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Background

Betel quid and its major ingredient, areca nut, are recognized by IARC as major risk factors in oral cancer development. Areca nut extract (ANE) exposure has been linked to OPMD progression and malignant transformation to OSCC. However, the detailed mechanism through which ANE acts on other cell types in the oral microenvironment to promote oral carcinogenesis remains elusive.

Methods

Immuno-profiling of macrophages associated with OPMD and OSCC was carried out by immunohistochemical and immunofluorescence staining. Phosphokinase and cytokine arrays and western blotting were performed to determine the underlying mechanisms. Transwell assays were used to evaluate the migration-promoting effect of ANE. Hamster model was finally applied to confirm the in vivo effect of ANE.

Results

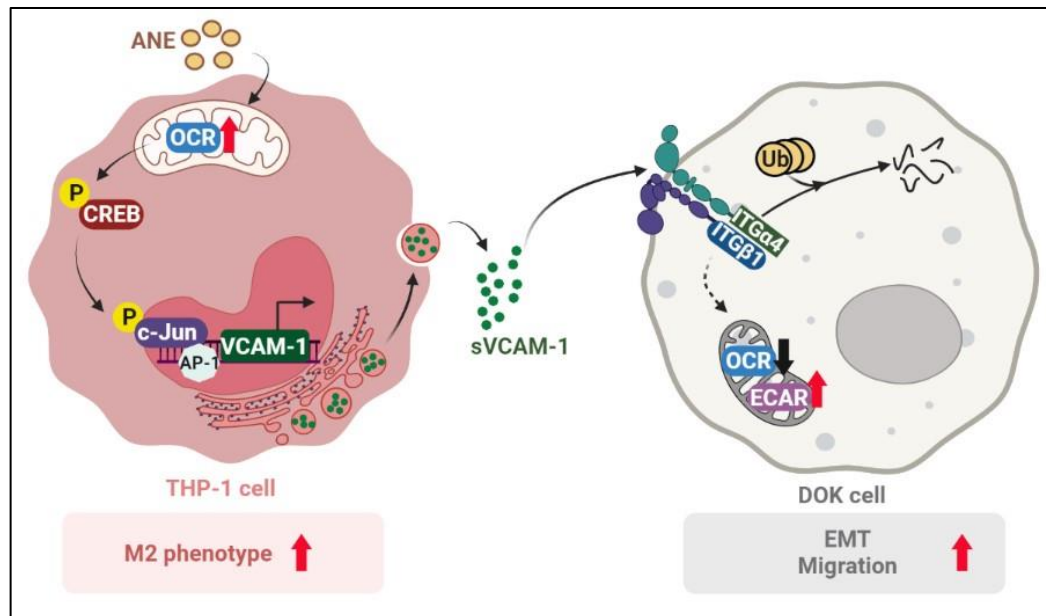
We reported that M2 macrophages positively correlated with oral cancer progression. ANE induced M2 macrophage differentiation, CREB phosphorylation and VCAM-1 secretion and increased mitochondrial metabolism. Conditioned medium and VCAM-1 from ANE-treated macrophages promoted migration and mesenchymal phenotypes in oral precancer cells. In vivo studies showed that ANE enhanced M2 polarization and related signaling pathways in the oral buccal tissues of hamsters.

Conclusion



Our study provides novel mechanisms for areca nut-induced oral carcinogenesis, demonstrating that areca nut promotes M2 macrophage differentiation and secretion of oncogenic cytokines that critically activate malignant transformation of oral premalignant cells.

Keywords: Areca nut, macrophage, OPMD, OSCC, mitochondrial metabolism



Schematic drawing for malignant transformation in oral premalignant cells via ANE-induced M2 macrophage differentiation.

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Research Team Introduction

Our research primarily focuses on the molecular mechanisms underlying cancer progression and the development of novel therapeutic strategies. We have explored the impact of the DNA repair protein Rad51 on tumor growth and metastasis in esophageal squamous cell carcinoma, identifying potential targets for therapeutic intervention. Currently, we aim to examine the cross-talk between senescence and cancer development. Given that aging plays a key role in cancer development and progression, understanding how defective DNA repair connects



senescence to malignancy could provide valuable insights. We believe our findings may help develop new precision medicine approaches and targeted therapies for cancer patients.

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