

METTL23 mutation alters histone H3R17 methylation in normal-tension glaucoma

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Normal-tension glaucoma (NTG) is a heterogeneous disease characterized by retinal ganglion cell (RGC) death leading to cupping of the optic nerve head and visual field loss at normal intraocular pressure (IOP). The pathogenesis of NTG remains unclear. Here, we described a single nucleotide mutation in exon 2 of the methyltransferase like 23 (METTL23) gene identified in a three-generation Japanese NTG family. This mutation caused METTL23 mRNA aberrant splicing, which abolished normal protein production and altered subcellular localization. *Mettl23* knock-in (*Mettl23+/-* & *Mettl23G/G*) and knockout (*Mettl23+/-* & *Mettl23-/-*) mice developed a glaucoma phenotype without elevated IOP. METTL23 is a histone arginine methyltransferase expressed in murine and macaque RGCs. However, the novel mutation reduced *Mettl23* expression in RGCs of *Mettl23G/G* mice, which recapitulated both clinical and biological phenotypes. Moreover, our findings demonstrated that *Mettl23* catalyzed the dimethylation of H3R17 in the retina, and was required for the transcription of *pS2*, an estrogen receptor α target gene that was critical to RGC homeostasis.

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