Correspondence

Re: Laïns et al.: Human plasma metabolomics study across all stages of age-related macular degeneration identifies potential lipid biomarkers

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TO THE EDITOR: The study by Inês Laïns et al. demonstrated that particular metabolites were identified in patients with age-related macular degeneration (AMD) when compared with controls, with most related to lipid pathways. The authors suggested these metabolites would be a biomarker for and related to the pathogenesis of AMD. However, we have several questions. First, did all the participants in this study have other systemic diseases excluded, such as hypertension and metabolic diseases, which would influence the blood lipid components? Furthermore, did the authors either measure the total blood lipid concentration, such as serum cholesterol levels, or confirm the varied metabolites were significantly different in this study via other methods? Notably, there would be some bias when using the single method of a broad-based mass spectrometry platform. In a previous study, these authors found only small changes in specific lipid moieties in with AMD using nuclear magnetic resonance spectroscopy. The results of the AMD biomarker found in the blood were different when compared with this study’s results.

Second, it was noted this study enrolled 30 controls and 90 patients with AMD; however, did the authors calculate the sample size? In their previous studies, they enrolled a total of 396 patients to test the plasma metabolomic profile in patients with AMD by nuclear magnetic resonance spectroscopy. Finally, the authors suggested the lower level of diacylglycerols and phosphatidylcholines found in the blood of patients with AMD imply a dysfunction of lipid metabolism in the retinal pigment epithelium. We wondered if the local dysfunction of lipid metabolism at the retinal pigment epithelium could be reflected in the blood.

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