

Same gene, different outcomes: Insights into the expanding landscape of RNA polymerase III disorders

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RNA polymerase III (Pol III) is a large enzymatic complex responsible for transcribing small noncoding RNAs. Pathogenic variants in multiple genes encoding Pol III subunits are known to cause neurological disorders such as hypomyelinating leukodystrophy (HLD), Wiedemann-Rautenstrauch syndrome (WRS), and spastic ataxia/paraplegia. These disorders, collectively known as POLR3-related disorders, primarily affect the central nervous system (CNS) and are caused by biallelic mutations to Pol III subunit genes.

Our group recently identified a patient with a de novo variant in the POLR3A gene encoding the largest Pol III subunit. The proband presented with early-onset, severe demyelinating Charcot-Marie-Tooth (CMT) disease which is a disorder of the peripheral nervous system (PNS). Through international collaboration, we identified ten additional patients from seven distinct families worldwide, all carrying monoallelic POLR3A variants linked to similar CMT-like clinical features. Notably, these patients do not show the cardinal CNS features typical for patients with biallelic POLR3-related disorders. Our functional genomics studies suggest that these newly identified POLR3A variants disrupt the Pol III complex assembly and cause downregulation of crucial RNA molecules transcribed by Pol III. Interestingly, the CMT-causing variants occur in close proximity to those causing biallelic POLR3-related disorders, yet they result in a distinct phenotype affecting the PNS rather than the CNS.

This discovery expands the clinical landscape of POLR3-related disorders beyond classical CNS phenotypes and underscores the importance of considering monoallelic POLR3A variants in the genetic evaluation of peripheral neuropathies, thus improving the diagnostic yield.