity to cisplatin and 5-FU by siRNA mediated silencing of HMGB2. Animal model based studies would be helpful to understand the role HMGB2 in HNSCC chemoresponsiveness and targeting HMGB2 might improve the HNSCC patient outcome effectively.