Comparison of MicroRNA Expression in Aqueous Humor of Normal and Primary Open-Angle Glaucoma Patients Using PCR Arrays: A Pilot Study

We read with great interest the article published by Jayaram et al.1 The investigators used a cost-effective approach to assay the microRNA (miRNA) expression in aqueous humor (AH) of normal patients and those with primary open-angle glaucoma (POAG). They found that miRNA expression within the AH of patients with POAG differed from that of age-matched controls. Only a few studies investigated the expression of miRNA within human AH samples.2–4 In the past, we also tried to identify the miRNA expression profile from patients with glaucoma using next-generation small RNA sequencing. Unfortunately, the high throughput screening technique is restricted by the pooled AH samples. We congratulate the investigators for their excellent work on this field. They firstly used preamplification to increase RNA yield before further analysis. This technique has an important apocalypse meaning for our future research and we would like to make some contributions and criticisms related to this study.

The first one is about patient selection. Six patients with stable POAG and eight age-matched controls were recruited for this study. However, 57.1% (8/14) of volunteers were suffering from additional ocular comorbidities. In particular, three patients diagnosed with dry age-related macular degeneration (AMD) were enrolled. Numerous studies have analyzed miRNA dysregulation in patients with AMD and some miRNAs have been shown to be involved in AMD pathology.5 Although no one has studied the change in miRNA expression in AH of patients with AMD, that possibility cannot be ruled out. Therefore, we feared that the selected patients may confound the results.

Secondly, we think that miRNA expression within the plasma is of equal importance to that of AH. The investigators found that six of the most abundant miRNAs in AH of both groups also were detected in human plasma. However, Williams et al.6 tested the miRNAs profile in cell-free serum and plasma from pregnant women and their husbands using deep sequencing of barcoded small RNA cDNA libraries. The differences among the volunteers and the methods of separating and detecting miRNAs as well as analyses of biological information may account for the different results. Conjoint analysis of the altered expression of specific miRNAs in AH and plasma may provide more useful information about the relationship between the pathogenesis of glaucoma and miRNA. So, what do you think?

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References

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