# RESULTS

# *RESULTS*

The normal chromosomal pattern of male mouse bone marrow revealed that the 40 chromosomes of mouse were acrocentric and vary only slightly in the length (Fig.4)

## A- First group (fed for 20 days):

### 1- Control:

a) **Negative control samples:** The results of these samples were collectively presented in (Table 1). The total examined metaphases were 500 for the ten mice where there were three gaps (Fig. 5), two breaks, two rings (Fig. 6), five chromatid separations (Fig. 7) and one fragment. The percentage of chromosomal aberrations comprising structural, hypoploidy (Fig. 8) and polyploidy (Fig. 9) were 2.6%, 2.4% and 2.2% respectively.

b) **Positive control samples:** The results of these samples were collectively presented in (Table 2). There were 38 gaps, 92 chromatid breaks, 15 isochromatid breaks, (Fig. 10), 12 rings, 27 chromatid separations, 518 fragments (Fig.11), 34 deletions (Fig.12), 7 end to end associations (Fig.13), and 25 pulverized cells (Fig.14). The percentage of chromosomal aberrations comprising structural, hypoploidy and polyploidy were 148.6%, 2.8% and 3% respectively. The percentage of abnormal cells to the examined cells was 35.6%.

### 2- Experimental samples:

a) **Erythrosine samples:** The results of these samples were collectively presented in (Table 3). There were three gaps, three

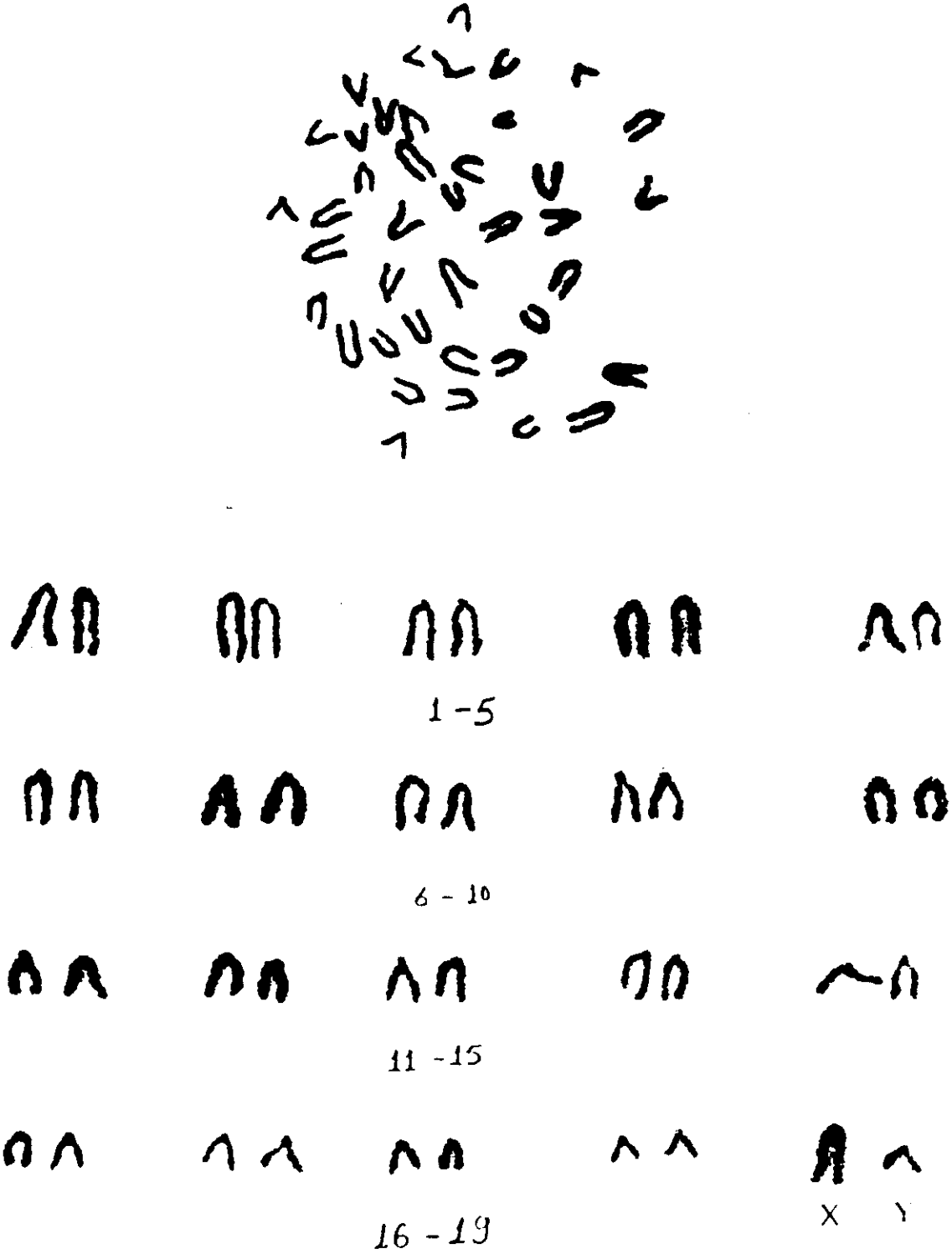



Fig. 4: A photomicrograph of a normal male mouse bone marrow metaphase spread showing 40 acrocenteric chromosomes.

( Giemsa stain, Objective x 100, Projective x 10 )

**Table 1:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in the negative control of the first group.

| Animal Number | Structural Anomalies (S.A.) | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | | | 1 | | | 1 | 2 | 1 |
| 2 | 1 | | | | | | 1 | | 2 |
| 3 | | | 1 | | 1 | | 2 | 2 | |
| 4 | | 1 | | 1 | | | 2 | 2 | |
| 5 | 1 | | | | | | 1 | 1 | 1 |
| 6 | | 1 | | 1 | | | 2 | | 1 |
| 7 | 1 | | | | | | 1 | 2 | 1 |
| 8 | | | 1 | | | | 1 | 1 | 2 |
| 9 | | | | | | | | 2 | 3 |
| 10 | | | | 2 | | | 2 | | |
| Total | 3 | 2 | 2 | 5 | 1 | 0 | 13 | 12 | 11 |
| Mean | 0.3 | 0.2 | 0.2 | 0.5 | 0.1 | 0.0 | 1.3 | 1.2 | 1.1 |
| ± SD | 0.48 | 0.42 | 0.42 | 0.71 | 0.32 | 0.0 | ± 0.67 | ± 0.92 | ± 0.99 |
| % | 0.6% | 0.4% | 0.4% | 1.0% | 0.2% | 0.0% | 2.6% | 2.4% | 2.2% |

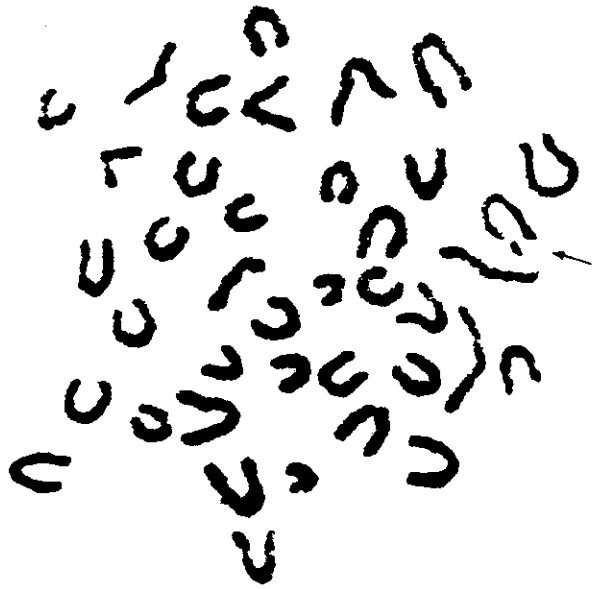


Fig. 5: A photomicrograph of a -ve control male mouse bone marrow metaphase spread showing a chromatid gap (arrow).

( Giemsa stain, Objective x 100, Projective x 10 )

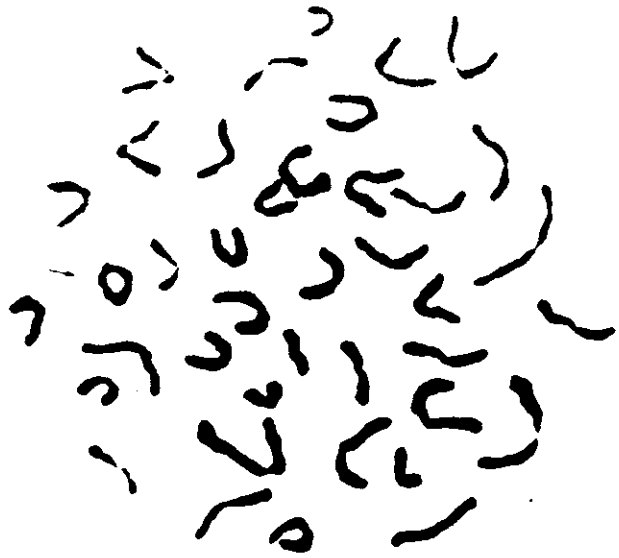


Fig. 6: A photomicrograph of a -ve control male mouse bone marrow metaphase spread showing a ring (arrow).

( Giemsa stain, Objective x 100, Projective x 10 )

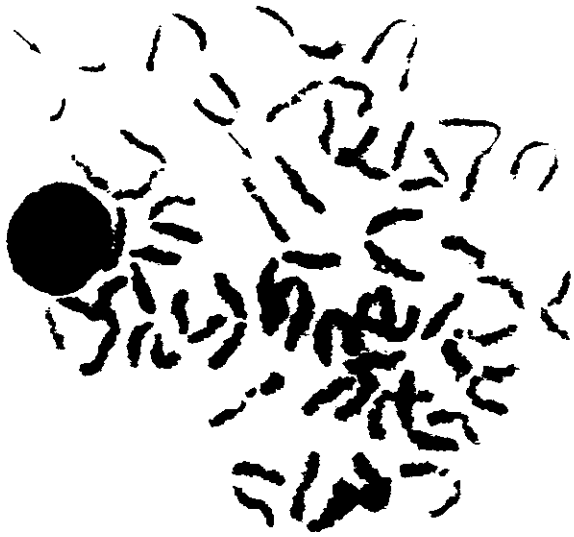


Fig. 7: A photomicrograph of a -ve control male mouse bone marrow metaphase spread showing chromatid separations (arrow).

( Giemsa stain, Objective x 100, Projective x 10 )

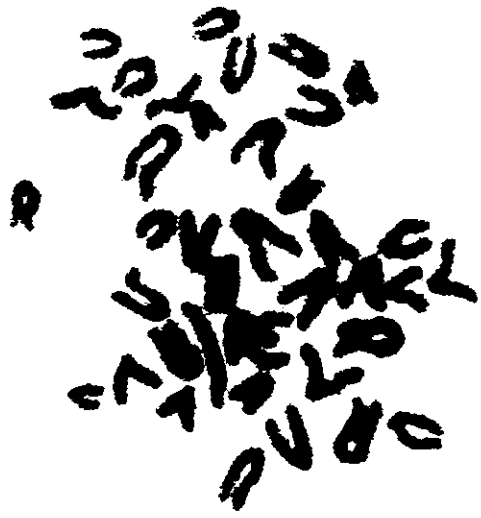


Fig. 8: A photomicrograph of a -ve control male mouse bone marrow metaphase spread showing hypoploidy (39 Chromosomes).

( Giemsa stain, Objective x 100, Projective x 10 )

Fig. 9: A photomicrograph of a -ve control male mouse bone marrow metaphase spread showing polyploidy.

( Giemsa stain, Objective x 100, Projective x 10 )

**Table 2:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in the positive contorl of the first group.

| Animal Number | Structural Anomalies | | | | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Chromatid Breaks | Isochromatid Breaks | Rings | Chromatid separations | Fragments | Deletions | End to end association | Summation | Pulverized cells | Hypoploidies | Polyploidies |
| 1 | 4 | 15 | 1 | 1 | 2 | 46 | 3 | 1 | 73 | 4 | 1 | 1 |
| 2 | 5 | 7 | 3 | 1 | 1 | 23 | 3 | 2 | 45 | 6 | 1 | 2 |
| 3 | 4 | 11 | 5 | | 5 | 60 | 2 | | 87 | 1 | 3 | 2 |
| 4 | 2 | 9 | | 3 | 7 | 63 | 1 | 1 | 86 | 4 | 1 | 1 |
| 5 | 6 | 6 | 1 | 2 | 3 | 68 | 5 | | 91 | 1 | | 1 |
| 6 | 3 | 7 | | 2 | 1 | 57 | 7 | 2 | 79 | 5 | 2 | 2 |
| 7 | 2 | 9 | 1 | 1 | 1 | 52 | 4 | | 70 | 1 | | 2 |
| 8 | 3 | 7 | 2 | | 2 | 69 | 5 | 1 | 89 | 2 | 2 | 1 |
| 9 | 4 | 12 | 1 | 2 | 2 | 37 | 2 | | 60 | 1 | 1 | 2 |
| 10 | 5 | 9 | 1 | | 3 | 43 | 2 | | 63 | | 3 | 1 |
| Total | 38 | 92 | 15 | 12 | 27 | 518 | 34 | 7 | 743 | 25 | 14 | 15 |
| Mean | 3.8 | 9.2 | 1.5 | 1.2 | 2.7 | 51.8 | 3.4 | 0.7 | 74.3 | 2.5 | 1.4 | 1.5 |
| ± SD | 1.32 | 2.78 | 1.51 | 1.03 | 1.95 | 14.67 | 1.84 | 0.82 | 15.00 | 2.07 | 1.07 | 0.53 |
| % | 7.6% | 18.4% | 3% | 2.4% | 5.4% | 103.6% | 6.8% | 1.4% | 148.6% | 5.0% | 2.8% | 3% |


Fig. 10 : A photomicrograph of an endoxan injected +ve control male mouse bone marrow metaphase spread showing chromatid (b) and isochromatid (ib) breaks.

( Giemsa stain, Objective x 100, Projective x 10 )

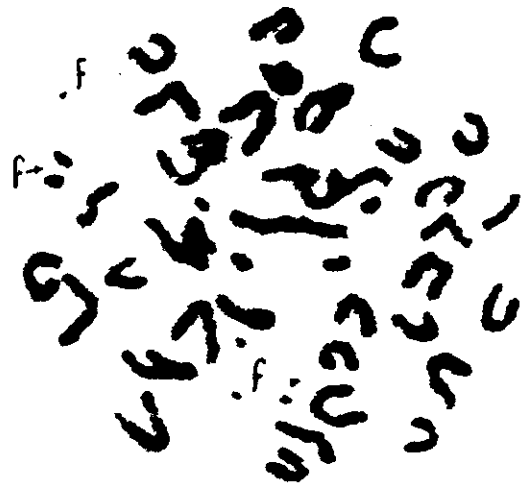



Fig. 11 : A photomicrograph of an endoxan injected +ve control male mouse bone marrow metaphase spread showing fragments(f).

( Giemsa stain, Objective x 100, Projective x 10 )

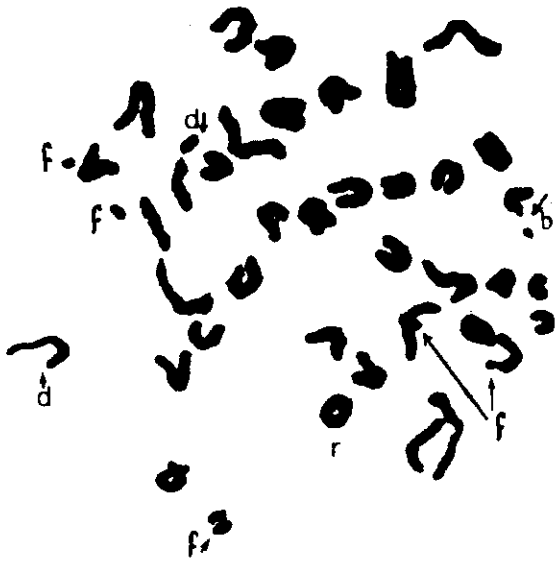



Fig. 12: A photomicrograph of an endoxan injected +ve control male mouse bone marrow metaphase spread showing deletions (d), ring (r), fragments (f) and chromatid break (b).

( Giemsa stain, Objective x 100, Projective x 10 )

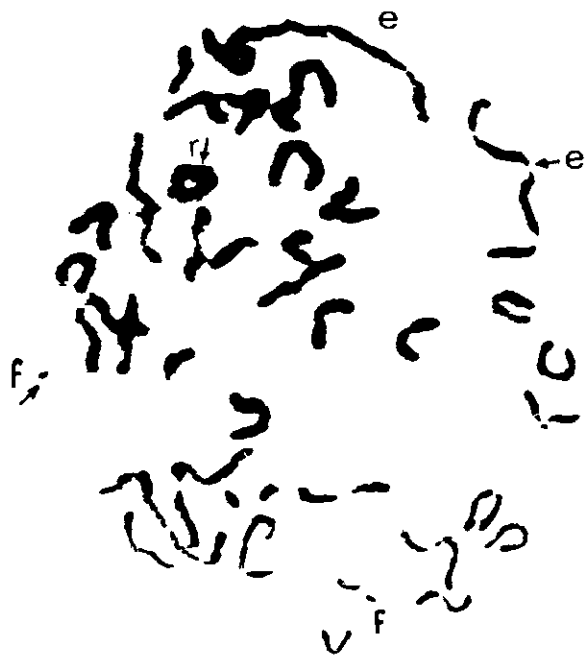



Fig. 13 : A photomicrograph of an endoxan injected +ve control male mouse bone marrow metaphase spread showing end to end associations (e), fragments (f) and a ring (r)

( Giemsa stain, Objective x 100, Projective x 10 )

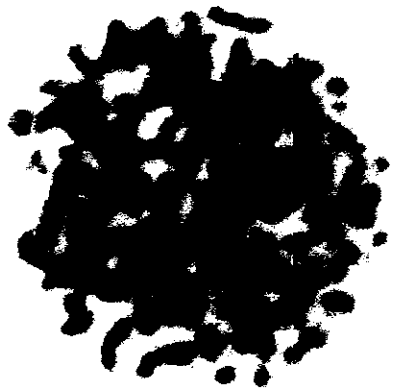


Fig. 14 : A photomicrograph of an endoxan injected +ve control male mouse bone marrow metaphare spread showing a pulverized cell.

( Giemsa stain, Objective x 100, Projective x 10 )

**Table 3:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in erythrosine fed animals in the first group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | | 1 | 1 | | | 2 | 1 | |
| 2 | | 1 | | 1 | | | 2 | | 1 |
| 3 | | | | | | | | 2 | 2 |
| 4 | 1 | | | | | | 1 | 2 | 2 |
| 5 | 1 | | | | | | 1 | | 1 |
| 6 | | 1 | | 1 | | | 2 | 1 | |
| 7 | | | | 2 | | | 2 | | 1 |
| 8 | | | 1 | | | | 1 | 2 | 1 |
| 9 | | | | | | | 1 | 1 | 1 |
| 10 | 1 | 1 | | 1 | | | 2 | 2 | 1 |
| Total | 3 | 3 | 2 | 6 | 0 | 0 | 14 | 11 | 10 |
| Mean | 0.3 | 0.3 | 0.2 | 0.6 | 0.0 | 0.0 | 1.40 | 1.10 | 1.00 |
| ± SD | 0.48 | 0.48 | 0.42 | 0.7 | 0.0 | 0.0 | ± 0.70 | ± 0.88 | ± 0.67 |
| % | 0.6% | 0.6% | 0.4% | 1.2% | 0.0% | 0.0% | 2.8% | 2.2% | 2.0% |

breaks, two rings and six chromatid separations.The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 2.8%, 2.2% and 2% respectively.

b) **Ponceau 4R samples** : The results of these samples were collectively presented in (Table 4). There were four gaps, two breaks, two rings, seven chromatid separations and one fragment. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 3.2%, 1.6% and 2.2% respectively.

c) **Sunset yellow samples:** The results of these samples were collectively presented in (Table 5). There were three gaps, one break, two rings, five chromatid separations and one deletion. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 2.4%, 1.6% and 1.8% respectively .

d) **Tartrazine samples:** The results of these samples were collectively presented in (Table 6). There were three gaps, two breaks, two rings, six chromatid separations and one fragment. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 2.8%, 1.8% and 2% respectively.

Indeed, the results of the different experimental samples of the first group showed non-significant difference when compared with their corresponding negative control (Table 7).

The means of structural anomalies, hypoploidies and polyploidies of the first group were presented in the histogram I (Fig. 15).

**Table 4:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in ponceau 4 R fed animals in the first group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | 1 | | | 1 | | | 2 | | 2 |
| 2 | | | | | | | | 1 | 2 |
| 3 | 1 | | 1 | 1 | | | 3 | 2 | 1 |
| 4 | | | | | 1 | | 1 | 1 | 1 |
| 5 | | 1 | | | | | 1 | 1 | |
| 6 | | | | 1 | | | 1 | 1 | |
| 7 | | 1 | | 1 | | | 2 | | 2 |
| 8 | 1 | | 1 | 1 | | | 3 | | |
| 9 | | | | 1 | | | 1 | | |
| 10 | 1 | | | 1 | | | 2 | 2 | 3 |
| Total | 4 | 2 | 2 | 7 | 1 | 0 | 16 | 8 | 11 |
| Mean | 0.4 | 0.2 | 0.2 | 0.7 | 0.1 | 0.0 | 1.60 | 0.80 | 1.10 |
| ± SD | 0.52 | 0.42 | 0.42 | 0.48 | 0.32 | 0.0 | ± 0.97 | ± 0.79 | ± 1.10 |
| % | 0.8% | 0.4% | 0.4% | 1.4% | 0.2% | 0.0% | 3.2% | 1.6% | 2.2% |

**Table 5:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in sunset yellow fed animals in the first group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | 1 | | | | | 1 | | 1 |
| 2 | | | 1 | 1 | | | 2 | 3 | 1 |
| 3 | 1 | | | | | | 1 | 1 | |
| 4 | | | 1 | 1 | | | 2 | | 2 |
| 5 | | | | 1 | | 1 | 2 | 1 | 1 |
| 6 | | | | | | | | | |
| 7 | | | | 1 | | | 1 | 1 | 1 |
| 8 | 1 | | | 1 | | | 2 | | |
| 9 | | | | | | | | | 2 |
| 10 | 1 | | | | | | 1 | 2 | 1 |
| Total | 3 | 1 | 2 | 5 | 0 | 1 | 12 | 8 | 9 |
| Mean | 0.3 | 0.1 | 0.2 | 0.5 | 0.0 | 0.1 | 1.20 | 0.80 | 0.90 |
| ± SD | 0.48 | 0.32 | 0.42 | 0.53 | 0.0 | 0.32 | ± 0.79 | ± 1.03 | ± 0.74 |
| % | 0.6% | 0.2% | 0.4% | 1.0% | 0.0% | 0.2% | 2.4% | 1.6% | 1.8% |

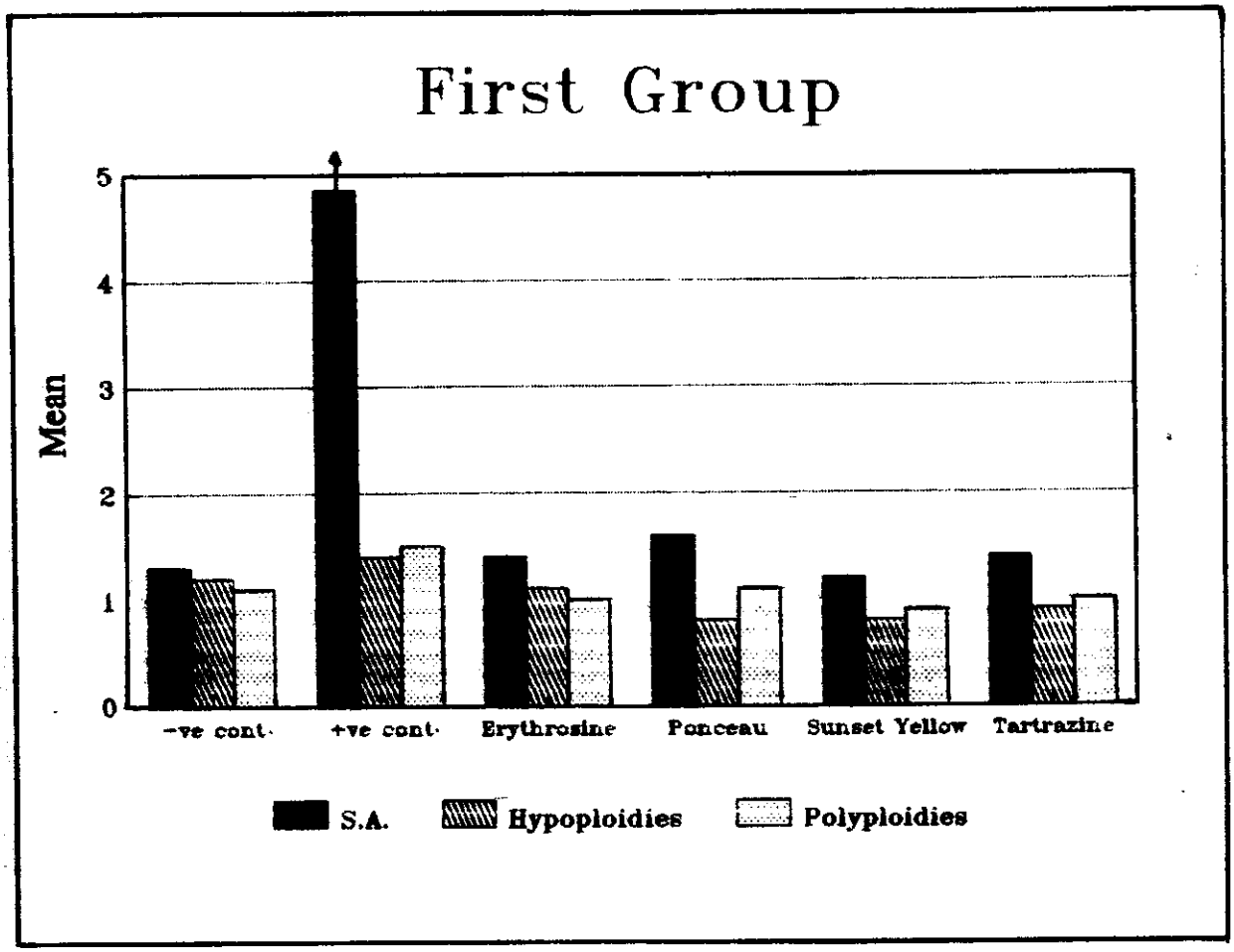
**Table 6:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in tartrazine fed animals in the first group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | | 1 | 1 | | | 2 | | 2 |
| 2 | 1 | | | | 1 | | 2 | 1 | |
| 3 | | | | | | | | 1 | 2 |
| 4 | | 1 | | | | | 1 | | 1 |
| 5 | 1 | | | 1 | | | 2 | 1 | |
| 6 | | | | | | | | 2 | 1 |
| 7 | | | | 1 | | | 1 | | |
| 8 | | | 1 | | | | 1 | | 1 |
| 9 | | 1 | | 1 | | | 2 | 1 | |
| 10 | 1 | | | 2 | | | 3 | 3 | 3 |
| Total | 3 | 2 | 2 | 6 | 1 | 0 | 14 | 9 | 10 |
| Mean | 0.3 | 0.2 | 0.2 | 0.6 | 0.1 | 0.0 | 1.40 | 0.90 | 1.00 |
| ± SD | 0.48 | 0.42 | 0.42 | 0.7 | 0.32 | 0.0 | ± 0.97 | ± 0.99 | ± 1.05 |
| % | 0.6% | 0.4% | 0.4% | 1.2% | 0.2% | 0.0% | 2.8% | 1.8% | 2.0% |

**Table 7:** Showing the means ± SD, values of t test and their significances in the first group.

| First group | Mean ± SD | t | P | Significance |
|---|---|---|---|---|
| **Negative control** | | | | |
| S.A. | 1.3 ± 0.67 | | | |
| Hypoploidies | 1.2 ± 0.92 | | | |
| Polyploidies | 1.1 ± 0.99 | | | |
| **Positive contorl** | | | | |
| S.A. | 74.3 ± 15 | 15.3700 | < 0.001 | H.S. |
| Hypoploidies | 1.4 ± 1.07 | 0.4472 | > 0.05 | I.S. |
| Polyploidies | 1.5 ± 0.53 | 1.1239 | > 0.05 | I.S. |
| **Erythrosine** | | | | |
| S.A. | 1.40 ± 0.70 | 0.3254 | > 0.05 | I.S. |
| Hypoploidies | 1.10 ± 0.88 | 0.2491 | > 0.05 | I.S. |
| Polyploidies | 1.00 ± 0.67 | 0.2641 | > 0.05 | I.S. |
| **Ponceau 4R** | | | | |
| S.A. | 1.60 ± 0.97 | 0.8050 | > 0.05 | I.S. |
| Hypoploidies | 0.80 ± 0.79 | 1.0445 | > 0.05 | I.S. |
| Polyploidies | 1.10 ± 1.10 | 0.0000 | > 0.05 | I.S. |
| **Sunset yellow** | | | | |
| S.A. | 1.20 ± 0.79 | 0.3046 | > 0.05 | I.S. |
| Hypoploidies | 0.80 ± 1.03 | 0.9150 | > 0.05 | I.S. |
| Polyploidies | 0.90 ± 0.74 | 0.5108 | > 0.05 | I.S. |
| **Tartrazine** | | | | |
| S.A. | 1.40 ± 0.97 | 0.2683 | > 0.05 | I.S. |
| Hypoploidies | 0.90 ± 0.99 | 0.7006 | > 0.05 | I.S. |
| Polyploidies | 1.00 ± 1.05 | 0.2182 | > 0.05 | I.S. |

I.S. = Insignificant. H.S. = Highly significant.




(Fig. 15) : A histogram I showing the means of structural anomalies, hypoploidies and polyploidies of the first group.

## B- Second group (fed for 4 months):

### 1- Control:

a) **Negative control samples:** The results of these samples were collectively presented in (Table 8). There were three gaps, two breaks, two rings, six chromatid separations and one deletion. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 2.8%, 2.4% and 1.6% respectively.

b) **Positive control samples:** The results of these samples were collectively presented in (Table 9). There were 43 gaps, 94 chromatid breaks, 8 isochromatid breaks, 10 rings, 18 chromatid separations, 461 fragments, 21 deletions, 8 end to end associations and16pulverized cells. The percentage of chromosomal aberrations per cell comprising structural, hypoploidy and polyploidy were 134.6%, 2.2% and 2.6% respectively. The percentage of abnormal cells to the examined cells was 32.6% .

### 2- Experimental samples:

a) **Erythrosine samples:** The results of these samples were collectively presented in (Table 10). There were two gaps, two breaks, one ring, nine chromatid separations and one deletion. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 3%, 1.6% and 3.2% respectively.

b) **Ponceau 4R samples:** The results of these samples were collectively presented in (Table 11). There were three gaps, two breaks, one ring, ten chromatid separations and one fragment. The

**Table 8:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in the negative contorl of the second group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | 1 | | 1 | | | | 2 | 2 | |
| 2 | | 1 | | 1 | | | 2 | 1 | 1 |
| 3 | | | | | | | | 2 | |
| 4 | | 1 | | 1 | | 1 | 3 | | 1 |
| 5 | | | | 1 | | | 1 | 1 | 1 |
| 6 | 1 | | | | | | 1 | 2 | 2 |
| 7 | | | | | | | | 1 | |
| 8 | | | | 1 | | | 1 | 2 | 1 |
| 9 | 1 | | | 2 | | | 3 | 1 | |
| 10 | | | 1 | | | | 1 | | 2 |
| Total | 3 | 2 | 2 | 6 | 0 | 1 | 14 | 12 | 8 |
| Mean | 0.3 | 0.2 | 0.2 | 0.6 | 0.0 | 0.1 | 1.4 | 1.2 | 0.8 |
| ± SD | 0.48 | 0.42 | 0.42 | 0.70 | 0.0 | 0.32 | ± 1.07 | ± 0.79 | ± 0.79 |
| % | 0.6% | 0.4% | 0.4% | 1.2% | 0.0% | 0.2% | 2.8% | 2.4% | 1.6% |

**Table 9:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in the positive contorl of the second group.

| Animal Number | Structural Anomalies | | | | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Chromatid Breaks | Isochromatid Breaks | Rings | Chromatid separations | Fragments | Deletions | End to end association | Summation | Pulverized cells | Hypoploidies | Polyploidies |
| 1 | 5 | 12 | 1 | | 2 | 40 | 4 | 1 | 65 | 2 | 1 | 1 |
| 2 | 3 | 14 | 2 | 2 | 1 | 54 | 3 | 2 | 81 | 3 | 1 | |
| 3 | 2 | 7 | | 1 | 2 | 47 | 2 | | 61 | 1 | 2 | 2 |
| 4 | 7 | 9 | 1 | | 4 | 60 | 3 | 1 | 85 | | | |
| 5 | 3 | 10 | 2 | 1 | 3 | 35 | 2 | 2 | 58 | 2 | 1 | 2 |
| 6 | 5 | 6 | | 2 | 1 | 53 | 1 | | 68 | 3 | 2 | 1 |
| 7 | 4 | 9 | 1 | | 2 | 62 | 1 | 1 | 90 | 1 | | 3 |
| 8 | 6 | 7 | | 3 | | 38 | 2 | | 56 | 1 | | 1 |
| 9 | 2 | 13 | 1 | 1 | 1 | 43 | 1 | | 62 | 1 | 1 | 1 |
| 10 | 6 | 7 | | | 2 | 29 | 2 | 1 | 47 | 2 | 3 | 2 |
| Total | 43 | 94 | 8 | 10 | 18 | 461 | 21 | 8 | 673 | 16 | 11 | 13 |
| Mean | 4.3 | 9.4 | 1.5 | 1.0 | 1.8 | 46.1 | 2.1 | 0.8 | 67.3 | 1.6 | 1.1 | 1.3 |
| ± SD | 1.77 | 2.8 | 0.79 | 1.05 | 1.14 | 10.98 | 0.99 | 0.79 | 13.81 | 0.97 | 0.99 | 0.95 |
| % | 8.6% | 18.8% | 1.6% | 2% | 3.6% | 92.2% | 4.2% | 1.6% | 134.6% | 32% | 2.2% | 2.6% |

**Table 10:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in erythrosine fed animals in the second group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | 1 | 1 | | 2 | | | 4 | | 1 |
| 2 | | | | 1 | | 1 | 2 | 1 | 3 |
| 3 | | | 1 | | | | 1 | 1 | 1 |
| 4 | 1 | | | 1 | | | 2 | 1 | 1 |
| 5 | | | | 1 | | | 1 | 1 | 1 |
| 6 | | | | | | | | | 2 |
| 7 | | | | | | | | 2 | 2 |
| 8 | | 1 | | 1 | | | 2 | | 2 |
| 9 | | | | 2 | | | 2 | 2 | 3 |
| 10 | | | | 1 | | | 1 | | |
| Total | 2 | 2 | 1 | 9 | 0 | 1 | 15 | 8 | 16 |
| Mean | 0.2 | 0.2 | 0.1 | 0.9 | 0 | 0.1 | 1.50 | 0.80 | 1.60 |
| ± SD | 0.42 | 0.42 | 0.32 | 0.74 | 0.0 | 0.32 | ± 1.18 | ± 0.79 | ± 0.97 |
| % | 0.4% | 0.4% | 0.2% | 1.8% | 0.0% | 0.2% | 3.0% | 1.6% | 3.2% |

**Table 11:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in ponceau 4 R fed animals in the second group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | 1 | | 1 | | | 2 | 1 | |
| 2 | | | | 2 | | | 2 | | 1 |
| 3 | 1 | | | | | | 1 | 5 | |
| 4 | | | | 1 | | | 1 | | 1 |
| 5 | | | | 2 | | | 2 | 1 | |
| 6 | | | | 1 | | | 1 | | 1 |
| 7 | | 1 | | 1 | | | 2 | 3 | 1 |
| 8 | 1 | | | | 1 | | 2 | | 2 |
| 9 | | | | 1 | | | 1 | | 3 |
| 10 | 1 | | 1 | 1 | | | 3 | 2 | 1 |
| Total | 3 | 2 | 1 | 10 | 1 | 0 | 17 | 12 | 10 |
| Mean | 0.3 | 0.2 | 0.1 | 1.0 | 0.1 | 0.0 | 1.7 | 1.2 | 1 |
| ± SD | 0.48 | 0.42 | 0.32 | 0.67 | 0.32 | 0.0 | ± 0.67 | ± 1.69 | ± 0.94 |
| % | 0.6% | 0.4% | 0.2% | 2.0% | 0.2% | 0.0% | 3.4% | 2.4% | 2.0% |

percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 3.4%, 2.4% and 2% respectively.

c) **Sunset yellow samples:** The results of these samples were collectively presented in (Table 12). There were three gaps, one chromatid and one isochromatid breaks, two rings and eight chromatid separations. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 3.0%, 1.6% and 1.6% respectively.

d) **Tartrazine samples:** The results of these samples were collectively presented in (Table 13). There were three gaps, two chromatid and one isochromatid breaks, one ring, seven chromatid separations, one fragment and one deletion. The percentage of chromosomal aberrations including structural, hypoploidy and polyploidy were 3.2%, 1.8% and 2.4% respectively.

In analogy to group I samples, the statistical analysis revealed non-significant difference between experimental and negative control samples (Table 14). The means of structural anomalies, hypoploidies and polyploidies of the second group were presented in the histogram II (Fig. 16).

However, in both groups I and II, the positive control samples revealed a strikingly increased level of structural anomalies which were, in most cases, innumerable due to severe damage of the chromosomes .

**Table 12:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in sunset yellow fed animals in the second group.

| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | 1 | | | 2 | | | 3 | 1 | 1 |
| 2 | | 1 | 1 | | | | 2 | 1 | |
| 3 | | | | 2 | | | 2 | | 1 |
| 4 | 1 | | | | | | 1 | | |
| 5 | | | | 1 | | | 1 | 1 | |
| 6 | 1 | | | | | | 1 | 2 | |
| 7 | | | | 1 | | | 1 | | |
| 8 | | 1* | | | | | 1 | 1 | 1 |
| 9 | | | | 1 | | | 1 | 1 | 3 |
| 10 | | | 1 | 1 | | | 2 | 1 | 2 |
| Total | 3 | 2 | 2 | 8 | 0 | 0 | 15 | 8 | 8 |
| Mean | 0.3 | 0.2 | 0.2 | 0.8 | 0.0 | 0.0 | 1.50 | 0.8 | 0.8 |
| ± SD | 0.48 | 0.42 | 0.42 | 0.79 | 0.0 | 0.0 | ±0.71 | ±0.63 | ±1.03 |
| % | 0.6% | 0.4% | 0.4% | 1.6% | 0.0% | 0.0% | 3.0% | 1.6% | 1.6% |

* Isochromatid break.

**Table 13:** Chromosome aberrations in direct preparations of mouse bone marrow cells in the examined 500 metaphases in tartrazine fed animals in the second group.

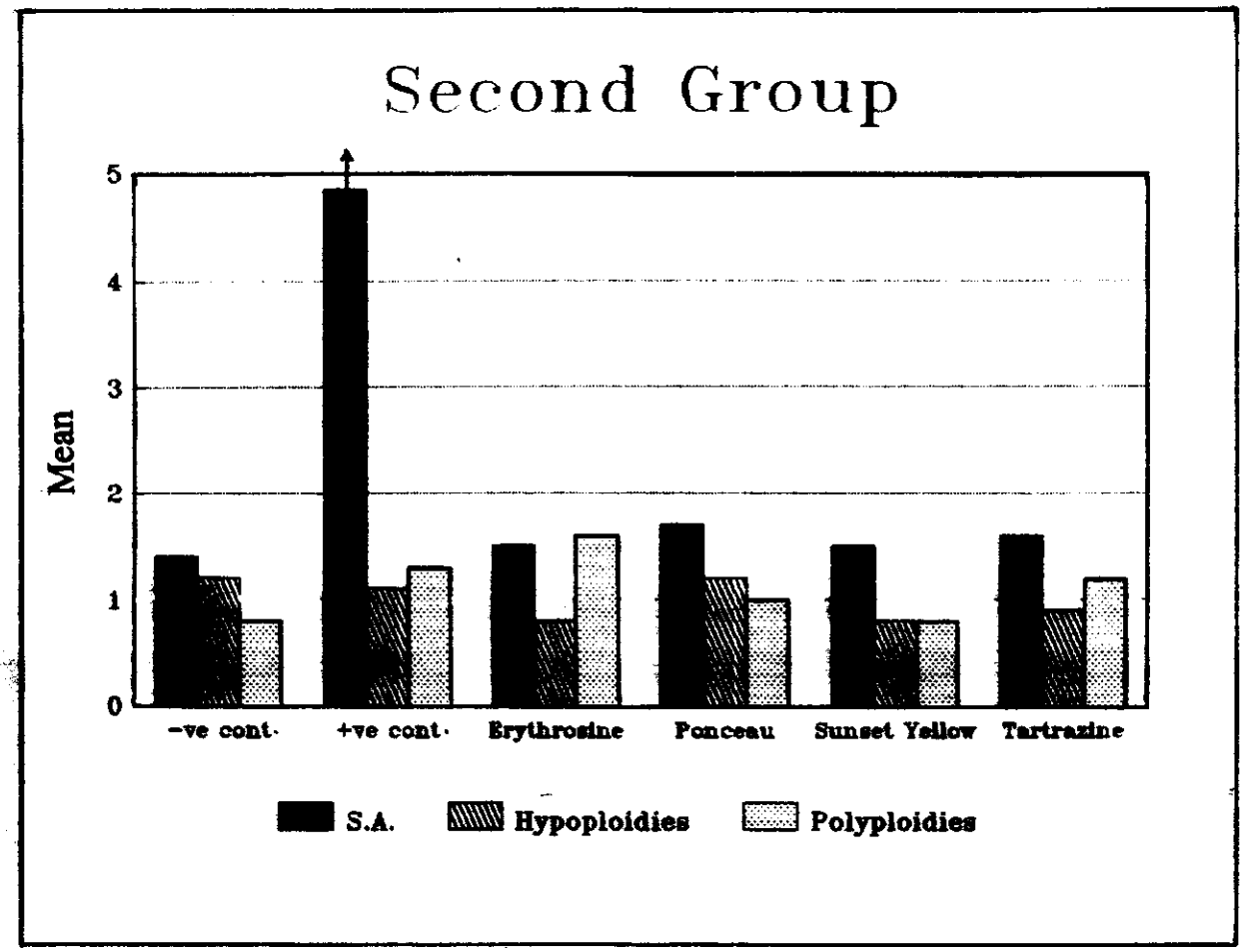
| Animal Number | Structural Anomalies | | | | | | | Numerical Anomalies | |
|---|---|---|---|---|---|---|---|---|---|
| | Gaps | Breaks | Rings | Chromatid separations | Fragments | Deletions | Summation | Hypoploidies | Polyploidies |
| 1 | | | | 2 | | | 2 | 2 | 2 |
| 2 | 1 | 1* | | | | 1 | 3 | 1 | |
| 3 | | | | | | | | 1 | |
| 4 | | | 1 | 1 | 1 | | 3 | 1 | 2 |
| 5 | | | | 1 | | | 1 | | 2 |
| 6 | | 1 | | | | | 1 | | 2 |
| 7 | | | | 1 | | | 1 | 1 | 1 |
| 8 | 1 | 1 | | 1 | | | 3 | 1 | 1 |
| 9 | 1 | | | | | | 1 | 1 | 1 |
| 10 | | | | 1 | | | 1 | 1 | 1 |
| Total | 3 | 3 | 1 | 7 | 1 | 1 | 16 | 9 | 12 |
| Mean | 0.3 | 0.3 | 0.1 | 0.7 | 0.1 | 0.1 | 1.6 | 0.9 | 1.2 |
| ± SD | 0.48 | 0.48 | 0.32 | 0.67 | 0.32 | 0.32 | ± 1.07 | ± 0.57 | ± 0.79 |
| % | 0.6% | 0.6% | 0.2% | 1.4% | 0.2% | 0.2% | 3.2% | 1.8% | 2.4% |

* Isochromatid break.

**Table 14:** Showing the means ± SD, values of t test and their significances in the second group.

| Second group | Mean ± SD | t | P | Significance |
|---|---|---|---|---|
| **Negative control** | | | | |
| S.A. | 1.4 ± 1.07 | | | |
| Hypoploidies | 1.2 ± 0.79 | | | |
| Polyploidies | 0.8 ± 0.79 | | | |
| **Positive contorl** | | | | |
| S.A. | 67.3 ± 13.81 | 15.0723 | < 0.001 | H.S. |
| Hypoploidies | 1.1 ± 0.99 | 0.0000 | > 0.05 | I.S. |
| Polyploidies | 1.3 ± 0.95 | 0.8187 | > 0.05 | I.S. |
| **Erythrosine** | | | | |
| S.A. | 1.5 ± 1.18 | 0.1982 | > 0.05 | I.S. |
| Hypoploidies | 0.8 ± 0.79 | 1.1339 | > 0.05 | I.S. |
| Polyploidies | 1.6 ± 0.97 | 2.0284 | > 0.05 | I.S. |
| **Ponceau 4R** | | | | |
| S.A. | 1.7 ± 0.67 | 0.7474 | > 0.05 | I.S. |
| Hypoploidies | 1.2 ± 1.69 | 0.0000 | > 0.05 | I.S. |
| Polyploidies | 1.0 ± 0.94 | 0.5145 | > 0.05 | I.S. |
| **Sunset yellow** | | | | |
| S.A. | 1.5 ± 0.71 | 0.2458 | > 0.05 | I.S. |
| Hypoploidies | 0.8 ± 0.63 | 1.2511 | > 0.05 | I.S. |
| Polyploidies | 0.8 ± 1.03 | 0.0000 | > 0.05 | I.S. |
| **Tartrazine** | | | | |
| S.A. | 1.6 ± 1.07 | 0.4160 | > 0.05 | I.S. |
| Hypoploidies | 0.9 ± 0.57 | 0.9762 | > 0.05 | I.S. |
| Polyploidies | 1.2 ± 0.79 | 1.1339 | > 0.05 | I.S. |

I.S. = Insignificant. H.S. = Highly significant.




(Fig. 16): A histogram II showing the means of structural anomalies, hypoploidies and polyploidies of the second group.