Professor
Ruben A. Mesa

Division of Haematology/
Oncology, Mayo Clinic,
Arizona, US

WILL THE LATEST GENETIC DISCOVERIES HAVE AN IMPACT ON CLINICAL MANAGEMENT IN ET AND MF?

BIOGRAPHY

Ruben A. Mesa, M.D., is chair of the Division of Hematology/Oncology in the Department of Internal Medicine at Mayo Clinic and deputy director at Mayo Clinic Cancer Center in Arizona.

Prof. Mesa is committed to improving therapies and quality of life for patients with chronic myeloid disorders such as myeloproliferative neoplasms, including polycythemia vera, essential thrombocythemia and myelofibrosis.

He has been principal investigator or co-principal investigator in more than 45 clinical trials for patients with myeloproliferative neoplasms or other myeloid disorders.

ABSTRACT

The management of patients with myeloproliferative neoplasms (MPNs) is a complex, and ideally individualized approach in 2014. Patients with essential thrombocythemia (ET) and myelofibrosis (MF) have a broad spectrum of disease burden and clinical needs in terms of risk of vascular events, symptomatic burden, clinical phenotype, and risk of mortality from the respective diseases. Choice of therapy relies on many factors including an assessment of risk for ET – International Prognostic Score for ET (IPSET); and for MF – Dynamic International Prognostic Scoring System (DIPSS or DIPSS Plus), clinical phenotype (including symptom burden), and expectations of the efficacy of the therapy. Currently, our understanding of the molecular mutation profile (i.e. status on common mutations *JAK2* V617F or *CALR*, or uncommon – *MPL, ASXL1, IDH 1/2, TET2*, etc) is evolving and not yet mature enough to guide medication utilization (nor are included in current risk scores). As evidence of this latter statement, current response criteria both for MF (IWG-MRT – Tefferi A, *et al. Blood*. 2013) and ET (ELN – Barosi G, *et al. Blood*. 2013) do not require a molecular response for either complete or partial responses. Clinical decision making, and responses, remain primarily focused on demonstration of impact on clinical factors likely to beneficially impact the patient (changes in blood counts, spleen size, symptoms, reduction of vascular events, or even bone marrow morphology). The reason for excluding molecular response from overall response is (for the moment) although molecular status has been found to have certain prognostic value, we have no evidence (yet) that choice of therapy should be influenced by the presence/absence of a mutation. Additionally we do not yet have evidence that altering the allele burden of a certain mutation impacts clinical outcomes.

CONFLICTS OF INTEREST:

• SHIRE • INCYTE • GENETECH • LILLY • CELGENE • PROMEDIOR • GILEAD • CTI

Presentation references:

• Barosi G, *et al. Blood*. 2013;121:4778-4781• Geyer HL, *et al. Blood*. 2014;123:3803-3810 • Mesa RA, *et al. Cancer.* 2007;109:68-76 • Passamonti F, *et al. Blood*. 2012;120:1197-1201 • Passamonti F, *et al. Blood*. 2010;115:1703-1708 • Scherber R, *et al. Blood*. 2011;118:401-408 • Tefferi A, *et al. Leukemia*. 2013;27:1874-1881• Tefferi A, *et al. Blood*. 2013;122:1395-1398.