**ABSTRACT**

Recent advances have made it possible to classify tumors not solely on their morphological phenotype, but also their molecular profile. Fibroblast growth factor receptor 1 (FGFR1) amplification is one of the most common genetic alterations in human cancers and has been reported in a variety of tumor types, including squamous cell carcinomas (SCCAs) of the lung. More recently, it has also been identified in SCCA of the head and neck. Increased FGFR1 copy number has been shown to be a predictor of poor outcomes. FGFR1 is an actionable therapeutic target for lung SCCAs and small-molecule FGFR inhibition therapy is currently in clinical trials. In addition to providing new therapeutic options to patients, they often have a better toxicity profile compared to conventional chemotherapies.

**METHODS**

This retrospective study employed formalin fixed paraffin embedded (FFPE) laryngeal SCCA tissue samples selected from the University of Mississippi Medical Center's Pathology Department. DNA was isolated from FFPE samples using the Qiagen Allprep kit and concentrations were determined using a nanodrop spectrophotometer. FGFR1 copy number (CN) was determined with respect to the reference gene RPPO using a primer/probe assay (Bio-Rad Inc., Hercules, CA). As recommended, DNA (15-50 ng/reaction) was fragmented by Hael1 enzyme digestion and assayed in duplicate (Bio-Rad Inc.). A droplet digital polymerase chain reaction (ddPCR) utilizing a water-in-oil emulsion droplet system employing multiplexed primer/probes was used for absolute quantitation.

**RESULTS**

A total of 78 FFPE samples were obtained for determination of FGFR1 copy number. Two 20 micron samples of tissue were obtained from each tissue block. DNA was isolated from 74 samples in sufficient concentration (≥ 10 ng/µl) and condition for CN analysis (Figure 1). Of these, 41.9% were from Caucasians, 55.4% from AA’s (African Americans), and 2.7% from Native Americans. The majority of specimens, 85%, were from males. This included Caucasians (27males, 4 females), AA (33 males, 8 females), and Native Americans (2 males).

As shown in Table 1, FGFR1 CN analysis revealed: 54% of samples had CN greater than the reported normal value (1.8-2.2 CN), and 41% of samples had CN values greater than 3 (range 3-9). As shown in Table 1, the mean and standard deviation FGFR1 CN was 4.17 ± 1.46 (range 2.21-9.07) CN for AA patients and 3.78 ± 1.85 (range 2.22-9.71) CN for Caucasian patients. Further, 60.9% of specimens from AA demonstrated increase FGFR1 CN compared to 48.4% from Caucasians. Of note, 3/74 samples had CN less than 2 (0.79, 1.7, and 1.2 CN).

**DISCUSSION**

FGFR1 amplification occurs in AA’s as well as Native Americans. The overall incidence of amplification is higher than previously reported. Future research will analyze the relationship of smoking and stage of diagnosis.

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**REFERENCES**


