

## GS02-2 **Comprehensive epigenetic analysis of oropharyngeal cancer**

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**Background:** The incidence of oropharyngeal squamous carcinoma (OPSCC) associated with Human Papilloma Virus (HPV) is dramatically increasing, mainly due to infection of HPV 16. Whereas HPV-associated OPSCC patients significantly correlate with better prognosis, 36% patients show worse prognosis.

**Methods:** To stratify OPSCC into distinct molecular subtypes, reflecting these different clinicopathological features, we performed genome-wide DNA methylation analysis by Infinium 450k using 89 OPSCC samples, and compared the data with 81 OPSCC samples of the Cancer Genome Atlas (TCGA).

**Results:** Hierarchical clustering analysis classified OPSCC into four epigenotypes. Analysis of methylome data of 170 OPSCC including 81 cases of TCGA, revealed that HPV(+) OPSCC samples correlated with higher methylation accumulation ( $P < 1 \times 10^{-5}$ , Fisher's exact test), and that high methylation subtype significantly correlated with better prognosis ( $P = 0.004$ , log-rank test).

**Conclusion:** It is indicated that OPSCC is stratified into several molecular subtypes reflecting distinct epigenetic features and prognosis.