

Multi-Center Evaluation of a New AI-Based Karyotyping Software

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Background & Introduction

- Cytogenetics laboratories are often challenged by the extensive time and effort required to prepare karyograms using conventional approaches, particularly for the analysis of bone marrow specimens.
- This multi-center study evaluates the performance of a new artificial intelligence (AI)-based karyotyping solution compared to existing processes.

Methods

- Standard preparation and staining procedures were applied to generate G-banded slides from specimens of both normal bone marrow and constitutional blood.
- The HiBand system (Applied Spectral Imaging) was used for scanning and analysis. Metaphases, automatically identified at 10X magnification, were imaged at 100X and twenty cells were automatically selected for each case based on a predefined quality score.
- The selected cells were karyotyped using the AI software while scanning. The automatically generated karyograms were reviewed and corrected by certified cytogenetic professionals. Number of manual changes and time required to correct and analyze each cell were recorded and compared to the conventional method.

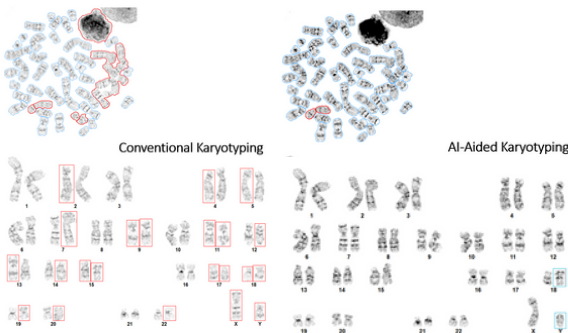


Figure 1 Representative example of automatically segmented chromosomes of a normal bone marrow metaphase (top) and automatic placement of chromosomes in the karyotype table following correction of segmentation errors (left: conventional method, right: AI-aided method, errors are highlighted in red and blue).

Results

- A total of 360 cells from 18 cases of bone marrow, and 40 cells from 2 cases of constitutional blood, were analyzed by 15 cytogenetic professionals from four independent laboratories. Each participant analyzed at least 10 cells with both conventional and AI-aided methods.
- The AI algorithm correctly segmented 90% of the 16,499 bone marrow chromosomes and 93% of the 1,838 constitutional blood chromosomes (less than 0.4% random losses were reported for both specimens).
- An average of 3.3 manual adjustments (0-10, median 3.5) were required to correct the blood metaphases and an average of 4.8 (0-15, median 4.0) to correct the bone marrow metaphases.
- The average time required to analyze each cell was 1.4±1.0 minutes for constitutional blood (0.1-6.3 min, median 1.4 min) and 1.6±1.0 minutes for bone marrow (0.3-5.0 min, median 1.5 min). This represents a 57% reduction in time spent segmenting and classifying each case when compared to the conventional method (p<0.001).

Conclusions

- This multi-center evaluation demonstrates that the new AI-based karyotyping method reduces by more than half the average time spent to prepare karyograms as compared to the current workflow.
- This enhanced efficiency is poised to significantly contribute to expediting turnaround times for the preparation of karyograms in cytogenetic labs, freeing precious time for chromosome analysis.

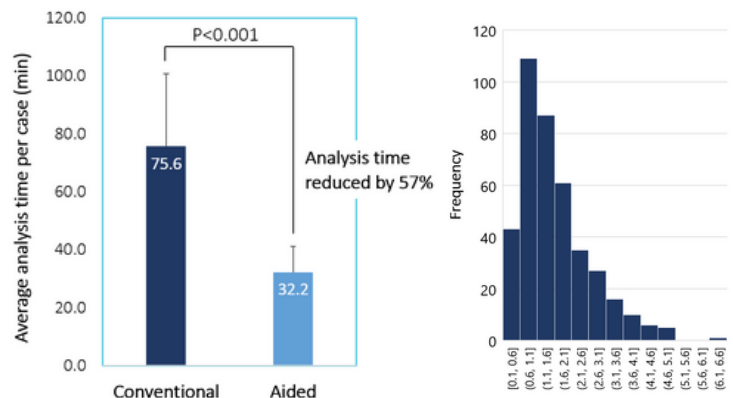


Figure 2 Compared average analysis time between conventional and aided methods for 20 normal cases (including 20 metaphases each). **Figure 3** Histogram of the time spent to prepare each metaphase (in min) using the aided method (mean 1.6±1.0 min).