CYTOGENETIC PROFILE OF ACUTE MYELOID LEUKEMIA IN 221 MEXICAN PEDIATRIC PATIENTS

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INTRODUCTION

Pediatric acute myeloid leukemia (AML) is a rare and heterogeneous disease, with an overall survival of approximately 70% and a relapse rate of 30%. The current WHO classification recognizes entities defined by specific cytogenetic and molecular abnormalities, which determine risk stratification and adapted therapy. In terms of clinical impact, adult classification systems, cannot be completely transferred to the classification of childhood AML, because risk associations are different according to age. Also, the distribution of *RUNX1-RUNXT1*, *PML-RARA*, *CBFB-MYH11* and *KMT2A-MLLT3* in the pediatric population with AML in many countries of Latin America is poorly unknown.

AIM

Provide an updated review of cytogenetics findings in pediatric AML according to WHO entities in Mexico.

METHOD

1. Sample collection: peripheral blood/bone marrow
2. Cell cultures without mitotic stimulants
3. GTG banding
4. Cytogenetic analysis
5. ISCN Report in effect

All the samples were referred to Mendel Laboratories from institutions all over Mexico between 2020 and 2025.

CONCLUSIONS

Our findings demonstrate a heterogeneous cytogenetic landscape in pediatric AML, with recurrent translocation identified in nearly half of the cases and t(15;17) [*PML::RARA*] as the most frequent rearrangement. The identification of adverse-risk abnormalities highlights the importance of comprehensive cytogenetic and molecular characterization for accurate risk stratification. These findings contribute to the limited data on pediatric AML in Latin America and support age- and population-specific approaches to disease classification and risk-adapted therapy.

RESULTS

We analyzed the cytogenetic abnormalities according to the age groups: infants (<2 years), children (2 to <13 years), and adolescents (13 to <18 years). The largest group was children, representing 56%, followed by adolescents (38%) with a female:male ratio of 5:6 **(Fig 1)**. Translocations (fusion genes) showed major prevalence in pediatric population (47%). *PML-RARA* was the most frequent, with 26%. *RUNX1-RUNX1T1* and *CBFB-MYH11* followed with 17% and 4.5%, respectively. Cytogenetically normal cases were present in the 30% of the cases. According to Creutzig et al.[1],the cytogenomic entities associated with the highest risk in our pediatric population are monosomy 7, inv(3)(q21q26) and del(5q) **(Fig 2)**.

Figure 1. Distribution of the pediatric cases by age group

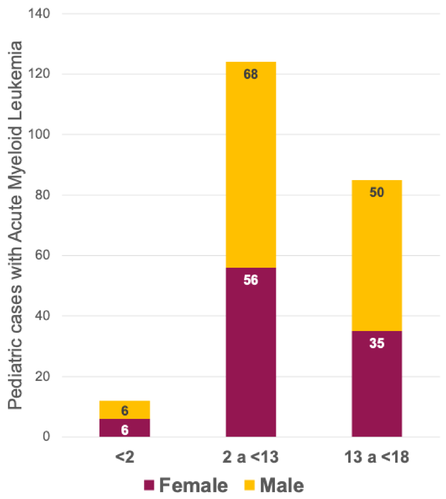
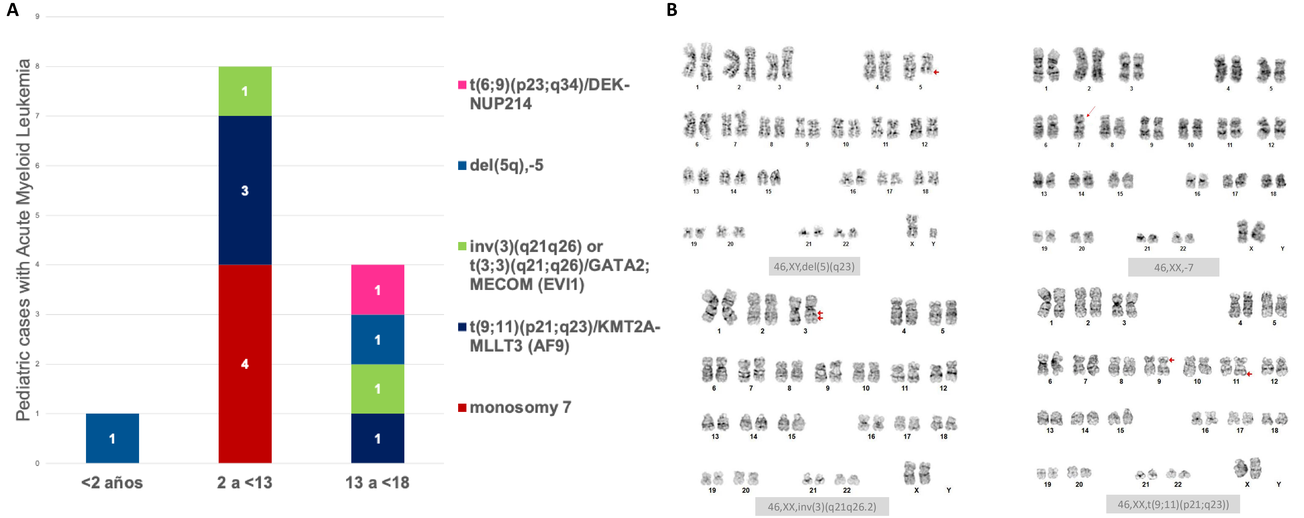


Figure 2. Intermediate and adverse abnormalities in pediatric cases. (A) Distribution of risk entities according to age group. (B) Chromosomal abnormalities.



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CONTACT INFORMATION

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