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Mining the biomarker from the blood of patients with endometriosis using proteomics and metabolomics approach

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Endometriosis is a gynecological disease characterized by the presence of endometrial tissue comprising the endometrium located outside the uterine cavity. It is often found at the peritoneum, ovary, or fallopian tube, and rarely at the pleura, lung, or brain. However, despite its prevalence, endometriosis is still poorly understood. The purposes of this study is to identify the differences in the protein expression between the endometriosis and non-endometriosis patients from the blood using the proteomics and metabolomics method in order to discover specific causable biomarker proteins and metabolites of endometriosis patients. In the profiling of the blood from women with or without endometriosis, 20 protein spots and 25 lipoidal hormones were found to be differentially expressed with changes in the density by two-fold or more with its down or up-regulation. Only 4 protein spots were found in the non-endometriosis patients. To confirm the possible involvement of these proteins and metabolites, we analyzed the change in these protein spots and metabolites from blood, classified by American Society for Reproductive Medicine (1997). In the classification system, the morphology of peritoneal and ovarian implants is categorized into four stages; minimal (stage 1), mild (stage 2), moderate (stage 3) and severe (stage 4). Among the candidate protein and metabolites, only the 4 protein spots and some lipoidal hormones decreased in stage 2, 3, and 4 compared to stage 1 of endometriosis. In the conclusion, this finding suggests possible involvement of these identified proteins in understanding the pathogenesis of endometriosis.

Biography

Dr. Hong-gu Lee has completed his Ph.D at the age of 33 years from Iwate University in Japan and research professor from Seoul National University. He has published more than 50 papers in SCI journals and 32 papers in domestic journals.