

論 文 要 旨

**Detecting Early-Stage Oral Cancer from Clinically
Diagnosed Oral Potentially Malignant Disorders by DNA
Methylation Profile**

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Abstract: Clinically, early-stage oral cancers are difficult to distinguish from oral potentially malignant disorders (OPMDs), and invasive tissue biopsy should be performed to determine a treatment strategy. Previously, we focused on gargle fluid as a noninvasive testing method and reported aberrant methylation in gargle fluid in patients with oral cancer. This study aimed to distinguish early-stage oral cancer from clinically diagnosed OPMDs using gargle fluid samples. We collected gargle fluid samples from 40 patients who were clinically diagnosed with OPMDs in the training set; among them, 9 patients were pathologically diagnosed with oral cancer. Methylation levels of 25 tumor suppressor genes were analyzed using the methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA) method. We found that a combination of six genes (TP73, CASP8, RARB, KLLN, GSTP1, and CHFR) could distinguish oral cancer from clinically diagnosed OPMDs with high diagnostic performance (area under the curve [AUC], 0.885; sensitivity, 77.8%; and specificity, 87.1%). Additionally, the panel comprised of the six methylated genes was validated in the test set. Furthermore, when compared with cytology testing, the panel could accurately detect oral cancer. The present methylated gene panel may serve as a novel biomarker for oral cancer.