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Abstract Topic: - Molecular effects of genetic variation

Abstract Title: - Assessment of graft function of kidney transplant recipients harboring genetic predisposition for Thrombotic Microangiopathy.

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Aims: - Our aim was to identify the role and importance of systemic testing of complement genes in post renal transplant TMA patients

Methods: - In this single center, prospective cohort study, we have assessed the incidence of Post-Renal transplant TMA from 2019-2023. About 8.3% (22 patients) developed TMA and were followed-up for a period of 1 year to 4 Years. All the prospective transplant patients were subjected to complement gene testing, using Next-Generation sequencing (NGS) and Multiplex Ligation-dependent Probe Amplification (MLPA).

Results: - : The mean age of TMA patients was 36.3±12.7 Years, with 20 (91%) Male patients and 2 (9%) Female patients. Mean time for TMA development from the date of transplant was observed to be 34.5±58.4 Days. Moreover, similar genetic change is observed in patients with normal functioning grafts and TMA. No changes were observed in CFHR4, CFB, C3, MCP, amongst the TMA cohort. Additionally using NGS variant in CFI was observed in one patient. there was no significant difference of estimated GFR between patients having a mutation and those who do not have a mutation.

Conclusions: - The interpretation of complement genetics in post-transplant TMA is quite complex, as TMA is not a classical monogenic disease. Most notably, factors other than complement genes might play an important role in the development of post-transplant TMA.

Keywords: - : The mean age of TMA patients was 36.3±12.7 Years, with 20 (91%) Male patients and 2 (9%) Female patients. Mean time for TMA development from the date of transplant was observed to be 34.5±58.4 Days. Moreover, similar genetic change is observed in patients with normal functioning grafts and TMA. No changes were observed in CFHR4, CFB, C3, MCP, amongst the TMA cohort. Additionally using NGS variant in CFI was observed in one patient. there was no significant difference of estimated GFR between patients having a mutation and those who do not have a mutation.