proceedings

MDPI

Extended Abstract

Prognostic Role of DNA Methylation Analysis from Oral Brushing in Oral Squamous Cell Carcinoma †

Valentina Russo [1,*], Jacopo Lenzi [2], Roberto Rossi [1], Luca Morandi [3], Achille Tarsitano [4], Andre Gabusi [1], Chiara Amadasi [1], Dora Servidio [1] and Davide B. Gissi [1]

[1] Section of Oral Sciences, Department of Biomedical and Neuromotor Sciences, University of Bologna, 40125, Bologna, Italy; roberto.rossi30studio.unibo.it (R.R.); andrea.gabusi3@unibo.it (A.G.); chiama90@live.it (C.A.); dora.servidio@gmail.com (D.S.); davide.gissi@unibo.it (D.B.G.)

[2] Section of Hygiene, Public Health and Medical Statistics, Department of Biomedical and Neuromotor Sciences, University of Bologna, 40126 Bologna, Italy; jacopo.lenzi2@unibo.it

[3] Functional MR Unit, Department of Biomedical and Neuromotor Sciences, IRCCS Istituto delle Scienze Neurologiche di Bologna, University of Bologna, 40139 Bologna, Italy; luca.morandi2@unibo.it

[4] Section of Maxillo-Facial Surgery at S. Orsola-Malpighi Policlinic, Department of Biomedical and Neuromotor SciencesUniversity of Bologna, 40138, Bologna, Italy; achille.tarsitano2@unibo.it

* Correspondence: valentina.russo15@studio.unibo.it; Tel: +39-051-208-8123

† Presented at the XV National and III International Congress of the Italian Society of Oral Pathology and Medicine (SIPMO), Bari, Italy, 17–19 October 2019.

Published: 11 December 2019

1. Introduction

The aim of this study was to investigate the prognostic role of methylation profile of 13 genes starting from oral brushing collected in a group of patients affected by oral squamous cell carcinoma (OSCC). To this purpose, we analyzed the relationship between the methylation profile of each gene and the appearance of a loco-regional relapse in a study sample of OSCC patients. We also calculated a unique prognostic score with the aim to predict survival of OSCC patients.

2. Materials and Methods

The study sample included 37 consecutive OSCC patients with a median follow-up period of 22 months (range 1–59).

Brushing cell collection was performed prior to any cancer treatment in the tumor mass. Two hundred forty-five CpG islands from a set of 13 previously described methylated genes in OSCC (ZAP70, KIF1A, LRRTM1, PARP15, FLI1, NTM, LINC0059, EPHX3, ITGA4, MIR193, GP1BB, MIR296, TERT) [1] were investigated by bisulfite-Target Next Generation Sequencing (NGS) using MiSEQ platform (Illumina, San Diego, CA, USA).

Univariable Cox proportional hazards models were used to analyze the association between each of the CpG sites and survival. Then, a Cox proportional hazards lasso model was used to select the prognostic markers of the candidate CpG sites. Lastly, a cross-validated prognostic score was computed for each patient, based on individual values of methylation and non-zero regression coefficients. Kaplan-Meier estimates were calculated to compare the survivor functions of the two groups (High-risk of relapse group and low-risk of relapse group). Statistical significance of the log-rank test was set at 0.05.

3. Results

Nine out of 37 (24%) OSCC patients developed a secondary neoplastic manifestation during the follow-up period. Cox proportional hazards lasso model selected 5 CpG sites significantly related with appearance of a second neoplastic event (ZAP70-position1, FLI1-position3, FLI1-position4,

ITGA4-position4 and MIR193-position3). A prognostic score for each patient was calculated, and OSCC patients were divided based on risk of relapse (high and low risk): 8/18 high-risk group patients developed a local relapse with respect to 1/19 low-risk group patients, this difference being statistically significant ($p < 0.001$).

4. Conclusions

Our study showed that a prognostic score based on DNA methylation analysis might be a useful indicator in surgical decision making, even if a larger cohort of patients is necessary to confirm these preliminary data.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Morandi, L.; Gissi, D.; Tarsitano, A.; Asioli, S.; Gabusi, A.; Marchetti, C.; Montebugnoli, L.; Foschini, M.P. CpG location and methylation level are crucial factors for the early detection of oral squamous cell carcinoma in brushing samples using bisulfite sequencing of a 13-gene panel.Clin Epigenetics. *Clin. Epigenet.* **2017**, *9*, 85