



The molecular landscape of myeloproliferative neoplasms associated with splanchnic vein thrombosis: Current perspective

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ABSTRACT

BCR::ABL1-negative myeloproliferative neoplasms (MPNs) are classically represented by polycythemia vera, essential thrombocythemia, and primary myelofibrosis. *BCR::ABL1*-negative MPNs are significantly associated with morbidity and mortality related to an increased risk of thrombo-hemorrhagic events. They show a consistent association with splanchnic vein thrombosis (SVT), either represented by the portal, mesenteric or splenic vein thrombosis, or Budd-Chiari Syndrome. SVT is also a frequent presenting manifestation of MPN. MPNs associated with SVT show a predilection for younger women, high association with *JAK2V617F* mutation, low *JAK2V617F* variant allele frequency (generally <10%), and low rates of *CALR*, *MPL*, or *JAK2* exon 12 mutations. Next-Generation Sequencing techniques have contributed to deepening our knowledge of the molecular landscape of such cases, with potential diagnostic and prognostic implications. In this narrative review, we analyze the current perspective on the molecular background of MPN associated with SVT, pointing as well future directions in this field.

1. Introduction

BCR::ABL1-negative myeloproliferative neoplasms (MPNs) are clonal myeloid neoplasms defined by the absence of *BCR::ABL1* fusion transcript and by the aberrant proliferation of differentiated myeloid cells in the bone marrow and peripheral blood. They are classically represented by Polycythemia Vera (PV), Essential Thrombocythemia (ET), Primary Myelofibrosis (PMF), either in the pre-fibrotic or overt fibrotic stage), and myeloproliferative neoplasms, unclassifiable (MPN-U) [1–4].

BCR::ABL1-negative MPNs are molecularly defined by alterations of the *JAK-STAT* pathway. *JAK2V617F* mutation leads to a constitutively activated *JAK/STAT* signaling; it is found in more than 95% of PV patients, and up to 60% of ET and PMF cases. *JAK2* exon 12 mutations are found in almost all *JAK2V617F*-negative PV cases while being absent in ET and PMF. On the other hand, *MPL* mutations, leading to an activation of the thrombopoietin receptor, are found in 5%–10% of patients with

ET and PMF and not in PV. Last but not least, calreticulin (*CALR*) mutations are found in up to 35% of ET and PMF cases, but again not in PV patients [1,3,5]. About 20% of ET and 10% of PMF cases do not show any of the above-mentioned driver mutations and are therefore termed “triple negative”; instead, they exhibit non-driver mutations as surrogate markers of clonal hematopoiesis [6]. Concomitant mutations in other genes, such as *TET2*, *ASXL1*, *IDH1/2*, *EZH2*, *SRSF2*, *U2AF1*, and *DNMT3A* can be variably encountered across *BCR::ABL1*-negative MPNs, especially within PMF in the overt fibrotic phase or MPN accelerated/blast phase [7]. *ASXL1*, *IDH1/2*, *EZH2*, *SRSF2*, and *U2AF1* mutations portend poorer prognosis as they guide disease progression and are therefore termed “High Molecular Risk” (HMR) mutations. Moreover, the acquisition of *TP53* mutation is a well-known leukemogenic factor in MPNs [1,8].

BCR::ABL1-negative MPNs show a consistent association with thrombosis, also involving unusual sites, such as cerebral veins and splanchnic vessels (SVT). SVT is an unusual thromboembolic

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phenomenon that manifests as portal (PVT), splenic, or mesenteric vein thrombosis, or Budd-Chiari syndrome (BCS), defined as hepatic venous outflow obstruction [9]. PVT is the most common SVT with a prevalence esteemed around 1 % [10], while BCS is, on the other hand, the least frequent (Fig. 1) [11]. *BCR::ABL1*-negative MPNs hold almost a 5-fold higher risk of venous thrombosis compared to controls [12], with a particular increase in SVT incidence; radiographic evidence of SVT is found in almost 1/3 of MPNs [13]. On the other hand, a *BCR::ABL1*-negative MPN diagnosis is made in 15 %–30 % of patients presenting with PVT and in up to 50 % of those with BCS [10,14,15].

This narrative review aims to describe current insights on specific molecular alterations of *BCR::ABL1*-negative MPNs associated with SVT (from now on, MPN-SVT), and their relationship with clinical and pathological features.

2. Epidemiology and natural history of MPN-SVTs

While other thrombotic events are more frequently reported in the elderly, MPN-SVT shows a distinct and unexplained predilection for female patients younger than 45 years old. Moreover, SVT risk is significantly higher within the first year of MPN diagnosis among younger patients compared to older ones [12]. This is probably due to a combination of environmental factors (i.e. oral contraceptive assumption), co-occurrence of thrombophilia disorders, low intensity of treatment, and/or higher prevalence of the *JAK2 46/1* haplotype, which is associated with a higher risk of MPN-SVT development and a presumed higher frequency among females [17–24]. The co-existence of hypercoagulable/thrombophilia disorders might have been an underestimated factor in the past, and it is found in almost 40 % of MPN-SVT [25].

Despite its significant association with MPNs, SVT risk is not uniformly distributed among different MPN subtypes. SVT shows in fact the strongest association with PV (37.1 % of MPN-SVT), followed by ET (34.4 %), PMF (17 %), and MPN-U (10.6 %) [25]. Accordingly, SVT prevalence among PV patients is significantly higher than in other MPNs (76 % vs. 26 %) [26], while PMF exhibits the lowest SVT prevalence, estimated at around 1 % [27]. However, MPNs should be suspected in all patients presenting with non-cirrhotic/non-malignant SVTs. BCS is associated with PV in 52.9 % of cases, with ET in 24.6 % and with PMF in 6.7 %, while PVT is associated with PV in 27.5 % of cases, with ET in 26.2 % and with PMF in 12.8 % [15].

Of interest, vascular complications, including SVT, seem to occur frequently within two years before MPN diagnosis, therefore assuming the role of a presenting sign of disease [28], especially in the context of MPN-U [16,29]. De Stefano et al. [30] have in fact identified SVT as the heralding manifestation of MPN in 58 % of their cohort composed of 181 patients. Interestingly, however, the reported association between MPN-U and SVT might be partly biased by the hypersplenism and hemodilution caused by the SVT itself, which hinders the expression of a full-blown MPN phenotype. Therefore, a consistent subset of MPN-SVT might be incorrectly termed as “unclassifiable” due to the inability to meet specific clinical criteria (such as hemoglobin and hematocrit thresholds for PV), an occurrence seen in about 40 % of MPN-SVT patients [15,16,30,31]. It should be noted, however, that tools such as red cell mass measurement and plasma volume measurement (with Cr^{51} -labeled RBC and I^{125} -labeled albumin respectively) consistently help in excluding hemodilution and/or hypersplenism and might be valuable in augmenting diagnostic accuracy for MPN-SVT, especially in the case of PV; unluckily, they are not commonly used and are available at few centers [32–34].

According to some authors [35], MPN-SVTs might have shorter age-corrected survival compared to conventional MPNs due to vascular complications (such as liver failure and major bleeding) and higher incidence of second cancers rather than to actual MPN progression. With specific regards to hemorrhagic complications, a multicenter study on chronic non-cirrhotic, non-tumoral PVT reported an incidence of newly developed varices of 2 % at 1 year and 22 % at 3 years, and a probability of worsening of existing esophageal varices of 13 % and 40 % at 1 and 3 years, respectively. The same study reported a probability of bleeding in patients with large esophageal varices of 9 % and 20 % at 1 and 3 years [36]. MPN-SVTs show high recurrence of thrombotic events, with an esteemed risk of 2.55 % per year; BCS, history of thrombosis, splenomegaly, and leukocytosis are all factors independently associated with SVT recurrence [30]. However, most studies agree on the general benign clinical behavior of MPN-SVT with low rates of leukemic evolution [25, 29,31,37–39]. A panoramic on epidemiologic and molecular features associated with MPN-SVT is offered in Fig. 2.

3. Pathogenesis of SVT IN *BCR::ABL1*-Negative MPNS

The exact mechanism leading to SVT in MPNs is yet to be fully understood. Higher hematocrit levels and increased platelet count (>400

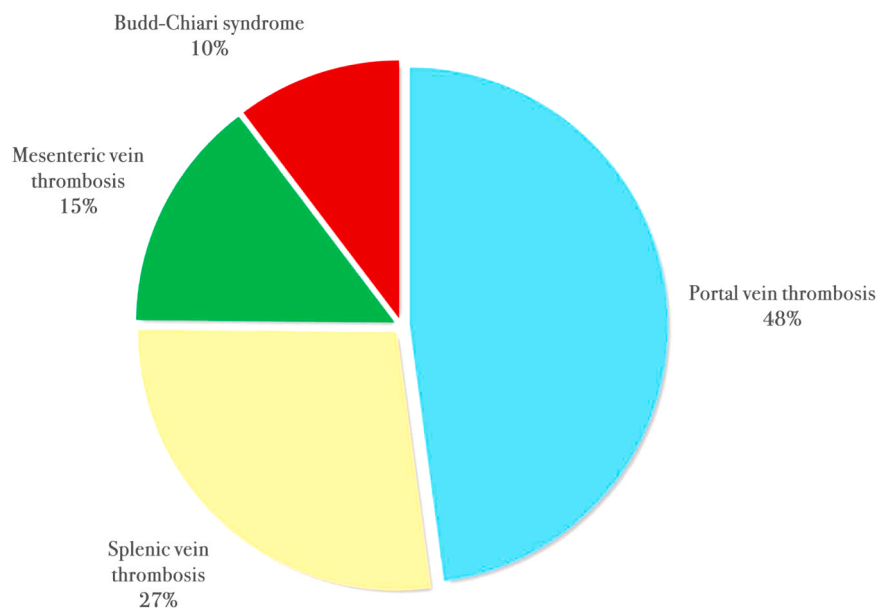


Fig. 1. Percentual distribution of different types of MPN-SVT based on the experience at our center [16].

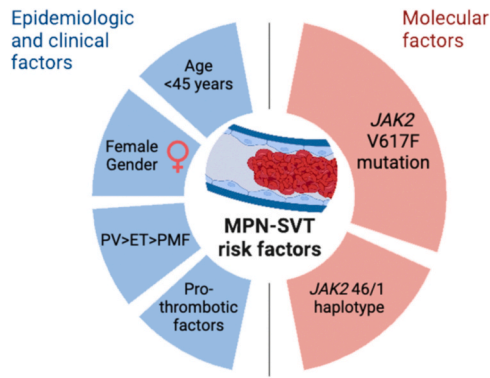


Fig. 2. Epidemiologic, clinical, and molecular features associated with MPN-SVT. (PV: polycythemia vera; ET: essential thrombocythemia; PMF: primary myelofibrosis). Image created with Biorender.com.

$\times 10^9/L$) have been predictably linked to thrombotic diathesis in MPN patients [40], thus representing important risk factors to be monitored. Hence, lowering hematocrit and platelet count represents one of the most important therapeutic interventions in MPNs. However, blood counts are not the only variable determining MPN-SVT. Several studies have demonstrated *JAK2V617F* mutation also in endothelial cells, which play a pivotal role in coagulation homeostasis [41–43]. This fascinating observation confirms a common cell of origin for hematopoietic and endothelial cells and provides further insights regarding the pro-thrombotic implications of *JAK2* mutations. Indeed, *JAK2V617F* mutations lead to an increased endothelial expression of von Willebrand factor (vWF) and P-selectin, which exhibit adjuvant functions in platelet adhesion and aggregation at sites of injury [44,45], and to a pro-coagulative endothelial phenotype as demonstrated by means of transcriptomic analysis [46].

Another significant aspect contributing to SVT might be represented by slow flow gradients within the splenic vein system [14] and the increase in circulating endothelial cells in MPN patients [47], which may both play additive pro-coagulative roles.

Lastly, several studies have highlighted a reduced bioavailability of nitric oxide (NO), increased cell adhesion molecules expression, and decreased fibrinolysis via *STAT* pathway activation in *JAK2*-mutated MPNs, deranging the hemostatic balance and therefore contributing to thrombosis [48–54].

Pathogenetic mechanisms involved in MPN-SVT are summarized in

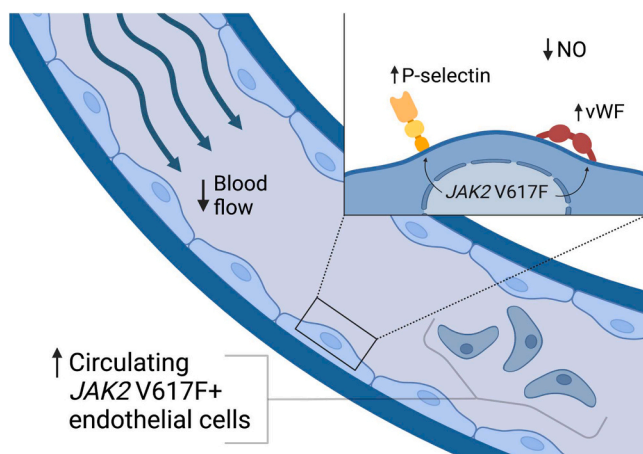


Fig. 3. Mechanisms involved in MPN-SVT pathogenesis include decreased blood flow in splanchnic veins, increase in circulating *JAK2*-mutated endothelial cells, and up-regulation of P-selectin and von Willebrand factor and downregulation of NO production by *JAK2* mutated endothelial cells. Image created with Biorender.com.

Fig. 3.

4. Molecular insights on *BCR::ABL1*-NEGATIVE MPNS associated with SVT

4.1. *JAK2* mutations in SVT: a molecular driver and a predictor of MPN?

JAK2V617F mutation is detected employing polymerase chain reaction (PCR) techniques in 4 %–32 % of SVTs, depending on different population samples [55–57], while its prevalence is significantly lower (less than 10 %) in non-SVT vascular complications. *JAK2V617F* mutation confers indeed a higher risk of SVT, with an odds ratio of 53.98 [55], and its screening reveals an underlying MPN in 17.1 % of BCS patients and 15.4 % of those with PVT [15]. Overt MPNs complicated with SVT seem to show even higher *JAK2V617F* mutation prevalence, ranging from 71 % to 100 % [25,58]. Moreover, the frequency of *JAK2V617F* mutation is significantly higher in ET and PMF associated with SVT compared to their control counterparts (85.1 % vs. 60.6 % and 84.6 % vs. 65.2 % respectively). No differences in this regard have been observed in PV patients, while MPN-U associated with SVT harbor the *JAK2V617F* mutation in almost 94 % of cases [25].

JAK2V617F variant allele frequency (VAF) has been studied by several authors in conventional MPNs with interesting results. First, PV patients show higher although heterogeneous *JAK2V617F* VAF compared to ET patients, with a median value of around 50 %. A VAF higher than 50 % in PV has been correlated by several studies with a higher risk of arterial and venous thrombotic events [59–61] and the development of secondary myelofibrosis [62]. On the other opposite of the spectrum, cases with low VAF (<1 %) might harbor additional genetic abnormalities such as *CALR* exon 9 or *MPL* mutations [63]. *JAK2V617F* VAF varies widely in MPN-SVT patients, with a mean value of 27 % [64]. Quite surprisingly, MPN-SVTs show a significantly lower *JAK2* allele burden compared to conventional MPNs. How *et al.* [65] found a median VAF value of 5 % in MPN-SVTs compared to a median of 36.3 % in MPNs ($p = 0.019$), with no patients showing a VAF greater than 10 %. This finding was subsequently confirmed by other authors [39,66,67]. In the large MPN-SVT cohort studied by Sant’Antonio *et al.* [25], however, median *JAK2V617F* VAF was 47.7% in PV, 29.5 % in ET, 30 % in overt PMF, 43 % in pre-fibrotic PMF, and 19.2 % in MPN-U. Moreover, the authors highlighted a higher *JAK2* allele burden among ET-SVT compared with ET controls (29.5 % vs. 22 %, $p = 0.029$), while results regarding other MPN-SVT phenotypes were not statistically significant.

JAK2V617F mutation is found in about 30 % of SVT without overt MPN [68,69]. In this regard, as mentioned in the epidemiology section, many authors have highlighted the inadequacy of peripheral blood count criteria for MPN diagnosis in the setting of MPN-SVT, mainly due to hypersplenism, bleeding from gastro-esophageal varices, and hemodilution: all these factors modify blood counts hampering the fulfillment of diagnostic clinical criteria and lead to underdiagnosis of MPN and/or overdiagnosis of MPN-U [16,25]. Hence, Yonal *et al.* [68] have suggested specific cut-off values for platelet ($>190 \times 10^9/L$) and white blood cell count ($>8.15 \times 10^9/L$) that may improve *JAK2V617F* diagnostic significance and therefore MPN diagnosis in SVT clinical setting: according to their study, these two parameters were the only ones that positively correlated with *JAK2V617F* mutational status. During the last twenty years, WHO classifications have progressively lowered PV hemoglobin/hematocrit thresholds and ET platelets cutoff to improve MPN diagnosis; however, the debate concerning the correct classification of *JAK2V617F* mutated SVTs without “overt” MPN is still ongoing. In this regard, the scientific community suggests performing *JAK2V617F* testing in the diagnostic workup of SVTs outside the cirrhotic or oncologic setting, as a useful tool to identify “latent” MPNs [64,66,70–75].

Of note, *JAK2* exon 12 mutations are extremely rare in MPN-SVT and have been documented only by means of Next-Generation Sequencing (NGS) or high-resolution melting (HRM) techniques (see paragraph 4.5)

[66,72,76,77].

4.2. The *JAK2* 46/1 haplotype and its role in MPN-SVT

As mentioned above, *JAK2* 46/1 (GGCC) haplotype on chromosome 9p.24.1 might have particular implications in MPN-SVT development. *JAK2* 46/1 haplotype is found in up to 45 % of the general population and is associated with a predisposition towards *JAK2* mutations, leading to a 5 times higher risk of MPN development. Interestingly, the 46/1 haplotype has also been linked to *MPL*-mutated MPNs, inflammatory diseases, and reduced defense against infections [22,78–80].

Different studies have explored the association between this haplotype and SVT or MPN-SVT. Colaizzo *et al.* have discovered a significantly higher frequency of the 46/1 haplotype among *JAK2*-unmutated SVTs [81], while Smalberg *et al.* demonstrated its higher expression among patients with *JAK2*-mutated BCS and *JAK2*-negative SVT associated with a documented MPN [21]. Additionally, Villani *et al.* observed a significantly higher prevalence of the 46/1 haplotype across MPN-SVTs compared to the normal population, while its frequency was not increased in idiopathic SVTs not associated with MPN [82].

In conclusion, *JAK2* 46/1 haplotype plays an important role as a susceptibility factor for MPN and therefore for MPN-SVT, while it is not presumably associated with SVT *per se* [83,84].

4.3. *CALR* mutations

Calreticulin (*CALR*) exon 9 mutations are the second most common driver mutation found in MPNs and determine a ligand-independent activation of the thrombopoietin receptor. *CALR* frameshift mutations lead to a novel C-terminal protein sequence, either represented by a 52-bp deletion (type 1 mutation) or a 5-bp insertion (type 2 mutation). Type 1 mutation is the most commonly found and presents a more favorable prognosis in PMF [1,85,86]. The prevalence of *CALR* mutations among MPN-SVT is deemed to be really low. Turon *et al.* [87] report a 1.9 % prevalence of *CALR* mutations among SVT patients and a 5.4 % prevalence in cases with an underlying MPN. Similar results have been reported in more or less wide cohorts by different authors [25,88–91]. In the work by Poisson *et al.* [88], all *CALR*-mutated patients had a spleen height ≥ 16 cm and a platelet count $>200 \times 10^9/L$; these criteria had a low positive predictive value but a 100 % negative predictive value and can be used to choose those patients who may benefit from *CALR* testing.

In light of these findings, *CALR* testing is not strongly recommended in the SVT diagnostic workup, with the obvious exception of *JAK2*-negative cases with features highly suggestive of MPNs as those reported by Poisson *et al.* [64,88,92]. Interestingly, a reason for *CALR*'s inconsistent association with MPN-SVT might be represented by lower thrombotic risk and lower platelet reactivity observed in *CALR*-mutated ETs [93–95].

4.4. *MPL* mutations

Missense *MPL* mutations represent the third most common molecular alteration in MPN. The most common *MPL* mutations (either W515L or W515K) lead to an amino acid substitution at the 515 position and to subsequent constitutive activation of thrombopoietin receptor signaling. *MPL* mutations in MPNs have been linked to older age at presentation and lower cell counts, although with no significant prognostic implications [96–98].

In a similar fashion to *CALR*, *MPL* mutations are infrequent among MPN-SVTs, with a presumed prevalence inferior to 1 % according to different cohorts and reports; these results probably reflect its overall low prevalence among all MPNs [25,64,72,76,99,100]. Bergamaschi *et al.* [76] identified 3/93 (3 %) SVT patients showing *MPL*W515 mutations: however, they were all confirmed ET and one harbored also a concomitant *JAK2*V617F mutation with *MPL* and *JAK2* VAF both inferior to 50 %.

4.5. Triple-negative cases and additional mutations. The role of Next-generation sequencing in MPN-SVTs

While triple-negative cases account for 10 %–15 % of MPNs, a precise evaluation of their contribution to the molecular background of MPN-SVTs is difficult, although some authors have reported a 3.5 % prevalence among MPN-SVTs [16].

Conventional quantitative polymerase chain reaction (qPCR) and digital droplet PCR (ddPCR) are the routinely used techniques to perform *JAK2*V617F evaluation in suspected MPNs, as they allow sensitive detection of low VAF. On the other hand, *CALR* and *MPL* mutations are usually detected by Sanger sequencing or PCR techniques in *JAK2*V617F-negative cases [101,102]. However, PCR does not permit the simultaneous complex screening of genetic variants, which is instead enabled by Next-Generation Sequencing (NGS). NGS has been applied to conventional MPNs with interesting results, although at present its use is still mainly considered for investigational purposes. NGS provides diagnostic improvements, especially in triple-negative cases, supplying molecular proof of clonal hematopoiesis [6,103–106]. Clonal markers alternative to classical driver mutations suggested for MPN diagnosis by the present classifications include *ASXL1*, *EZH2*, *TET2*, *DNMT3A*, *IDH1*, *IDH2*, *SRSF2*, and *SF3B1* mutations, and/or translocations such as those involving *ABL1* [1,4]. Many of these mutations, implied in spliceosome or chromatin remodeling, have been also linked to a more aggressive disease course in MPNs.

Likewise, NGS techniques have been suggested to improve the diagnosis of underlying MPNs in SVT patients lacking conventional MPN molecular alterations. Magaz *et al.* showed that 2/5 (40 %) cases originally categorized as triple negative MPN-SVT harbored *JAK2* exon 12 mutations [107]. Moreover, they highlighted additional mutations in *TET2*, *DNMT3A*, and *ASXL1* genes in more than 1/3 of SVT patients, supporting a putative role as predictors of thrombotic events. Indeed, *TET2* mutations might be an independent thrombotic risk factor in PV [108] and in the study by Magaz *et al.* patients with additional mutations in the above-mentioned genes exhibited a trend towards recurrent thrombosis. *TET2* mutations have been previously documented in almost 15 % of SVT patients [109,110]. However, despite being more frequent than *CALR* and *MPL* mutations in MPN-SVT, *TET2* alterations co-occur frequently with *JAK2*V617F mutations, and their contribution to thrombosis and prognosis is yet to be fully understood. More recently, in a single-center experience evaluating the clinical-morphological and molecular data of 58 consecutive patients with MPN-SVT, the authors showed a high prevalence of *TET2* mutations (28.5 %) compared with other previous studies (roughly 14 %) [111]. This evidence, together with a reported increased prevalence of cases with homozygous *JAK2*V617F mutations, which have been shown to precede those of *TET2* in the majority of subjects, allowed the authors to hypothesize a genetically determined prothrombotic phenotype in MPN patients affected by SVT.

In contrast with these findings, Kiladjian *et al.* [112] failed to highlight any additional mutations in triple-negative SVTs by means of NGS, although they were able to prove clonal hematopoiesis for 1 case out of 5 triple-negative MPN-SVT (20 %) harboring a *DNMT3A* mutation.

Ultra-deep NGS, which consists of multiple repetitions of genomic region sequencing, has been able to detect *JAK2*V617F and *MPL*W515R mutations in about 30 % of blood samples from an SVT cohort composed of 44 patients, including 7 mutations whose VAF was under the conventional NGS detection threshold of 2 % and a co-occurrence of both *JAK2* and *MPL* mutations [67]. Ultra-deep NGS has high sensitivity, and it might therefore predict MPN diagnosis and increase MPN prevalence among SVT patients by identification of low and ultra-low driver mutation allele burdens.

Finally, Debureaux *et al.* [39] illustrated a molecular profiling scheme for MPN-SVT delineating a high-risk subset of patients defined by the presence of at least one of the following: (a) *JAK2*-mutant allele burden ≥ 50 %, (b) chromatin, spliceosome or *TP53* mutations detected

by NGS. These patients showed worse event-free and overall survival, representing 29 % of the analyzed cohort. This elegant study parallels analogous results found in conventional MPN, where additional mutations affecting chromatin or spliceosome (i.e., *TET2*, *DNMT3A*, and *ASXL1* mutations) negatively impact survival [113]. NGS might therefore identify high-risk patients who might benefit from disease-modifying therapies. However, due to conflicting pieces of evidence, the prognostic value of *TET2* mutations in MPN has been significantly downplayed by current WHO and ICC classifications, which identify only *EZH2*, *IDH1*, *IDH2*, *SRSF2*, *ASXL1*, and *U2AF1* alterations as "high molecular risk" (HMR) mutations [1,4].

4.6. Practical recommendations on laboratory and molecular testing in MPN-SVTs

To summarize, considering the scientific evidence and expert recommendations, the initial assessment of suspected MPN-SVTs involves physical examination, complete blood counts, and ultrasounds or CT scans. These serve as the fundamental tools for disease characterization and the localization of SVTs, helping to point toward a potential MPN diagnosis. If the blood counts do not raise suspicion of MPN, additional tests such as red cell mass or plasma volume measurements, available in selected centers, can be useful in ruling out the effects of hypersplenism and hemodilution [34].

When confronted with clinical indicators suggestive of MPN-SVT, it is essential to conduct *JAK2* V617F testing using conventional PCR methods. A positive result necessitates a bone marrow biopsy for the classification of the underlying MPN. In cases of negative results, patients should be screened for *MPL*, *CALR* and *JAK2* exon12 mutations [72,88]. If any of these mutations is present, a bone marrow biopsy is always required for MPN characterization. However, if these tests yield negative results and there is a strong suspicion of an underlying MPN (indicated for example by a spleen height of ≥ 16 cm and a platelet count $>200 \times 10^9/L$), further investigations, ranging from bone marrow biopsy to NGS or Ultradeep NGS, may be considered to detect extremely low *JAK2* VAF or surrogate markers of clonality, with potential prognostic implications. It is however important to note that, as of now, NGS use in MPN is mainly limited to scientific research and is not currently applied to routine clinical practice. Testing for the *JAK2* haplotype 46/1 does not have clinical implications and is not recommended, either for individual cases or for familial screening purposes [34,39,64].

5. Treatment of MPN-SVTs

MPN-SVT treatment, although poorly defined, must be focused on two main tasks: (a) thrombosis management via anticoagulation, and (b) MPN management via cytoreduction.

5.1. Anticoagulation therapy

Anticoagulation is the main therapeutic intervention in patients with SVT and MPNs, as it may promote vascular recanalization and prevent thrombosis recurrence, and in the acute phase it does not differ from that of patients without MPNs [114]. Anticoagulation with full-dose low molecular weight or unfractionated heparin followed by vitamin K antagonists (VKA) should be initiated as soon as possible in MPN-SVT patients, with the caveat of patients showing frank portal hypertension (especially in BCS), for whom it may increase bleeding risk [14,115]. During past years, oral anticoagulation choices have been almost exclusively restricted to VKA; however, newer direct oral anticoagulants have been safely and successfully tested in SVT as well as in MPNs, and they might be preferable in terms of patient convenience. Anticoagulation therapy should be continued indefinitely in MPN-SVT, considering the presence of a permanent risk factor for thrombosis, such as underlying MPN [116,117], and patients should be monitored for portal hypertension and gastro-esophageal varices [14,118–120]. In

fact, in a multicenter prospective registry of SVT patients, anticoagulant drugs were used in almost all MPN patients [121], as recommended by the American College of Chest Physicians guidelines [122]. The addition of anti-platelet drugs such as aspirin or clopidogrel to anticoagulants is of little use, but it should be considered in patients with SVT recurrence while on anticoagulation or suffering from arterial thrombosis, although it may increase major bleeding occurrence [14,30,123]. In this context, it should also be considered that hemorrhagic events not related to portal hypertension occur in approximately 10 % of patients with cirrhosis treated with anticoagulants [124]. This rate does not appear to be higher than that observed in patients with cirrhosis and PVT not receiving anticoagulation nor in patients without cirrhosis receiving anticoagulation [124,125], although in cirrhotic patients treated with VKA, a PLT count $< 50 \times 10^9/L$ was predictive of bleeding [126]. Unexpectedly, bleeding events related to portal hypertension are less frequent in patients receiving anticoagulation than in those without anticoagulation, possibly due to a beneficial effect of anticoagulation on intrahepatic vascular resistance [124,125,127]. Therefore, the administration of anticoagulants does not imply more frequent screening for gastroesophageal varices nor more intense prophylaxis for portal hypertension-related complications [128].

Additionally, if there is clinical worsening despite anticoagulation, cytoreductive therapy, and supportive care, including sodium restriction, diuretic therapy, and paracentesis, patients with BCS should be considered for invasive procedures, such as angioplasty with or without stenting, or transjugular intrahepatic portosystemic shunt (TIPS) [116]. The latter might be applied to those patients with a high risk of liver failure secondary to SVT. Predictably, TIPS improves recanalization rates, especially in *JAK2*V617F mutated SVTs that show the lowest recanalization rates [129,130]. Liver transplantation should be considered an effective treatment for rapidly progressive BCS after failure of conventional strategy or portosystemic shunting, occurring in 10–20 % of patients [14,121].

5.2. Cytoreductive treatment

The second pillar of MPN-SVT management is MPN cytoreductive treatment. Cytoreduction is generally obtained through hydroxyurea, pegylated interferon, or *JAK1/2* inhibitor ruxolitinib, and should be adapted to specific MPN subtypes [131,132]. In detail, PV patients with SVT are classified at high risk of thrombosis recurrence, even if they are young and have only a moderate increase of hemoglobin or hematocrit [14]. Therefore, cytoreductive therapy is indicated, in addition to phlebotomy, with the goal of maintaining hematocrit $<45\%$ [133] and, possibly, PLT count $\leq 400 \times 10^9/L$ and WBC count $<10 \times 10^9/L$ [134]. According to current recommendations [131], either hydroxyurea (HU) or pegylated interferon (PEG-IFN) represent first-line cytoreductive therapy at any age. In PV patients resistant or intolerant to HU [135], both the *JAK1/2* inhibitor ruxolitinib and PEG-IFN can be appropriate second-line therapies [72,131,136–138]. Current guidelines also favor HU as first-line therapy for ET patients requiring cytoreduction, including those with SVT [131,139], while anagrelide or PEG-IFN are the recommended second-line therapies in case of resistance or intolerance to HU [131,136,140–142]. Regarding PMF, current prognostication systems are based on the risk of mortality rather than thrombosis [143–145]; consequently, the presence of SVT does not change the risk classification of PMF patients. Regardless of risk categories, if cytoreductive treatment is indicated to reduce leukocytosis or thrombocytosis, the first-line drug of choice is HU [131]. In the subgroup of PMF patients with SVT ruxolitinib could also represent an effective therapeutic option, reducing disease-related symptoms and spleen size, as well as the resistivity indices of the hepatic and splenic intraparenchymal arteries, with a substantial stabilization of esophageal varices grade [146]. This compares favorably with a prospective study of non-cirrhotic, non-tumoral PVT, in which the probability of worsening of existing esophageal varices at 1 year was 13 % [36].

That said, the most difficult context is represented by MPN-U patients with SVT who present with normal blood counts, therefore not satisfying all the diagnostic criteria required for another MPN, and for whom the need for cytoreduction is still uncertain [114]. Indeed, since approximately half of these patients will not develop an overt MPN during follow-up [16,25,29,111], and exhibit an indolent clinical course [147], there is no evidence to prescribe cytoreductive regimens [114, 132]. An expert panel identified the appropriateness of myeloproliferative-targeted therapy in patients with SVT-associated MPN as an unmet clinical need and provided methodological suggestions to address this issue [148].

It should also be kept in mind that, despite reaching MPN control, there is no evidence that cytoreductive therapies significantly impact SVT recurrence [146,149,150].

6. Conclusions and future perspectives

MPN-SVT represents a unique and fascinating subset of *BCR::ABL1*-negative MPN that poses diagnostic and therapeutic challenges. MPN-SVT molecular biology has been partly unraveled during the last few years, revealing a strong association with *JAK2V617F* mutation, although with a lower allele burden compared to conventional MPNs. On the other hand, *JAK2 exon 12*, *CALR*, and *MPL* mutations are exceedingly rare in MPN-SVT. Recent papers have successfully explored the application of NGS to SVTs, leading to diagnostic improvements and higher detection rates of MPNs among these patients. Although conventionally less sensitive compared to PCR, NGS identifies *JAK2* mutations and additional somatic mutations that might serve as proof of clonal hematopoiesis or molecular prognosticators, in a similar fashion to what is reported in conventional MPNs. Moreover, the application of ultrasensitive molecular techniques, such as Ultradeep NGS, might aid the recognition of SVT patients at risk of developing subsequent MPN (or with “incipient” MPN) by pointing out cases with low or “ultra-low” allele burden. Indeed, since early MPNs are presumably associated with low *JAK2V617F* VAF, low allele burden in MPN-SVTs reinforces SVT identification as a precocious manifestation of MPN. However, further studies are needed to deepen the contribution of low allele burden to MPNs in general and specifically to MPN-SVTs. Additionally, the combination of low/undetectable *JAK2V617F* allele burden with low blood counts secondary to SVT-related hypersplenism might dramatically hinder MPN diagnosis in SVT patients, or it may misleadingly suggest an MPN-U diagnosis. Therefore, the MPN-U category might also include a considerable group of MPN-SVTs. Further MPN-U series are required to fully uncover such aspects; moreover, the role of blood counts as well as *JAK2V617F* allele burden in specific MPN settings might need substantial revision, and techniques such as red cell mass and plasma volume measurements, although not easily accessible, might help to avoid underdiagnosing of MPN-SVT.

In summary, the integration of PCR, sequencing, and NGS methods has played a crucial role in uncovering the intricate molecular aspects of MPN and MPN-SVT. Continued research endeavors are expected to facilitate the development of a molecular theragnostic approach for MPN-SVT. This advancement will enhance diagnostic precision, identify prognostic and predictive factors, and ultimately aid in making informed decisions regarding treatment options.

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CRediT authorship contribution statement

Conceptualization, AI, UG, CP; methodology, CP, GL, DC; formal analysis, GL, DC; investigation, CP, GL; resources, CP, GL, DC, CB; data curation, CP, GL, DC; writing—original draft preparation, CP, GL; writing—review and editing, AI, UG, DC, CP, GL, CB; visualization, AI, UG,

CP; supervision, AI, DC, UG. All authors reviewed the results and approved the final version of the manuscript.

Declaration of Competing Interest

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