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**JAK2 46/1 HAPLOTYPE AND JAK2 VARIANT ALLELIC FREQUENCY
CORRELATE WITH THE DEVELOPMENT OF POLYCYTHEMIC
PHENOTYPE IN JAK2-MUTATED ESSENTIAL THROMBOCYTEMIA
PATIENTS**

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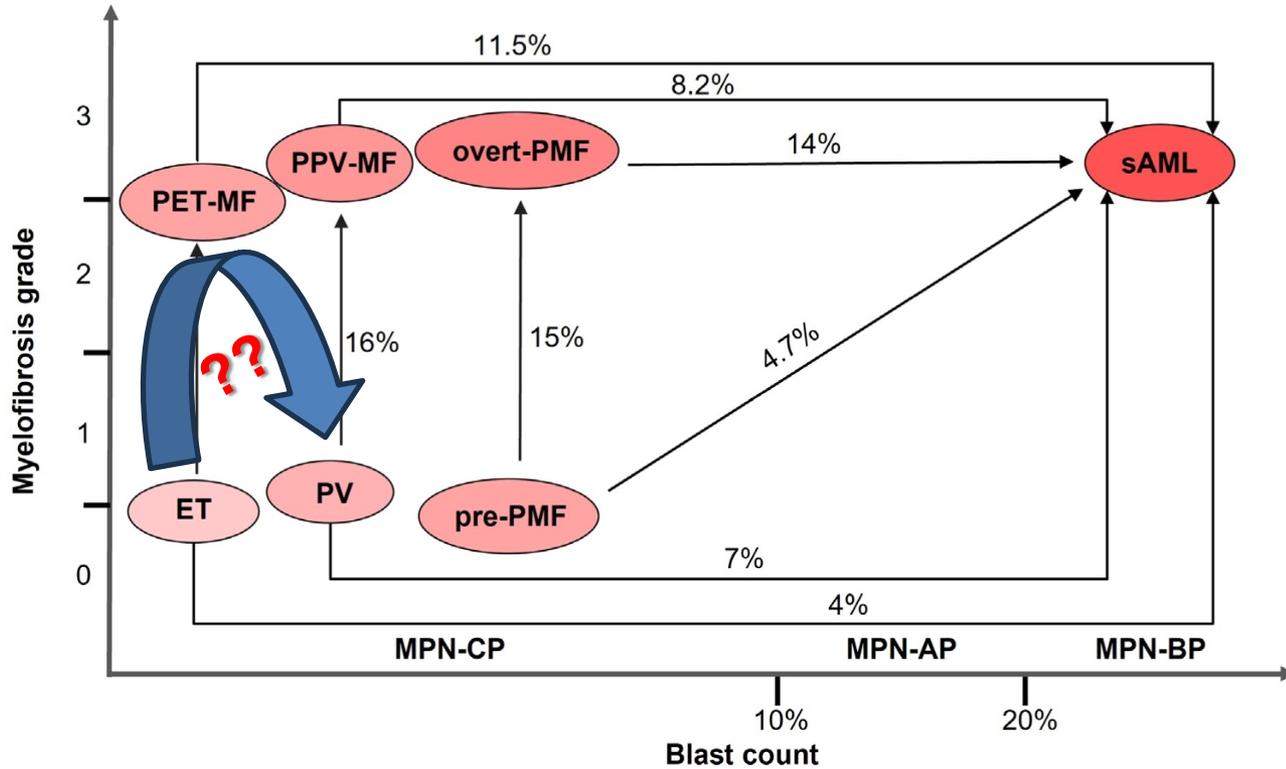
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Palazzo degli Affari



Disclosures of Giulio Capecchi

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
GSK							x
AOP							x

Clinical plasticity represents an intrinsic property of all MPNs



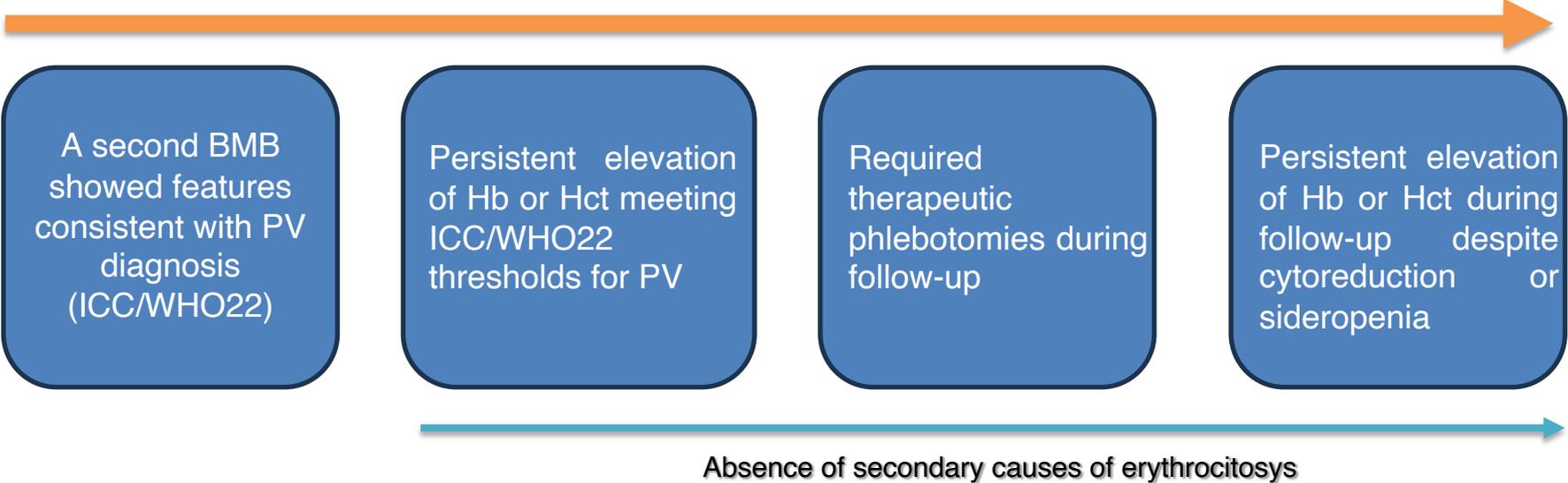
Aims

- To estimate the incidence of polycythemic phenotype development
- To identify distinctive clinical and molecular features both at diagnosis and during follow up
- To explore potential predisposing factors for the progression of ET to PV

Methods

- **411 *JAK2*-mutated** ET patients from the CRIMM Database were analyzed and compared

Definition of polycythemic phenotype

A flowchart illustrating the definition of a polycythemic phenotype. It consists of four blue rounded rectangular boxes arranged horizontally, connected by a light blue arrow pointing from left to right. Above the boxes is a long orange arrow pointing right. Below the boxes is a long light blue arrow pointing right, with the text 'Absence of secondary causes of erythrocytosis' centered underneath it.

A second BMB showed features consistent with PV diagnosis (ICC/WHO22)

Persistent elevation of Hb or Hct meeting ICC/WHO22 thresholds for PV

Required therapeutic phlebotomies during follow-up

Persistent elevation of Hb or Hct during follow-up despite cytoreduction or sideropenia

Absence of secondary causes of erythrocytosis

Results from 411 *JAK2*-mutated ET patients – clinical data

We identified **45** patients who developed a polycythemic phenotype, representing **11%** of the population

Variable	Study group (n = 45)	Control group (n = 366)	P value
Age at diagnosis years, median (range)	47 (17 – 77)	63 (19 – 92)	< 0 .001
Age at diagnosis >60 years, n (%)	6 (13.3)	210 (57.4)	< 0.001
Male gender, n (%)	15 (33.3)	118 (32.2)	1.0
WBC x10 ⁹ /L, median (range)	8.7 (4.5 – 13.9)	8.7 (4 – 23.4)	0.17
Hb g/dl, median (range)	14.2 (11.3 – 16)	14.5 (10 – 17.5)	0.17
PLT x10 ⁹ /L, median (range)	638 (449 – 971)	655 (460 – 1881)	0.21
MF progression, n (%)	2 (4.4)	10 (2.7)	0.63
AML Progression, n (%)	1 (2.2)	9 (2.5)	1.0
Deaths, n(%)	2 (4.4)	52 (14.2)	0.1

Variable	Study group (n=45)	Control group (n=366)	P value
Palpable splenomegaly, n (%)	2 (4.4)	41 (11.4)	0.20
Pruritus, n (%)	14 (31.1)	53 (14.7)	0.01
Constitutional symptoms, n (%)	2 (4.4)	17 (4.7)	1.0
Microvascular symptoms, n (%)	14 (31.1)	110 (30.4)	1.0
JAK2V617F VAF, % (DS)	23 (±12)	23 (± 14)	0.48

We found no significant differences in neither SMF-FS, BP-FS nor OS.

Aims

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Methods

- **411 JAK2-mutated** ET patients from the CRIMM Database were analyzed and compared
- 1:3 Propensity score matching was performed to identify **45 cases and 135 matched controls** (Age, FU duration, *JAK2 VAF*, gender)
- *JAK2 VAF*, NGS, and SNP analysis were performed

Results from matched analysis – clinical features

No clinical features showed any association with the evolution toward a polycythemic phenotype

Variable	Study group (n = 45)	Matched group (n = 135)	P value
Age at diagnosis, median (range)	47 (17 – 77)	48 (19 – 79)	0.63
Male gender, n (%)	15 (33.3)	49 (36.3)	0.86
WBC x10 ⁹ /L, median (range)	8.6 (4.5 – 13.9)	8.2 (3.5 -16.6)	0.79
Hb g/dl, median (range)	14.2 (11.3 – 16)	14.4 (11.7 – 17.2)	0.31
PLT x10 ⁹ /L, median (range)	638 (460 – 971)	631 (346 – 1500)	0.94
MF progression, n (%)	2 (4.4)	7 (5.2)	1.0
AML Progression, n (%)	1 (2.2)	4 (3.0)	1.0
Deaths, n (%)	2 (4,4)	11 (8.1)	0.52

Variable	Study group (n = 45)	Matched group (n = 135)	P value
Palpable splenomegaly, n (%)	2 (4.4)	11 (8.1)	0.52
Pruritus, n (%)	14 (31.1)	25 (18.5)	0.09
Constitutional symptoms, n (%)	2 (4.4)	9 (6.7)	0.73
Microvascular symptoms, n (%)	14 (31.3)	51 (37.8)	0.48

We found no significant differences in neither in SMF-FS, BP-FS or OS.

Results from matched analysis – Thrombosis

Patients in the study group experienced **fewer thrombotic events**, particularly after diagnosis

Variable	Study group (n = 45)	Matched group (n = 135)	P value
≥1 Thrombotic event (TE), n (%)	11 (24,4)	50 (37)	0.15
≥1 TE at/before diagnosis, n (%)	9 (20)	27 (20)	1.0
≥1 TE during follow up, n (%)	4 (8.9)	31 (23.0)	0.049
Arterial TE at or before diagnosis, n (%)	8 (17.8)	19 (14.1)	0.63
Arterial TE during follow up, n (%)	3 (6.7)	23 (17.0)	0.14

Arterial events: AMI (14), stroke (20), SAT (1), angina (1), TIA (5), PAD (19), other (2)

Venous events: DVT (11), SVT (4), Budd-Chiari (7), CVST (1), retinal thrombosis (9), other (1)

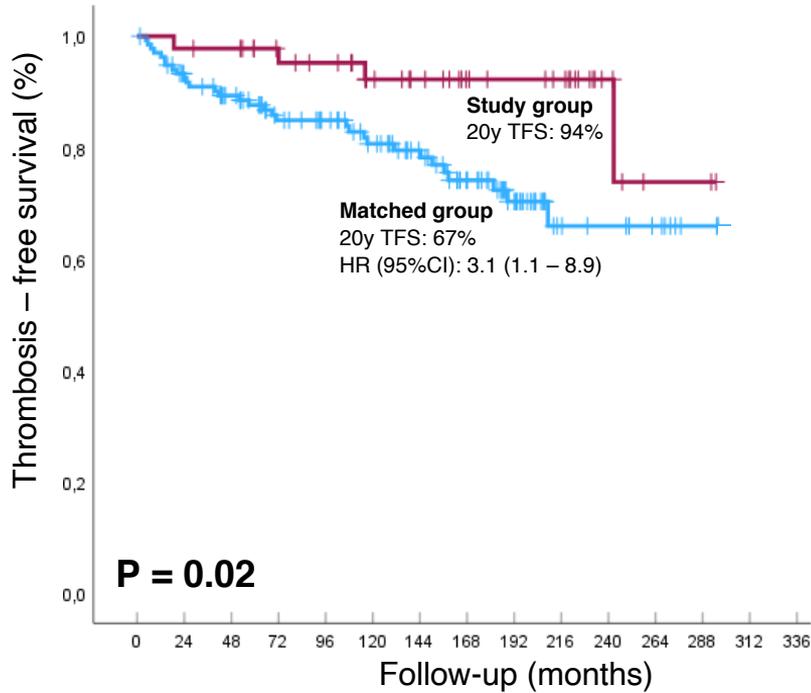
Variable	Study group (n = 45)	Matched group (n = 135)	P value
Venous TE at/before diagnosis, n (%)	1 (2.2)	8 (5.9)	0.45
Venous TE during follow up, n (%)	2 (4.4)	14 (10.4)	0.36
Bleeding events, n (%)	5 (11.1)	31 (23.0)	0.13
Major Bleeding, n (%)	3 (6.7)	13 (9.6)	0.76
Minor bleeding, n (%)	2 (4.4)	23 (17.0)	0.044

We found no differences in the use of **antiplatelet/anticoagulant** prophylaxis (100% vs 98.5% p = 1.0) nor **cytoreductive therapy** (53.3% vs 63.6% p = 0.34).



Results from matched analysis – Thrombosis

Patients in the study group experienced **fewer thrombotic events**, particularly after diagnosis





Results from matched analysis – *JAK2V617F* VAF

Patients in the study group showed a **significant increase in *JAK2V617F* VAF** over time

Variable	Study group	Matched group	P value
Baseline <i>JAK2V617F</i> VAF %, median (\pm SD); n=180	23 (\pm 12)	20 (\pm 12)	0.85
<i>JAK2V617F</i> VAF % on follow up, median (\pm SD); n=89	34 (\pm 28)	24 (\pm 17)	0.035
<i>JAK2V617F</i> VAF % annual increase, median (\pm SD); n=89	+ 6.1 (\pm 33)	+ 1.5 (\pm 14)	0.01
<i>JAK2V617F</i> VAF >50% at baseline, n (%); n=180	0 (0.0)	3 (2.2)	0.57
<i>JAK2V617F</i> VAF >50% at follow up, n (%); n=89	12 (30.8)	3 (6.0)	0.003

Median time to the second sample was comparable between the two groups 10.9 y vs 8.7 y p = 0.20

Results from matched analysis – *JAK2* 46/1

Patients showed no significant differences in *JAK2* 46/1 allele distribution

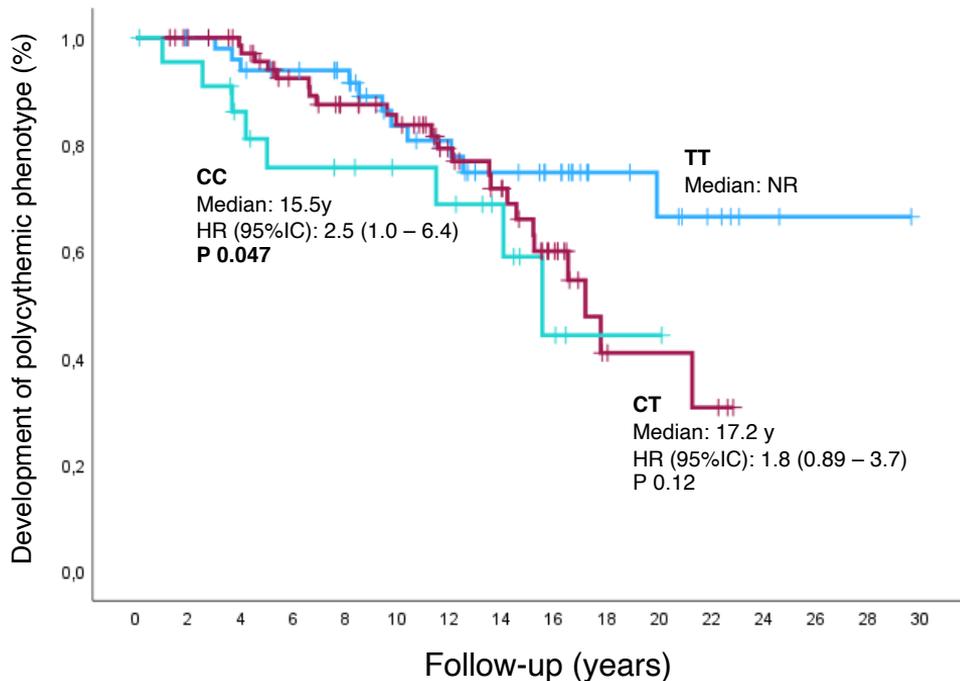
46/1 Status (n = 149)	Study group	Matched group	P value = 0.4
TT, n (%)	11 (26.2)	40 (37.4)	
CT, n (%)	23 (54.8)	52 (48.6)	
CC, n (%)	8 (19.0)	15 (14)	

46/1 Status (n = 149)	Study group	Matched group	P value
Non-TT, n (%)	31 (73.8)	67 (62.6)	0.25
CC, n (%)	8 (19.0)	15 (14)	0.46

- C = 46/1 allele
- T = non-46/1 allele

JAK2 46/1 correlates – development of polycythemic phenotype

Patients harbouring *JAK2* 46/1 alleles showed a faster development of the polycythemic phenotype



C = 46/1 allele
T = non-46/1 allele

Results from matched analysis – iron metabolism

Patients showed no significant differences evaluated iron parameters

	Study group	Matched group	P value
Ferritin ng/ml, Median (range) n = 140	61.5 (7- 276)	55.5 (9 – 564)	0.29

The HFE SNP rs79220007 has been previously linked to PV in genome-wide association studies.

	Study group	Matched group	P value
HFE variants, n (%) M = 140	1 (2.6)	4 (4.0)	1.0

All 5 patients presented HFE variants in heterozygosity

Results from matched analysis – NGS

Patients in the study presented **fewer additional mutation** at diagnosis

Variable	Study Group (n = 39)	Matched Group (n=26)	P Value
Additional mutation in myeloid gene, n (%);	9 (23.1)	9 (34.6)	0.40

Gene	Study Group (n=39)	Matched Group (n=25)	P value
<i>ASXL1</i> , n (%)	1 (2.6)	2 (7.7)	0.56
<i>SH2B3</i> , n (%)	2 (5.1)	1 (3.8)	1.0
<i>DNMT3A</i> , n (%)	1 (2.6)	2 (7.7)	0.56
<i>TET2</i> , n (%)	2 (5.1)	4 (15.4)	0.21
<i>BCOR</i> , n (%)	1 (2.6)	0 (0.0)	0.5
<i>SF3B1</i> , n (%)	1 (2.6)	1 (3.8)	1.0
<i>RUNX1</i> , n (%)	0 (0.0)	1 (3.8)	0.4

No variants were identified at diagnosis in the following genes: *EZH2*, *IDH1/2*, *SRSF2*, *N/K/H RAS*, *CBL*, *TP53*, *SETPB1*, *U2AF1*, *ZRSR2*, *CSF3R*, *PTPN11*

Results from matched analysis – paired NGS

Patients in the study presented **fewer additional mutation** at diagnosis, but **clonal progression** was frequent at the development of the polycythemic phenotype

Matched NGS analysis was available in 35 study group patients. **8 (23%) acquired ≥ 1 mutations** in myeloid genes.

TET2 and **TP53** mutations were acquired in 3 patients, **ASXL1** mutations in 2 patients and **SF3B1** in 1 patient each.

Two of these patients already presented an additional mutation at ET diagnosis.

One patient acquired more than one gene mutation (**TET2** and **SF3B1**).

Variable	ET diagnosis	Polycythemic phenotype	P Value
Additional mutation in myeloid gene, n (%); n = 35	8 (22.9)	14 (40.0)	0.2

Gene	ET diagnosis	Polycythemic phenotype	P value
ASXL1 , n (%)	1 (2.9)	3 (8.6)	0.61
SH2B3 , n (%)	2 (5.7)	2 (5.7)	1.0
TET2 , n (%)	2 (5.9)	5 (14.7)	0.21
SF3B1 , n (%)	1 (2.9)	2 (5.7)	1.0
TP53 , n (%)	0 (0.0)	3 (8.6)	0.24

Discussion

- This study investigated the characteristics of a large cohort of *JAK2V617F*-mutated ET patients who developed a polycythemic phenotype.
- The **incidence** of development of a polycythemic phenotype in our study **was 11%**, higher than what is reported in previous works.
- Patients who would develop a polycythemic phenotype **receive MPN diagnosis earlier** than controls, but clinical features are similar, except for **pruritus**.
- In matched analysis, study population experienced **fewer thrombotic events during follow up and longer Thrombosis-FS**, but no differences in clinical features and outcomes were noted

Discussion

- The development of a polycythemic phenotype was followed by an **increase of *JAK2V617F* VAF** with almost than one third of patients raising over 50% of VAF
- Patients harbouring ***JAK2 46/1* alleles** showed a faster development of the polycythemic phenotype
- **NGS** analysis showed a trend to a lower incidence of additional mutations in the study group, but clonal progression was frequent
- **Iron metabolism** showed no significant differences in the variables under investigation

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