

Analysis of esophageal cancer with molecular genetics and molecular epidemiology

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【Outline of survey】

Esophageal cancer is one of the most difficult cancers to treat. To progress the curability, it is important to understand its biological behavior more and more. For this purpose, we decided to clarify the nature of esophageal cancer from the view points of single nucleotide polymorphism, gene expression profile, and epidemiologic findings. To obtain reliable data, we will analyze more than 1000 patients and more than 1000 control volunteers. The patients will be collected from National Cancer Center Hospital, Tokyo, Juntendo University Hospital, Tokyo, Saitama Cancer Center Hospital, Saitama, Kurume University Hospital, Fukuoka, and Kyushu University Hospital at Beppu, Oita.

【Expected results】

This study will clarify the important single nucleotide polymorphisms that are associated with esophageal cancer development. In addition, it will clarify the important gene expression profiles that are associated with poor prognosis, chemosensitivity, radiosensitivity, and so on.

【References by the principal researcher】

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【Term of project】 FY 2005-2009

【Budget allocation】 86,200,000 yen

【Homepage address】 http://www.mib-beppu.kyushu-u.ac.jp/MIB_hosp/byouinn.html