

## Advances and Insights in Molecular Monitoring for Myeloproliferative Neoplasms

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Molecular monitoring has become a central component of disease assessment and therapeutic decision-making in myeloproliferative neoplasms (MPN). The identification of driver mutations in *JAK2*, *CALR*, and *MPL* has established a molecular framework that not only enables precise diagnosis but also supports risk stratification and individualized treatment strategies. Beyond these canonical lesions, the detection of high-molecular-risk (HMR) mutations—including *ASXL1*, *SRSF2*, *U2AF1*, *IDH1/2*, and *EZH2*—has further refined prognostic models by identifying patients at elevated risk for disease progression, leukemic transformation, and inferior survival.

Quantitative monitoring of variant allele frequencies (VAFs) across treatment courses provides an emerging tool to evaluate clonal dynamics, offering insights into disease biology and response. Reductions in driver-mutation burden may correlate with deeper responses to interferon-based therapies, whereas persistently rising VAFs may signal loss of disease control or therapy resistance. With the advent of next-generation sequencing and ultrasensitive digital PCR, measurable residual disease (MRD) assessment is becoming increasingly feasible, enabling earlier detection of molecular relapse and informing treatment modification.

Despite these advances, challenges remain. The relationship between molecular response and long-term clinical outcomes is still being clarified, and standardization of testing platforms and reporting thresholds is needed. Furthermore, clonal hematopoiesis, age-related mutations, and heterogeneous treatment exposures complicate interpretation in real-world settings.

This talk will highlight recent advances in molecular monitoring for MPN, explore its prognostic and therapeutic implications, and discuss how integrating molecular metrics with clinical and pathological features can improve disease management in the era of precision hematology.