DNA content, ploidy level and number of nuclei in the human heart after myocardial infarction

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Abstract

Objective: Cardiac hypertrophy due to a prolonged functional activity is associated with an increase of cell size and polyploidization of the myocyte nuclei. Myocardial infarction is characterized by loss of myocytes. Increased load and as a consequence hypertrophic growth of the surviving myocardium has to be expected. The aim of this study was to investigate the response of cardiomyocytes after infarction. Method: Biochemical and cytophotometric analysis was performed on myocyte and connective tissue nuclei to determine whether the human heart after myocardial infarction is accompanied by an increase in the ploidy level, DNA content and in the number of nuclei. A total of 15 hearts obtained from autopsy material was studied, among them 8 after myocardial infarction. The number of nuclei was measured by indirect computation. Results: We found a decrease of 4c and no significant difference of 2c nuclei in infarcted hearts. DNA ploidy level (> 8c) as well as the proportion of aneuploid myocyte nuclei were increased in infarcted hearts. DNA concentration and total DNA content were increased in the hearts after myocardial infarction. Numerical ratio of connective tissue nuclei/myocyte nuclei, total number of nuclei, number of myocyte nuclei and number of connective tissue nuclei were increased in infarcted hearts. Conclusion: Polyploidization and nuclear hyperplasia of myocytes may represent an adaptive response of the myocardium to an ischemic injury. © 1997 Elsevier Science B.V.

Keywords: Myocardial infarction; DNA measurement; Polyploidization; Nuclear hyperplasia; Human

1. Introduction

Myocardial infarction is characterized by loss of heart muscle cells and myocardial scarring. This loss of muscle mass may lead to an increased load on the surviving myocardium.

Hemodynamic conditions created by the increased load on the spared myocardium in the presence of cardiac failure and a decreased systolic stress may be the most important variable in the initiation of myocyte hypertrophy or hyperplasia [1]. It is a general contention that myocardial hypertrophy in the adult heart is accomplished by enlargement of the cardiomyocytes [2–4]. However, investigations have provided strong supportive evidence that myocyte nuclear and cellular hyperplasia may occur under pathological conditions [5–7]. Further on, polyploidization as well as an increased number of polyploid nuclei during physiological growth and increased load on the myocardium were described [8,9].

Several reports have suggested that myocytes in the adult human heart may reenter the cell cycle and synthesize DNA [1,6,9,10]. Therefore, the cell capacity for reactive DNA synthesis under pathological conditions is one of the central questions of regeneration.

The purpose of this study was to investigate the reaction of the human myocardium after myocardial infarction. Using different morphological, biochemical and cytophotometrical parameters of cardiac cells we analyzed the capacity for polyploidization, DNA synthesis and changes in the number of nuclei.
2. Method

A total of 15 human hearts obtained from autopsy cases were studied. Our material comprised eight hearts of patients aged between 32 and 83 (median 65) who had suffered from coronary arteriosclerosis accompanied by myocardial infarction with location in the anterior wall. Area of myocardial injury was on average 4 cm². Time after heart attack was between 1 and 2 years and the infarcts were healed. Out of this material, seven hearts were obtained from patients aged between 22 and 54 (median 41), who died from various non-cardiac or pulmonary causes.

Post-mortem examinations were carried out within 24 h of death. After weighing (total heart weight), the hearts were freed from vessels, atria, heart valves, tendinous fibres and subepicardial fatty tissue and then ventricular weight (= right + left ventricle) was determined. Samples of muscle tissue measuring approximately 0.3 cm × 1.0 cm × 1.2 cm were studied biochemically and cytophotometrically at 8 different norm sites (ns) of both ventricles (anterior wall right ventricle (1), posterior wall right ventricle (2), right papillary muscle (3), anterior (4) and posterior (5) wall left ventricle, pulmonary outflow tract (6), septum (7) and left papillary muscle (8)). In hearts with myocardial infarction in the region adjacent to scar 6 samples (0.3 cm × 1.0 cm × 1.2 cm) of viable myocardium were taken in addition.

2.1. Biochemical DNA determination

After fresh weight had been determined, tissue pieces of approximately 0.3 cm × 0.5 cm × 1.2 cm, were minced, mechanically homogenised and centrifuged. The sediment was washed three to five times in 0.25 mol perchloride at 0°C. Before use, 20 ml of the diphenylamine reagent were added to 1 ml of a freshly prepared acetaldehyde solution 9.8 ml distilled water + 0.2 ml acetaldehyde. For controls we use Salm DNA (Carl Roth, Karlsruhe, Germany) with a standard solution containing 10 mg DNA in 40 ml 0.5% perchloride acid. Calibrated curves were made out for 50 µg, 100 µg, 150 µm, 200 µg and 250 µg DNA.

For measuring of the absorbance of the DNA solutions a spectrophotometer PQM II (Carl Zeiss, Oberkochen, Germany) was used at a wave length of 595 nm (filter 0).

2.2. Cytophotometric DNA determination

Tissue samples with approximately 0.3 cm × 0.5 cm × 1.2 cm were mechanically homogenised using an ultraturrax (Janke and Kunkel, Staufen im Breisgau, Germany) in 3 ml of cooled physiological saline solution. A few drops of the homogenate were spread on glass slides. After the material had been dried, it was fixed in a Carnoy solution for 1 h, put into 96% alcohol for 2 × 15 min and into distilled water for 5 min.

The smear preparations were stained according to Feulgen [13]: Hydrolysis in HCl for 12 min at 60°C, Schiff’s reagent according to Graumann [14]. Stained bull spermatozoa were used as control for haploid DNA content. Fifty nuclei per sampling area were then measured on a Deeley integrating microdensitometer (Barr and Stroud, Glasgow, Scotland). Mean values of myocyte nuclei ploidy classes differed by no more than 3%. To investigate reproducibility we performed repeated measurement on five nuclei per sampling area of each heart (S.E. ± 0.05).

2.3. Determination of the numerical ratio of connective tissue nuclei/myocyte nuclei

To determine the numerical ratio of connective tissue nuclei/myocyte nuclei conventionally processed paraffin-embedded material in 5 µm sections was used. Nuclei were analyzed and the number of connective tissue nuclei per 100 myocyte nuclei was counted. Analysis was performed at a magnification of ×500.

2.4. Determination of the number of nuclei

The absolute number of myocyte nuclei can be obtained from the values of the total DNA amount determined by biochemical measurements, the percentage proportion of the various ploidy classes in the myocyte nuclei and the numerical ratio of connective tissue nuclei/myocyte nuclei [15,16]. First of all, mean DNA amount of heart cells was determined (taking into account the percentage proportion of the various ploidy classes):

\[ 2c_{\text{nucleus}} = N_{\text{CTN}} + N_{2c} + 1.5N_{3c} + 2N_{4c} + 3N_{6c} + 4N_{8c} + \ldots / (N_{\text{CTN}} + 100\, MN) \]

with CTN = connective tissue nuclei; MN = myocyte nuclei; \( 2c_{\text{nucleus}} \) = mean DNA amount; \( N_{\text{CTN}} \) = number of CTN/100 MN = number of genomes of CTN/100 MN, because CTN are diploid; \( N_{2c} \) = number of genomes with regard to the percentage of diploid myocyte nuclei; 1.5\( N_{3c} \) = number of genomes with regard to the percentage of triploid myocyte nuclei, etc.

Since \( 6 \times 10^{-12} \) g DNA are present within a diploid nucleus [17,18], it is possible to determine the median DNA amount found in the total genomes:

\[ \text{DNA amount}_{\text{nucleus}} = 2c_{\text{nucleus}} \times 6 \times 10^{-12} \, \text{g}. \]
The total number of nuclei is calculated from the ratio of the biochemically estimated total amount of DNA in the myocardium and the total amount of the genome determined on the basis of cytophotometric measurements:

\[
N_{\text{total number of nuclei}} = \frac{\text{total DNA amount} \times (2c_{\text{nuclei}} \times 6 \times 10^{-12} \text{g})}{(\text{number of CTN} / 100 \text{ MN}) + 100 \text{ MN}}
\]

and ratio of the total number of connective tissue nuclei/total number of nuclei correlates to the numerical ratio of (number of CTN/100 MN)/(number of CTN/100 MN + 100 MN):

\[
N_{\text{total number of CTN}} / N_{\text{total number of nuclei}} = N_{\text{CTN}} / (N_{\text{CTN}} + 100 \text{ MN})
\]

Total number of connective tissue nuclei can be calculated:

\[
N_{\text{total number of CTN}} = N_{\text{CTN}} / (N_{\text{CTN}} + 100 \text{ MN}) \times N_{\text{total number of nuclei}}
\]

And, the number of myocyte nuclei can be calculated:

\[
N_{\text{number of MN}} = N_{\text{total number of nuclei}} - N_{\text{total number of CTN}}
\]

2.5. Data collection and analysis

It should be recognized, however, that the number of hearts and variability in age may influence the quantitative results.

Statistical significance for comparisons between two measurements was determined with the Mann–Whitney–Wilcoxon test. Values of \( P < 0.05 \) were considered significant.

The investigations conform with the principles outlined in the Declaration of Helsinki [19].

3. Results

3.1. Ploidy of myocyte nuclei

Frequency distribution of DNA content was measured by image cytophotometry in myocyte nuclei in normal and infarcted hearts (Table 1). Quantitatively, the percentage of diploid myocyte nuclei did not change significantly, whereas tetraploid nuclei decreased from 59.1% to 39.1% in infarcted hearts (\( P < 0.001 \)). High ploidy nuclei (> 8c) are mainly present in infarcted hearts. Polyploid myocyte nuclei were hardly observed in normal hearts. 32c nuclei were only found in infarcted hearts.

Increased number of aneuploid nuclei was detected after myocardial infarction: 3c nuclei occur with a mean frequency of 6.1% (normal hearts 0.1%), 5c nuclei with 3.9% (normal hearts 0%), 6c nuclei with 4.5% (normal hearts 1.7%), 10c nuclei with 2.2% (normal hearts 0%), 12c nuclei with 0.9% (normal hearts 0.1%) and 20c nuclei with 0.2% (normal hearts 0%). Therefore, significant difference between normal and infarcted hearts could be found in 6c, 12c, 16c myocyte nuclei (\( P < 0.05 \)), in 5c myocyte nuclei (\( P < 0.005 \)), and in 3c, 4c and 10c myocyte nuclei (\( P < 0.001 \)).

Table 2 specifies the distribution of the DNA content in normal hearts and in infarcted hearts. In infarcted hearts the distribution of ploidy classes in the tissue from the right ventricle, left ventricle and in the region adjacent to scar is similar. In normal hearts no significant difference of ploidy levels between the right and left ventricle could be found.

In summary, great variability of myocyte ploidy could be found in normal hearts and in hearts after myocardial infarction. DNA ploidy level (> 8c) as well as the proportion of aneuploid myocyte nuclei were increased in infarcted hearts.

3.2. DNA concentration and total amount of DNA

Biochemically estimated DNA concentration could be found in Table 3. In the case of hearts with old infarction, the DNA concentration of the norm sites and in the region adjacent to scar was specified separately. In comparison with normal hearts (242 \( \mu \text{g/g} \)) mean DNA concentration in infarcted hearts (321 \( \mu \text{g/g} \)) was increased (\( P < 0.05 \)). No correlation between ventricular weight and DNA concentration could be found in normal as well as in infarcted hearts.

The total amount of myocardial DNA resulted from the product of myocardial weight (g) multiplied by the average DNA concentration (\( \mu \text{g/g} \)) (Table 3). Increased total DNA content could be found after myocardial infarction (\( P < 0.05 \)). Positive correlation between the ventricular weight and DNA concentration could be found in normal as well as in infarcted (I) hearts (\( r = 0.84, P < 0.05; I: r = 0.87, P < 0.01 \)).

<table>
<thead>
<tr>
<th>No.</th>
<th>2c (%)</th>
<th>3c (%)</th>
<th>4c (%)</th>
<th>5c (%)</th>
<th>6c (%)</th>
<th>8c (%)</th>
<th>10c (%)</th>
<th>12c (%)</th>
<th>16c (%)</th>
<th>20c (%)</th>
<th>32c (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>I mean</td>
<td>15.5</td>
<td>6.1</td>
<td>39.1</td>
<td>3.9</td>
<td>4.5</td>
<td>23.3</td>
<td>2.2</td>
<td>0.9</td>
<td>3.9</td>
<td>0.2</td>
<td>0.3</td>
</tr>
<tr>
<td>± SD</td>
<td>4.0</td>
<td>3.4</td>
<td>3.4</td>
<td>2.9</td>
<td>0.6</td>
<td>4.5</td>
<td>0.8</td>
<td>0.4</td>
<td>1.3</td>
<td>0.1</td>
<td>0.2</td>
</tr>
<tr>
<td>N mean</td>
<td>22.5</td>
<td>0.1</td>
<td>59.1</td>
<td>0.0</td>
<td>1.7</td>
<td>15.4</td>
<td>0.0</td>
<td>0.1</td>
<td>1.2</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>± SD</td>
<td>2.3</td>
<td>0.2</td>
<td>6.2</td>
<td>0.0</td>
<td>2.4</td>
<td>7.7</td>
<td>0.0</td>
<td>0.4</td>
<td>2.1</td>
<td>0.0</td>
<td>0.0</td>
</tr>
</tbody>
</table>
Table 2
Distribution of ploidy classes (myocyte nuclei) in infarcted hearts I and normal hearts N hearts (rv = right ventricle, lv = left ventricle and ras = region adjacent to scar).

<table>
<thead>
<tr>
<th>No.</th>
<th>2c (%)</th>
<th>3c (%)</th>
<th>4c (%)</th>
<th>5c (%)</th>
<th>6c (%)</th>
<th>8c (%)</th>
<th>10c (%)</th>
<th>12c (%)</th>
<th>16c (%)</th>
<th>20c (%)</th>
<th>32c (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>I rv</td>
<td>13.3</td>
<td>6.8</td>
<td>44.3</td>
<td>5.5</td>
<td>4.3</td>
<td>21.0</td>
<td>1.2</td>
<td>0.7</td>
<td>1.7</td>
<td>0.0</td>
<td>0.1</td>
</tr>
<tr>
<td>± SD</td>
<td>3.4</td>
<td>1.0</td>
<td>3.6</td>
<td>2.0</td>
<td>0.8</td>
<td>4.7</td>
<td>0.4</td>
<td>0.3</td>
<td>0.7</td>
<td>0.0</td>
<td>0.1</td>
</tr>
<tr>
<td>I lv</td>
<td>15.8</td>
<td>5.9</td>
<td>36.9</td>
<td>3.1</td>
<td>4.6</td>
<td>24.3</td>
<td>2.5</td>
<td>1.2</td>
<td>4.8</td>
<td>0.4</td>
<td>0.3</td>
</tr>
<tr>
<td>± SD</td>
<td>4.4</td>
<td>1.4</td>
<td>4.1</td>
<td>0.8</td>
<td>0.7</td>
<td>4.9</td>
<td>1.1</td>
<td>0.5</td>
<td>1.9</td>
<td>0.2</td>
<td>0.3</td>
</tr>
<tr>
<td>I ras</td>
<td>14.3</td>
<td>5.3</td>
<td>37.3</td>
<td>2.7</td>
<td>4.7</td>
<td>23.1</td>
<td>3.3</td>
<td>1.1</td>
<td>6.4</td>
<td>0.6</td>
<td>0.6</td>
</tr>
<tr>
<td>± SD</td>
<td>4.9</td>
<td>1.7</td>
<td>5.2</td>
<td>0.8</td>
<td>0.7</td>
<td>5.0</td>
<td>1.7</td>
<td>0.7</td>
<td>2.9</td>
<td>0.4</td>
<td>0.5</td>
</tr>
<tr>
<td>N rv</td>
<td>22.4</td>
<td>0.1</td>
<td>59.3</td>
<td>0.0</td>
<td>1.8</td>
<td>15.1</td>
<td>0.0</td>
<td>0.1</td>
<td>1.1</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>± SD</td>
<td>3.2</td>
<td>0.2</td>
<td>5.9</td>
<td>0.0</td>
<td>2.4</td>
<td>7.8</td>
<td>0.0</td>
<td>0.4</td>
<td>2.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>N lv</td>
<td>18.2</td>
<td>0.1</td>
<td>62.8</td>
<td>0.0</td>
<td>1.6</td>
<td>16.1</td>
<td>0.0</td>
<td>0.0</td>
<td>1.2</td>
<td>0.0</td>
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</tr>
<tr>
<td>± SD</td>
<td>7.3</td>
<td>0.3</td>
<td>12.7</td>
<td>0.0</td>
<td>1.3</td>
<td>7.2</td>
<td>0.0</td>
<td>0.0</td>
<td>2.6</td>
<td>0.0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

In summary, DNA concentration and total DNA content increased after myocardial infarction. Positive correlation between total amount of myocardial DNA and ventricular weight could be found in both normal and infarcted hearts.

3.3. Numerical ratio of connective tissue nuclei/myocyte nuclei

In order to calculate the absolute number of myocyte nuclei, the numerical ratio of connective tissue nuclei/myocyte nuclei (CTN/MN) was determined (Table 3). Results demonstrated that the mean numerical ratio was 297 CTN/100 MN in infarcted hearts and 221 CTN/100 MN in normal hearts (P < 0.001).

In summary, increase of the ratio of connective tissue nuclei/myocyte nuclei was detected after myocardial infarction.

3.4. Number of nuclei

The availability of the total DNA amount, the percentage proportion of the various ploidy classes in myocyte nuclei and the numerical ratio of CTN/100 MN allowed the evaluation of the total number of nuclei, number of myocyte nuclei and number of connective tissue nuclei. In infarcted hearts 9.818 × 10⁹ nuclei, 2.380 × 10⁹ myocyte nuclei and 7.440 × 10⁹ connective tissue nuclei could be found. In normal hearts total number of...
nuclei was $6.107 \times 10^8$, number of myocyte nuclei was $1.956 \times 10^9$ and $4.293 \times 10^9$ connective tissue nuclei.

Further on, number of myocyte nuclei and connective tissue nuclei per ventricular weight have been calculated. The ratio myocyte nuclei/ventricular weight did not change significantly, whereas the ratio connective tissue nuclei/ventricular weight was increased ($P < 0.01$).

In summary, myocardial infarction was associated with an increase of the number of connective tissue nuclei, number of myocyte nuclei and total number of nuclei ($P < 0.05$), respectively.

4. Discussion

Mortality with acute infarction is approximately 35% and, an additional 15 to 20% of survivors die in the first year following myocardial infarction [20]. If patient survives the acute infarction, granulation tissue ingrowths the necrotic area and the scarring are well advanced by the end of the sixth week, but the time required for total replacement depends, of course, on the size of the original lesion. The myocardial damage and loss of contractile myocytes may lead to an increased load on the spared myocardium in the presence of cardiac failure and a decreased systolic stress. The present study investigated, if heart is accompanied by increase of ploidy level, DNA content and number of nuclei after myocardial infarction.

4.1. Ploidy in myocyte nuclei

Cardiac myocytes have been claimed to be terminally differentiated cells. However, DNA synthesis in adult cardiac myocytes after myocardial infarction in rats [21] as well as in humans [10] was described. Further on, observations in humans have provided strong supportive evidence that myocyte cellular hyperplasia [5,6] and polyploidization [9] may occur under pathological conditions characterized by large and prolonged stress on the myocardium. However, the perennial issue of whether DNA replication leads exclusively to the formation of ploidy or to nuclear mitotic division has been a matter of controversy [10].

The first evidence of polyploid myocyte nuclei has been published in 1964 [22]. As in other reports [8,23,24] we found a distribution of ploidy levels with 10–30% diploid (2c) and 50–70% tetraploid nuclei (4c) and a small fraction of high ploidy nuclei in normal hearts (weighing < 500 g). The myocyte ploidy did not exceed the 16c level. No significant differences in the distribution of ploidy levels between left and right ventricle could be found.

Increased ploidy level could be found in cardiac hypertrophy [9,15,25]. And, reactive hypertrophy of the unaffected ventricular mass is an early event that characterizes the myocardial response to infarction. Hypertrophic growth of the myocyte population after infarction in rats is characterized by increases in myocyte diameter and length, which both contribute to cellular enlargement [26]. However, there is the existence of a so-called critical cell volume, which leads to doubling of the chromosomal content [27] in order to guarantee the synthesis of contractile proteins and cell metabolism [28].

In hearts after myocardial infarction we found a decrease of the percentage distribution of tetraploid myocyte nuclei, no significant change of 2c, 8c, 20c and 32c nuclei and an increase of 3c, 5c, 6c, 10c, 12c and 16c myocyte nuclei. 32 c nuclei could only be found in infarcted hearts. Aneuploid nuclei (3c, 5c, 6c, 10c, 12c, 18c, 20c) appearing in infarcted hearts can be defined as cells in the S-phase [15], incomplete variants of induced mitosis [9] or may be mitosis accompanied by nuclear fragmentation [10].

However, myocyte cellular hypertrophy occurs after myocardial infarction and myocyte enlargement is an early event that progresses throughout the healing process. When left-side pump failure is present, the right ventricle hypertrophies by enlarging its myocyte population in attempt to maintain the pressure gradient across the pulmonary bed [29]. Therefore, we did not find any significant differences in the distribution of ploidy levels in the left and right ventricle.

After myocardial infarction changes in the percentage distribution of ploidy levels was detected. We found an increase and new appearance of high ploidy levels. Thus, infarction activate the DNA replicatory machinery of the remaining viable cells.

4.2. DNA content

After myocardial infarction DNA concentration as well as total DNA content were increased. For a long time it was not clear, whether this increase was caused only by connective tissue nuclei or also by myocyte nuclei. Analyzing the DNA by using cytophotometric and biochemical measurement methods, increase of the higher ploidy levels of myocyte nuclei as well as increase of the number of connective tissue nuclei could be detected. These cells mainly influence the DNA concentration and total DNA content, respectively.

4.3. Number of nuclei

As a consequence of myocardial necrosis, a decrease of the myocytes has to be expected. Results in our investigation indicate that the activation of DNA synthesis in myocytes was involved in the myocardial response after infarction. Beside an increase of higher ploidy levels, we detected that the number of myocyte nuclei was not decreased in healed infarction. Therefore it must be presumed that nuclear hyperplasia may occur after infarction. Similar results could be detected in coronary artery narrowing-induced cardiomyopathy in rats [7].

Recently it could be shown that the number of nuclei per myocyte was similar in control hearts and in patho-
logic hearts. Aging, cardiac hypertrophy and ischemic cardiomyopathy do not change the percentage of mononucleated and multinucleated myocyte in the ventricular myocardium [30]. Therefore, it must be presumed, that beside nuclear hyperplasia myocyte hyperplasia may have occurred in ischemic hearts.

However, nuclear hyperplasia may be present more frequently than expected and masked by the phenomenon of cell loss [31]. The analyzed heart (II) came from a patient with tumour cachexia; therefore, the small number of myocyte nuclei must be interpreted as atrophy.

Although myocyte loss and proliferation could be detected, stimulation of interstitial cells exceed the reaction of myocytes leading to myocardial fibrosis.

4.4. Remodelling of the myocyte nucleus

The specific function of myocytes depends on its genetic structure in such a way, that this combination represents an adequate safety device for the physiological function. We assume that prolonged and increased functional activity of the myocardium and especially the compensating hyperfunction during the break-down of a part of the myocardium is naturally leading to an increased activity of the synthesis of protein and nucleic acid in preserved myocytes [9,32].

The mechanisms of cell division and polyploidization are basically the same [33]. Replacement of cell division by polyploidization itself may be favourable for permanently functioning cells, since polyploidization does not require cell junctions and extracellular structures to be reconstructed [34].

Polyploidization is associated with increased cell size, accompanied by longer diffusion distance for oxygen and calcium, and, in addition, ischemia caused by pathologic findings in infarcted hearts leads to trophic disturbance of cardiac fibres. In this process, the reaction of larger nuclei upon critical metabolism and trophic seems to cause the division of the myocyte nuclei [35]. However, functioning of the cell is determined by the sum of its DNA content.

In conclusion, myocardial infarction was associated with an increase in DNA synthesis of the surviving myocardium. Ventricular remodelling after myocardial infarction involved myocyte loss, myocyte nuclear polyploidization and hyperplasia.

References


[22] Sandritter W, Scomazzoni G. Deoxyribonucleic acid content (Feuligen photometry) and dry weight (interference microscopy) of normal and hypertrophic heart muscle fibres. Nature 1964; 202:100.
