Zagazig University Medical Journal
www.zumj.journals.ekb.eg

https://dx.doi.org/10.21608/zumj.2020.20514.1638 Volume 28, Issue 5, September 2022(999-1008)

**Manuscript ID** ZUMJ-1912-1638 (R1)
**DOI** **10.21608/zumj.2020.20514.1638**

**ORIGINAL ARTICLE**

# Abnormalities of Chromosome 17 in Patients with Myeloid Malignancies

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**Submit Date** 2019-12-06
**Revise Date** 2020-01-13
**Accept Date** 2020-01-18

## ABSTRACT

**Background:** chromosome 17 abnormalities are non-random cytogenetic events that occur in hematological and myeloid malignancies. Their prognostic impact is mostly related to alteration of tumor suppressor gene p53 by deletion or mutation. The aim of this study is to detect the frequency and types of chromosome 17 abnormalities and their prognostic effect in myeloid malignancies patients.

**Methods:** the study included 50 patients of newly diagnosed myeloid malignancies divided into three groups: group 1 included 28 AML patients, group 2 included 7 MDS patients and group 3 included 15 CML patients. All studied patients groups were subjected to history taking, clinical examination, routine laboratory investigations, conventional cytogenetic analysis and FISH for detection of chromosome 17 abnormalities.

**Results:** Chromosome 17 abnormalities were positive in 52% of myeloid malignancies patients; structural abnormalities were more frequent (40%) than numerical abnormalities (12%). Chromosome 17 abnormalities was detected in 67.9% of AML patients, 28.6% of MDS patients, and in 33.3% of CML patients.

**Conclusions:** Chromosome 17 abnormalities were frequent cytogenetic events that occur in various myeloid neoplasms and have poor prognostic impact related to alteration of tumor suppressor gene (*p53*).

**Keywords**
Chromosome 17 abnormalities, Acute myeloid leukemia, Myelodysplastic syndrome, chronic myeloid leukemia.

## INTRODUCTION

Myeloid malignancies are clonal disorders that affect hematopoietic stem cells (HSCs) and myeloid progenitor cells producing excessive proliferation, abnormal self-renewal, and/or differentiation defects. [1]
The major categories of myeloid neoplasms include myeloproliferative neoplasms (MPN), myelodysplastic syndromes (MDS), myelodysplastic/myeloproliferative neoplasms (MDS/MPN), acute myeloid leukemia (AML) and related neoplasms, mastocytosis, myeloid neoplasms with germ line predisposition, and myeloid/lymphoid neoplasms with eosinophilia.[2]

Chromosome 17 is a submetacentric autosome that span more than 83 million base pairs and contains between 1,200 and 1,500 genes. One of the most important genes located on the short arm of chromosome 17 is the tumor suppressor gene *(TP53)* that encodes a DNA-binding protein which responds to DNA damage by either stimulating DNA repair or inducing cell death. Loss or inactivation of *TP53* plays a critical role in the pathogenesis of many cancers.**[3]**

The presence of chromosome 17 abnormalities confer poor outcome and resistance to chemotherapeutic drugs in several hematologic malignancies, the prognostic significance of

chromosome 17 abnormalities may be due to loss of 17p13.1 that harbor the genetic locus of the tumor suppressor gene (*TP53*) **[4]**. The aim of this study was reporting aberrations of chromosome 17 in patients with myeloid malignancies, and to assess their prognostic impact.

## METHODS

The study was conducted on 50 patients with newly diagnosed myeloid malignancies (27 males & 23 females), they were categorized into three main groups; AML, MDS, and CML. Informed written consents were obtained from all patients (or their guardians) to use their samples and clinical data in this study according to the Declaration of Helsinki using a dedicated form. Approval of Institutional Review Board (IRB) was obtained ahead of study.

All studied patients groups were subjected to the following: history taking, clinical examination, Routine Laboratory Investigations including; CBC, liver and kidney function tests, (LDH), (ESR) (BM) examination supplemented with cytochemical stains, and finally immunophenotyping and flow-cytometric analysis.

**Specific laboratory investigations including:**

***Conventional cytogenetic analysis***

Samples from bone marrow aspirates or peripheral blood were cultured then harvested to obtain metaphase chromosomes, after that banding and staining were done. Finally microscope examination of 20 metaphases in order to detect numerical abnormalities and gross structural abnormalities.

***Fluorescence In Situ Hybridization using***

-Xcyting arm specific chromosome paint 17 (XCAP 17) (Metasystem, Germany).

-P53 deletion probe (cytocell, Camridge, UK ).

- PML/RARα (RAR) translocation, dual fusion probe (cytocell, Camridge, UK ).

After dropping of cell pellet, the slides were dehydrated using ethanol with three concentrations, then FISH probe were applied on the target cells, after that denaturation and hybridization was done using Dako Hybrite, then non-specific signals were removed by wash process. Finally DAPI counter stain was applied to visualize signals which was examined using Fluorcent microscope Olympus BX63.

## STATISTICAL ANALYSIS

All data were collected, tabulated and statistically analyzed using IBM SPSS Statistics for Windows, Version 20.0. Armonk, NY. Quantitative data were expressed as the mean ± SD and qualitative data were expressed as absolute frequencies (number) & relative frequencies (percentage). Continuous data were checked for normality by using Shapiro Walk test. For Independent samples Student's t-test was used to compare between two groups of normally distributed variables while. F (anova) test was used to compare between more than two independent groups of normally distributed variables. Kruskall Wallius test was used to compare between more than two independent groups of non-normally distributed variables. Percent of categorical variables were compared using Chi-square test or Fisher exact test when appropriate. All tests were two sided. P-value $< 0.05$ was considered statistically significant (S), p-value $<0.001$ was considered highly significant (HS) and p-value $\geq 0.05$ was considered statistically insignificant (NS).

## RESULTS

The demographic features and laboratory data of the studied patients groups are illustrated in tables (1) and (2)

Chromosome 17 abnormalities were positive in ( 26 out of 50) 52% of myeloid malignancies patients. Regarding frequency of various chromosome 17 abnormalities in myeloid malignancies patients; structural abnormalities were found in 20 patients representing (40%), they were more frequent than numerical abnormalities which were detected in 6 patients (12%). The most frequent among structural abnormalities was *t(v;17)* 18% followed by *t(15;17)* and *del 17(p13) (p53)* representing 8% for each and finally *Iso(17q)* 6% of myeloid malignancies patients. The most frequent among numerical abnormalities was *monosomy 17* representing 10% followed by *tetrasomy 17* which was present in 2% of patients.

Chromosome 17 abnormalities was detected in 67.9% of AML patients, 28.6% of MDS patients, and in 33.3% of CML patients with no statistically significant differences between the three groups.

The types of chromosome 17 abnormalities detected in the three patients' groups are illustrated in table (3) in which numerical abnormalities were more frequent in AML patients than CML patients, however not found in MDS patients. While structural abnormalities were detected in the three patients groups being more frequent among AML patients. In AML group the most frequent numerical abnormality was monosomy

17 and the most frequent detected structural abnormality was t(v;17). In MDS group only two patients had structural abnormalities one was t(v;17) and the other was iso(17q). In CML group only one patient had monosomy 17, while structural abnormalities were detected in four patients including del 17 (p13) (p53) and iso(17q) . There were statistically non-significant differences between the three groups regarding the distribution of chromosome 17 abnormalities.

Regarding association with standard prognostic parameters; AML patients with abnormal chromosome 17 had significant higher total leucocyte count also they were significantly related to unfavorable cytogenetic risk group, however no significant association with age, sex, hemoglobin concentration, and platelet count as showed in table (4).

MDS patients with chromosome 17 abnormalities showed no Statistically significant association with standard prognostic parameters such as; age, sex, WHO subtype, hemoglobin concentration, absolute neutrophil count, Platelet count, number of cytopenias, percent of bone marrow blast, and IPSS risk group as showed in table (5).

Patients with CML showed Statistically non-significant differences positive and negative for chromosome 17 abnormalities regarding; age, sex, spleen size, total leukocyte count, hemoglobin concentration, and platelet count as showed in table (6).

**Table 1**: Demographic data of the studied groups:

| | Group 1 AML (No=28) | | Group 2 MDS (No=7) | | Group 3 CML (No=15) | | F test | p |
|---|---|---|---|---|---|---|---|---|
| **Age Mean ± SD Range** | 44.3±15.3 (18-64) | | 57.14±9.5 (48-73) | | 42.7±13.7 (25-64) | | 1.9 | 0.14 (NS) |
| **Sex** | No | % | No | % | No | % | $\chi^2$ | 0.99 (NS) |
| Male | 15 | 53.6 | 4 | 57.1 | 8 | 53.3 | 0.086 | |
| Female | 13 | 46.4 | 3 | 42.9 | 7 | 46.7 | | |

SD: standard deviation NS: non-significant F: Anova test of significance $\chi$2: chi square No: number of subjects AML: acute myeloid leukemia MDS: myelodysplastic syndrome CML: chronic myeloid leukemia

**Table 2:** Laboratory data of myeloid malignancies patients groups (AML, MDS & CML)

| Variable | Group 1 AML (No=28) | Group 2 MDS (No=7) | Group 3 CML (No=15) | KW test | P |
|---|---|---|---|---|---|
| **Total leucocyte count (x109/L) Mean ± SD Range** | 35.6±29.7 (1-121.7) | 4.5±6.1 (1.2-20.2) | 159.2±127.6 (3.3-354.3) | 19.7 | <0.0001(S) |
| **Peripheral blood blasts(%) Mean± SD Range** | 61.1±27.1 (5-95) | 0.71±1.25 (0-3) | 7.3±7.5 (0-26) | 35.5 | <0.0001(S) |
| **Hemoglobin(gm/dl) Mean± SD Range** | 7.6±1.6 (4.6-11.7) | 7.5±0.79 (6.5 -8.7) | 9±1.97 (4.2-12.5) | F=4.045 | 0.024(S) |
| **Platelets(x109/L) Mean± SD Range** | 41.3±36.5 (9-140) | 147±171.8 (19-487) | 331±216 (45-826) | 25.9 | <0.0001(S) |
| **Bone marrow blasts (%) Mean± SD Range** | 71±19.3 (34-96) | 4.1±5.1 (0-11) | 12.3±14.8 (0-51) | 35.2 | 0.0(S) |
| **ESR (mm/hr) Mean± SD Range** | 95.5±26 (50-160) | 48±20.4 (20-80) | 61±32.2 (20-120) | 19.36 | <0.0001(S) |

| Variable | Group 1 AML (No=28) | Group 2 MDS (No=7) | Group 3 CML (No=15) | KW test | P |
|---|---|---|---|---|---|
| **LDH (IU/L) Mean± SD Range** | 697±308.7 (280-1321) | 167.4±29.9 (135-225) | 774±255.8 (354-1442) | 18.17 | <0.0001(S) |

KW: Kruskall Wallius test s: significant AML: acute myeloid leukemia
MDS: myelodysplastic syndrome CML: chronic myeloid leukemia

**Table 3:** Types of chromosome 17 abnormalities in myeloid malignancies patients groups (AML, MDS& CML)

| Chromosome 17 abnormalities | Group 1 AML (No=28) | | Group 2 MDS (No=7) | | Group 3 CML (No=15) | | $\chi^2$ test | P |
|---|---|---|---|---|---|---|---|---|
| | No | % | No | % | No | % | | |
| **Numerical abnormalities** | | | | | | | | |
| Positive | 5 | 17.9 | 0 | 0 | 1 | 6.7 | 2.3 | 0.3(NS) |
| Negative | 23 | 82.1 | 7 | 100 | 14 | 93.3 | | |
| **Monsomy 17** | | | | | | | | |
| Positive | 4 | 14.3 | 0 | 0 | 1 | 6.7 | 1.5 | 0.46(NS) |
| Negative | 24 | 85.7 | 7 | 100 | 14 | 93.3 | | |
| **Tetrosomy 17** | | | | | | | | |
| Positive | 1 | 3.6 | 0 | 0 | 0 | 0 | 0.18 | 0.67(NS) |
| Negative | 27 | 96.4 | 7 | 100 | 15 | 100 | | |
| **Structural abnormalities** | | | | | | | | |
| Positive | 14 | 50 | 2 | 28.6 | 4 | 26.7 | 2.66 | 0.26(NS) |
| Negative | 14 | 50 | 5 | 71.4 | 11 | 73.3 | | |
| **del 17 (p13)(p53)*** | | | | | | | | |
| Positive | 2 | 7.1 | 0 | 0 | 2 | 13.3 | 1.2 | 0.54(NS) |
| Negative | 26 | 92.9 | 7 | 100 | 13 | 86.7 | | |
| **t(15;17)** | | | | | | | | |
| Positive | 4 | 14.3 | 0 | 0 | 0 | 0 | 3.4 | 0.18(NS) |
| Negative | 24 | 85.7 | 7 | 100 | 15 | 100 | | |
| **t(v;17)** | | | | | | | | |
| Positive | 8 | 28.6 | 1 | 14.3 | 0 | 0 | 5.4 | 0.06(NS) |
| Negative | 20 | 71.4 | 6 | 85.7 | 15 | 100 | | |
| **Iso(17q)** | | | | | | | | |
| Positive | 0 | 0 | 1 | 14.3 | 2 | 13.3 | 4.1 | 0.13(NS) |
| Negative | 28 | 100 | 6 | 85.7 | 13 | 86.7 | | |

$\chi^2$: chi square test No: number of patients NS: non-significant AML: acute myeloid leukemia MDS: myelodysplastic syndrome CML: chronic myeloid leukemia
*del 17 (p13)(p53) that was present as a sole anomaly as all cases with iso(17q), monosomy 17 and some cases with t(v;17) were associated with del 17 (p13)(p53)

**Table 4:** Association between chromosome 17 abnormalities in group 1 (AML) patients and standard prognostic parameters

| Parameters | Chromosome 17 abnormalities | | | | Test | P |
|---|---|---|---|---|---|---|
| | Negative(No=9) | | Positive(No=19) | | | |
| | No | % | No | % | | |
| **Age (years)** | | | | | | |
| **<60** | 6 | 66.7 | 12 | 63.2 | Fisher Exact | 0.99(NS) |
| **≥60** | 3 | 33.3 | 7 | 36.8 | | |
| **Sex** | | | | | | |
| **Male** | 5 | 55.6 | 10 | 52.6 | Fisher Exact | 0.99(NS) |
| **Female** | 4 | 44.4 | 9 | 47.4 | | |
| **Hemoglobin** | | | | | | |
| **<8 gm/dl** | 4 | 44.4 | 12 | 63.2 | Fisher Exact | 0.43(NS) |
| **≥8 gm/dl** | 5 | 55.6 | 7 | 36.8 | | |
| **Total leucocyte count** | | | | | | |
| **<50 x10^9/l** | 6 | 66.7 | 5 | 26.3 | Fisher Exact | 0.0008**(HS)** |
| **≥50 x10^9/l** | 3 | 33.3 | 14 | 73.7 | | |
| **Platelet count** | | | | | | |
| **<80 x10^9/l** | 8 | 88.9 | 15 | 78.9 | Fisher Exact | 0.99(NS) |
| **≥80 x10^9/l** | 1 | 11.1 | 4 | 21.1 | | |
| **Cytogenetic risk group** | | | | | | |
| **Favorable** | 2 | 22.2 | 4 | 21.1 | $\chi^2$ =10.7 | 0.005 **(S)** |
| **Intermediate** | 6 | 66.7 | 2 | 10.5 | | |
| **Unfavorable** | 1 | 11.1 | 13 | 68.4 | | |

$\chi^2$: chi square test No: number of patients
NS: non-significant S: significant
HS: highly significant

**Table 5:** Association between Chromosome 17 abnormalities in group 2 (MDS) patients and standard prognostic parameters

| Parameters | Chromosome 17 abnormalities | | | | Test | P |
|---|---|---|---|---|---|---|
| | Negative (No=5) | | Positive(No=2) | | | |
| | No | % | (2) | % | | |
| Age (years) | | | | | Fisher Exact | 0.14(NS) |
| <60 | 4 | 80 | 0 | 0 | | |
| ≥60 | 1 | 20 | 2 | 100 | | |
| Sex | | | | | Fisher Exact | 0.99(NS) |
| Male | 3 | 60 | 1 | 50 | | |
| Female | 2 | 40 | 1 | 50 | | |
| WHO (2016)subtype | | | | | $\chi^2$=3.7 | 0.15(NS) |
| MDS-SLD | 2 | 40 | 0 | 0 | | |
| MDS-MLD | 2 | 40 | 0 | 0 | | |
| MDS-EB | 1 | 20 | 2 | 100 | | |
| Hemoglobin | | | | | Fisher Exact | 1.0(NS) |
| <10 gm/dl | 5 | 100 | 2 | 100 | | |
| ≥10 gm/dl | 0 | 0 | 0 | 0 | | |
| Absolute neutrophil count | | | | | Fisher Exact | 0.43(NS) |
| <1.8 x10^9/l | 2 | 40 | 2 | 100 | | |
| ≥1.8 x10^9/l | 3 | 60 | 0 | 0 | | |
| Platelet count | | | | | Fisher Exact | 0.43(NS) |
| <100 x10^9/l | 2 | 40 | 2 | 100 | | |
| ≥100 x10^9/l | 3 | 60 | 0 | 0 | | |
| Cytopenias | | | | | Fisher Exact | 0.99(NS) |
| 0-1 | 2 | 40 | 0 | 0 | | |

| Parameters | Chromosome 17 abnormalities | | | | Test | P |
|---|---|---|---|---|---|---|
| | Negative (No=5) | | Positive(No=2) | | | |
| | No | % | (2) | % | | |
| 2-3 | 3 | 60 | 2 | 100 | | |
| BM Blast percent | | | | | Fisher Exact | 0.29(NS) |
| <5% | 4 | 80 | 0 | 0 | | |
| ≥5% | 1 | 20 | 2 | 100 | | |
| | | | | | | |
| **IPSS risk group*** | | 80 | | | Fisher Exact | 0.99(NS) |
| Low risk MDS | 4 | | 1 | 50 | | |
| | | 20 | | | | |
| High risk MDS | 1 | | 1 | 50 | | |

*low risk MDS includes: low and intermediate-1 while high risk MDS includes intermediate-2 and high IPSS risk groups

$\chi^2$: chi square test No: number of patients NS: non-significant

MDS: Myelodysplastic syndrome, MDS-SLD: MDS with single lineage dysplasia, MDS-MLD: MDS with multi lineage dysplasia, MDS-EB: MDS with excess blast

**Table 6:** Association between Chromosome 17 abnormalities of group 3 (CML) and standard prognostic parameters

| Parameter | Chromosome 17 abnormalities | | | | Test | P |
|---|---|---|---|---|---|---|
| | Negative(No=10) | | Positive(No=5) | | | |
| | No | % | No | % | | |
| **Age (years)** | | | | | | |
| **<60** | 7 | 70 | 5 | 100 | Fisher Exact | 0.55(NS) |
| **≥60** | 3 | 30 | 0 | 0 | | |
| **Sex** | | | | | | |
| **Male** | 7 | 70 | 1 | 20 | Fisher Exact | 0.12(NS) |
| **Female** | 3 | 30 | 4 | 80 | | |
| **Spleen size** | | | | | | |
| **Moderate** | 3 | 30 | 2 | 40 | Fisher Exact | 0.33(NS) |
| **Huge** | 7 | 70 | 3 | 60 | | |
| **Total leukocyte count** | | | | | | |
| **<100 x10^9/l** | 4 | 40 | 3 | 60 | Fisher Exact | 0.61(NS) |
| **≥100 x10^9/l** | 6 | 60 | 2 | 40 | | |
| **Hemoglobin** | | | | | | |
| **<10 gm/dl** | 6 | 60 | 5 | 100 | Fisher Exact | 0.23(NS) |
| **≥10 gm/dl** | 4 | 40 | 0 | 0 | | |
| **Platelet count** | | | | | | |
| **<600 x10^9/l** | 9 | 90 | 5 | 100 | Fisher Exact | 0.99(NS) |
| **≥600 x10^9/l** | 1 | 10 | 0 | 0 | | |

No: number of patients

NS: non-significant

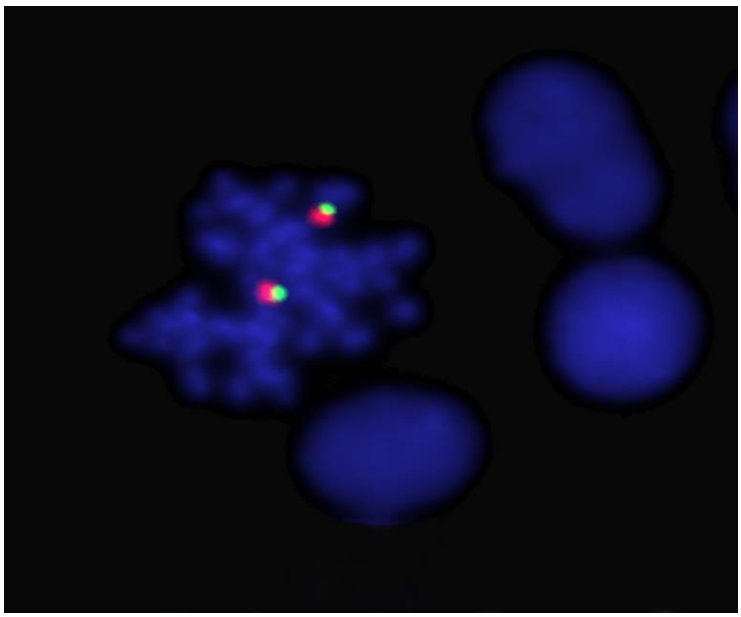

**Figure 1:** Normal chromosome 17 by arm specific probe

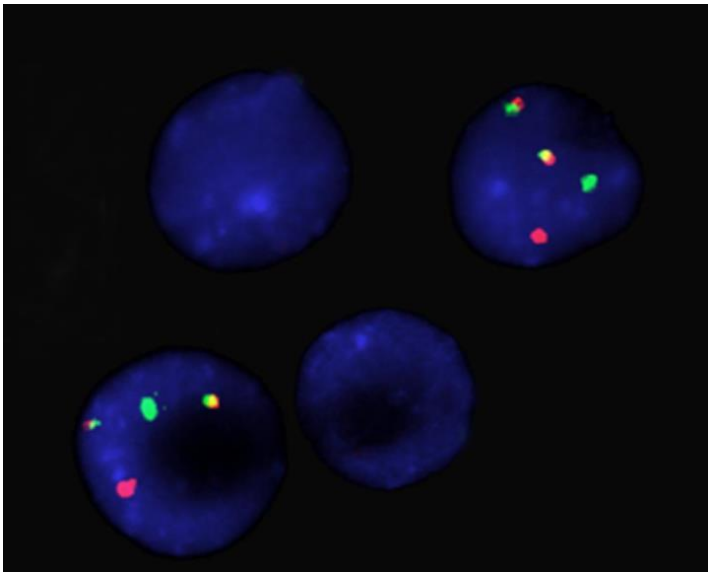

**Figure 2:** t(15;17) by dual fusion probe

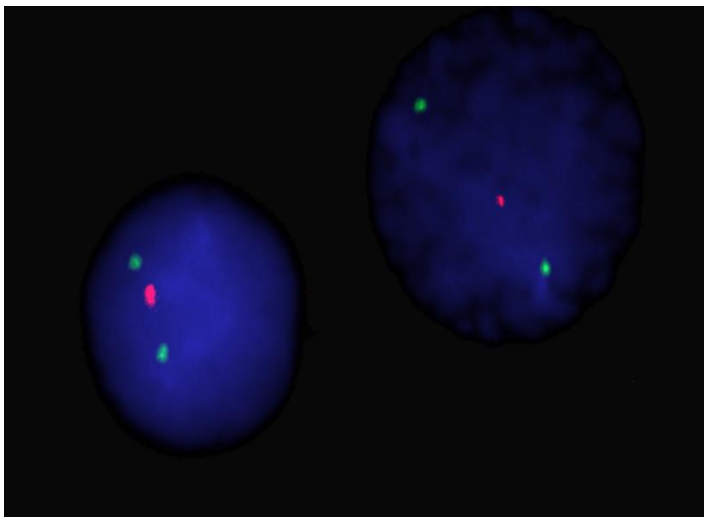

**Figure 3:**del 17(p13) (p53) by locus specific identifier (LSI)

## DISCUSSION

Myeloid malignancies are clonal disorders which affect hematopoietic stem cells and myeloid progenitor cells resulting in excessive proliferation, abnormal self-renewal, and/or differentiation defects [1].

High frequency of chromosome 17 abnormalities has been reported in some human cancers. The presence of chromosome 17 abnormalities confer poor outcome and resistance to chemotherapeutic drugs in several hematologic malignancies, which may be due to loss of the tumor suppressor gene p53 [4].

In the present study; Chromosome 17 abnormalities were detected in 52% (26/50) of the studied myeloid malignancies patients including 67.9% (19/28) of AML, 28.6% (2/7) MDS, and 33.3% (5/15) CML patients with no significant difference between the three groups. These results are in accordance with that reported by another Chinese study [5]. However higher than reported previously in AML [6], MDS [7] and CML [8].

The majority of abnormalities detected in this work were structural especially Chromosome 17 translocations , numerical abnormalities (monosomy and tetrasomy) were less frequent. These findings agree with the result of another study except for that the only detected numerical abnormality was monosomy 17 [5]. Trisomy 17 was previously reported in 70% of well and moderately differentiated oral squamous cell carcinoma [9]

In this work structural abnormalities were present in 50% (14/28) AML, 28.6% (2/7) MDS, and 26.7% (4/15) CML patients with statistically non-significant difference. Quite similar frequencies in AML 56.3% (9/16) and CML 33.3% (12/36) were reported by another study in which structural abnormalities were detected at higher percent of MDS patients 56.3% (9/16) [5] this difference may be attributed to the genetic variations among studied populations.

In the present study numerical abnormalities were found in 17.9% (5/28) AML, 6.7% (1/15) CML and not detected in MDS patients, there was no statistically significant difference between the three patient groups. These results agree with another earlier study in the reported frequency in AML patients 14.2% (3/21), and disagree with it regarding the frequency in CML 13.9% (5/36) and MDS 18.8% (3/16) patients [5].

In the present study AML patients show no significant difference between normal and abnormal chromosome 17 regarding age and sex. On the other hands previous studies reported significant differences regarding age and sex [6], [10], age not sex [12]. The differences may be related to the variation in sample size.

As regard to hematological data of AML patients; the current study revealed highly significant association of chromosome 17 abnormalities with higher total leucocyte count and no significant association with hemoglobin concentration and platelet count. These findings go hand in hand with previously reported results that significant association with TLC [10], [12] and non-significant association with hemoglobin concentration and platelet count [12]

In this work; it was revealed that 68.4% of AML patients with chromosome 17 abnormalities are significantly related to unfavorable, cytogenetic risk category this is in accordance with an earlier study [6]. Moreover; other authors reported statistically significant association between *p53* deletion and complex karyotype [12].

In the present study the two MDS patients with chromosome 17 abnormalities were older than 60 years, one patient was male and the other was female, chromosome 17 abnormalities were not significantly associated with age and sex. This is in agreement with previously reported results [4], [11].

In this work the two MDS patients with abnormal chromosome 17 were of MDS-EB-1 and MDS-EB-2 subtypes according to WHO (2016) classification with no significant association between chromosome 17 abnormalities and WHO subtypes. This is consistent with previously reported results [4]. Another earlier study classifies MDS patients according to WHO (2008) and reported that the most commonly encountered subtypes among patients positive for chromosome 17 abnormalities were RAEB-1 and RAEB-2 [11]

In our recent study; concerning hematological parameters the two MDS patients positive for chromosome 17 abnormalities had pancytopenia with hemoglobin less than 10 gm/dl, absolute neutrophil count less than 1.8x10^9/l and platelet count less than 100x10^9/l, there was no significant association between chromosome 17 abnormalities and hematological parameters which is similar to that reported by other authors [4]. Another larger study reported that

anemia, neutropenia, and thrombocytopenia were detected in (72.4%), (65.9%), (58.6%) of patients with abnormal chromosome 17; respectively [11]

Bone marrow examination of MDS patients with chromosome 17 abnormalities revealed more than 5% blast with no significant association between presence of abnormality and bone marrow blast percent. On the other hand the threshold of 5% blast was previously exceeded at lower frequency 68.2% [11] and significant association was previously reported [4] . The possible explanation for these differences may be attributed to small sample size in this study when compared with the others.

Concerning IPSS risk stratification the present study showed that MDS patients with abnormal chromosome 17 non-significantly related to intermediate-1 and intermediate-2 risk groups. This finding partially agrees with another larger study in which MDS patient with abnormal chromosome 17 were distributed among intermediate-1, intermediate-2, and high IPSS risk categories [11].

Moreover other authors used revised IPSS-R for risk stratification of MDS patients into five risk groups and the majority of chromosome 17 abnormalities positive patients were significantly related very high risk group [4]. This difference is possibly related to the small number of MDS patients in the present study.

Chromosome 17 abnormalities although relatively uncommon in MDS, they may be prognostically significant especially due to their correlation with loss of *TP53*. The presence of chromosome 17 abnormalities were associated with lower OS related to the fact that, if iso(17q) was excluded as it was found only as an isolated abnormality most of them were present in association with complex karyotype or chromosome 7 abnormalities that confer poor survival [4]. Moreover; abnormal chromosome 17 was associated with lower MCV that has poor prognosis [4], [13]. The prognosis of patients with chromosome 17 abnormalities may be altered by the use of hypomethylating agents [4]

Iso(17q) is the only abnormality of chromosome 17 that has already been characterized and used in the prognostic scoring systems for MDS as it has been defined as an intermediate cytogenetic risk lesion in the IPSS-R. It occurs in correlation with male sex, mixed myelodysplastic and myeloproliferative features, pseudopelger anomaly of neutrophil nuclei, and high risk for acute myeloid leukemia [4]**.**

In the present study all CML patients with chromosome 17 abnormalities were less than 60 years old, 80% of them were females. There was no significant difference between patients with and without abnormalities regarding age and sex. Similar findings were previously reported [8]. Other study revealed lower incidence in females [14].

Regarding spleen size; 60% of CML patients associated with abnormal chromosome 17 had huge splenomegaly, and 40% had moderate splenomegaly and no significant association between presence of abnormality and the size of the spleen. These findings agree with another Egyptian study [8].

Concerning hematological parameter; CML patients showed that chromosome 17 abnormalities were not significantly associated with total leucocyte counts, hemoglobin concentration and platelet count. This is in agreement with other authors who found also significant association between iso(17q) and bad patients outcome, shorter event-free survival in all phases. [8], [15]

Ph-negative myeloid neoplasms with isolated iso(17q) represent a clinicopathologic entity associated with a high risk for leukemic transformation [16].

Previous study concluded that the genetic or functional inactivation of the *p53* pathway plays an important role as regard to disease progression from the CP to BP and imatinib treatment response in CML and this was in accordance with our recent work [17].

## CONCLUSIONS

Chromosome 17 abnormalities were frequent cytogenetic events that occur in various myeloid neoplasms.Structural abnormalities of chromosome 17 were much more frequent than numerical.Chromosome 17 abnormalities have poor prognostic impact related to alteration of tumor suppressor gene (p53).

**Conflict of Interest:** None

**Financial Disclosures**: None

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**To Cite**
Easa, M., Shawky, N., Al-Azizi, N., Haggag, R. Abnormalities Of Chromosome 17 In Patients With Myeloid Malignancies.. *Zagazig University Medical Journal*, 2022; (999-1008): -. doi: 10.21608/zumj.2020.20514.1638