











Analyzing all results (including above figures), we can formulate the following conclusions:

- All parameters combinations allows to isolate the area of a high-order repeat alpha satellite (27000bp-176000bp) and areas with monomeric alpha satellite in the front domain and back domain of genomic sequence;
- Repeats length (~171bp) is shown by the first horizontal line at a frequency  $f=0.00585$ ;
- Repetition number (16) is given by the number of equidistant lines starting from  $f=0.00585$  but appears clearly only in Fig. 3 and Fig. 4 ( $L=19$ );
- Due to the large number of repeats contained in sequence good results are obtained even for small values of L parameter ( $L=3$  and Fig. 1);
- $M_m$  values affect the quality of the results. Too small or too large values lead to the deterioration of results. The best results were obtained for values of 30-40% of  $L$  value. The values of this parameter are chosen on biological criteria.

#### **4 Conclusions**

Spectral analysis and grey level spectrograms provides a robust detection method for higher order periodicity. Repeats are easily recognizable by regular horizontal lines, which give information about repeat length and number of repeats.

A polynomial-like representation of DNA sequences and an appropriate mapping algorithm provides a single numerical sequence that can be used directly in spectral analysis and yields improved results. This method can be successfully applied to alpha satellite DNA detection and yields more accurate results.

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