Use of artificial intelligence to enhance karyotyping efficiency of both normal and abnormal cases – A first mexican experience

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Introduction

Recent advancements in artificial intelligence (AI) have been integrated into karyotyping systems. This significantly reduce the turnaround time for analysis compared to traditional processing technologies. Multicenter studies have reported that AI methods reduce, by approximately, half of the time necessary to review and correct cytogenetically normal peripheral blood (BL) and bone marrow (BM) karyograms.

Aim

The present study is a first account of the use of the AI chromosome analysis technology assessing time gains for both normal and abnormal samples in a cytogenetic laboratory located in Mexico.

Objectives

Evaluate the effectiveness of AI chromosomal analysis technology specifically in terms of reducing turnaround time compared to traditional methods in constitutional and oncological cases.

Summary

This study demonstrates that the new AI-based karyotyping method reduced by almost 70% the time spent on karyotyping peripheral blood (BL) specimens and by almost 30% the time spent on karyotyping bone marrow (BM) samples. This time reduction was similarly significant for both cytogenetically normal and abnormal cells of both types. Exposing algorithm models to larger data pools is projected to further improve the turnaround time. Moreover, as AI technology progresses, additional tools are envisioned to assist in the detection of aberrations improving time to report results for abnormal cells.

Methods

Retrospective study conducted on G-banded slides of both normal and abnormal BL and BM specimens. The slides were prepared by standard methods and scanned using the HiBand system (Applied Spectral Imaging). Analyzed and karyotyped cells were selected for each case based on established laboratory analysis protocols. The time required to analyze cases with the traditional non-AI software was compared to the time needed with the new AI tools. Statistical significance was assessed using the two-sample t-test with unequal variance. A p-value lower than 0.05 was considered significant.

References

1.The AGT Cytogenetics Laboratory Manual, *WILEY Blackwell*
2.ISCN 2024, *S.Karger AG*

Results

A total of 307 cases were analyzed by six expert cytogenetics professionals with various degrees of training. Among these cases, 214 were cytogenetically normal and 93 cytogenetically abnormal. A total of 142 cases were processed using the non-AI software (72 BL and 70 BM) and 165 using the new AI software (86 BL and 79 BM). When using the AI method, the average time spent to prepare and analyze a karyotype decreased by 69% from 15.8±5.1 to 5.0±1.7 minutes for BL cells ($p<0.001$) and by 28% from 10.0±3.7 to 7.2±2.2 minutes for BM cells ($p<0.001$). The time gain was similarly significant for both normal and abnormal BL and BM cells.

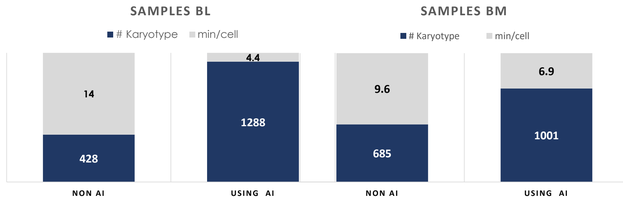


Fig 1. Comparison of time reduction and # karyotypes (min/cell) using AI

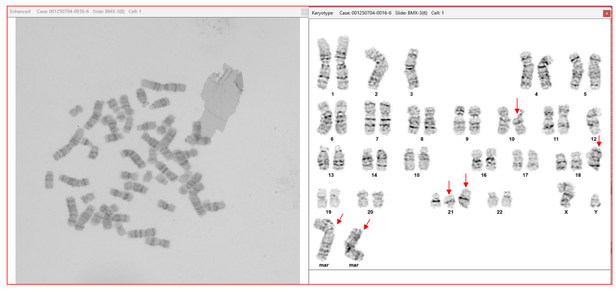


Fig 2. Example of errors in cropping and assembling the karyotype using AI

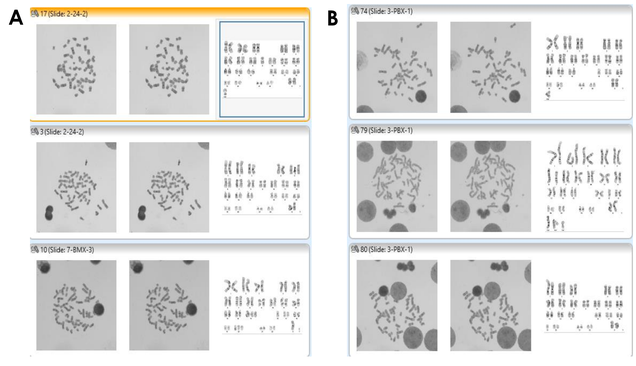


Fig 3. Automatic karyotyping of peripheral blood (A) and bone marrow sambles (B).

Discussion

Although the results are promising, it is important to consider that the effectiveness of AI technology may depend on the quality and quantity of the metaphases obtained. Integrating additional AI tools may allow for more accurate and rapid detection of chromosomal abnormalities. This study demonstrates that AI-based karyotyping technology is a valuable tool for improving efficiency and accuracy in cytogenetic analysis. The results suggest that implementing this technology can have a significant impact on clinical practice and cytogenetic research.

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