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Characteristics Analysis of Patients with SET-NUP214 Fusion Gene-Positive Acute Leukemia

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Abstract: Patients with SET-NUP214 fusion gene-positive acute leukemia are mainly young and middle-aged males, most of whom are diagnosed with T-cell acute lymphoblastic leukemia (T-ALL). Immunophenotyping is often accompanied by the expression of myeloid markers such as CD13 and CD33. Karyotype analysis presents normal karyotypes in some patients and abnormalities, including 9q34 deletion, in others. This type of leukemia is frequently accompanied by mutations of PHF6, NOTCH1, JAK3, and other genes. In terms of treatment, conventional chemotherapy has a low remission rate and tends to induce drug resistance, while allogeneic hematopoietic stem cell transplantation can bring benefits to some patients. The expression level of SET-NUP214 can be used as an indicator for follow-up of minimal residual disease and prognostic monitoring, but further expansion of sample size is required for verification to achieve better detection results.

Keywords: SET-NUP214; Fusion gene; Acute leukemia; Patient characteristic analysis

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1. Introduction

Acute leukemia is a malignant tumor of the hematological system with diverse pathogenesis, among which chromosomal abnormalities and the generation of fusion genes play decisive roles. Numerous fusion genes have been identified, and the SET-NUP214 fusion gene is relatively special and rare. Previous studies have found that SET-NUP214-positive acute leukemia shares common clinical and biological characteristics. Clinically, this disease mostly occurs in young and middle-aged males and is predominantly T-cell acute lymphoblastic leukemia, accounting for a relatively high proportion of adult T-cell acute lymphoblastic leukemia cases in the same period. Patients usually suffer from fever, hepatosplenomegaly, lymphadenopathy, and other symptoms, mostly accompanied by elevated white blood cell counts and a relatively high proportion of bone marrow blasts at onset. Biologically, immunophenotyping often shows expression of myeloid markers; karyotype analysis demonstrates normal karyotypes in some patients and complex karyotypes in a certain proportion of cases. This fusion gene frequently coexists with mutations of PHF6, NOTCH1, JAK3, and other genes. These mutant genes participate in the occurrence and progression

of leukemia, leading to diverse clinical phenotypes and prognoses [1]. In-depth analysis of the characteristics of patients with SET-NUP214-positive acute leukemia helps improve the understanding of this disease and guide clinical practice.

2. Overview of SET-NUP214 fusion gene-positive acute leukemia

The SET-NUP214 fusion gene is a rare subtype of fusion gene detected in acute leukemia [2]. Its formation is usually associated with chromosomal abnormalities such as t(9;9) (q34;q34) or del(9) (q34.11q34.13), which result in the fusion of the SET gene and the NUP214 gene [3]. This fusion gene plays an important role in the initiation and progression of acute leukemia. The abnormal fusion protein encoded by it may interfere with normal physiological functions of cells, affect cell proliferation, differentiation, apoptosis, and other processes, and further induce leukemia [4].

3. General characteristics of patients with SET-NUP214 fusion gene-positive acute leukemia

3.1. Age and gender distribution

Multiple studies have shown that SET-NUP214 fusion gene-positive acute leukemia mainly affects young and middle-aged people [5]. Retrospective analysis of patients admitted to our hospital with SET-NUP214 fusion gene-positive acute leukemia shows a median age of 36 years (range 18–50 years), with a high proportion of male patients. For example, one study included 13 patients, among whom there were 11 males and 2 females [6]. Another study analyzing 17 newly diagnosed patients over 14 years old also found a higher proportion of males. The predominance of male patients with SET-NUP214 fusion gene-positive acute leukemia may be related to patients' genetic background, hormone levels, lifestyles, and other factors, yet the specific mechanism needs further research [7].

3.2. Disease subtype distribution

SET-NUP214 fusion gene-positive acute leukemia is mainly T-cell acute lymphoblastic leukemia (T-ALL)/ T-lymphoblastic lymphoma (T-LBL). Relevant studies show a large proportion of T-ALL/T-LBL patients: among 13 enrolled patients, 10 were diagnosed with T-ALL/T-LBL, accounting for 12.20% (10/82) of adult T-ALL patients in the same period. Among 17 newly diagnosed patients over 14 years old, 13 suffered from ALL (all T-ALL, including 3 ETP, 6 Pro-T-ALL, 3 Pre-T-ALL, and 1 Medullary-T-ALL), 3 suffered from AML (2 M5 and 1 M0), and 1 patient was diagnosed with acute leukemia of ambiguous lineage (ALAL). These results indicate that the SET-NUP214 fusion gene is closely associated with T-lineage acute leukemia and may participate in abnormal regulation during T-cell development to trigger leukemia.

4. Clinical characteristics of patients with SET-NUP214 fusion gene-positive acute leukemia

4.1. Symptoms and signs

Patients often present with fever, anemia, and hemorrhage, consistent with general symptoms of acute leukemia. Fever may be caused by infection or pyrogenic substances released by leukemic cells; anemia

occurs because leukemic cells inhibit normal hematopoiesis and reduce erythropoiesis; hemorrhage is associated with thrombocytopenia and abnormal coagulation function. Physical signs such as hepatosplenomegaly and lymphadenopathy can also be observed occasionally. One study reported extramedullary infiltration in all 13 patients at admission, suggesting that SET-NUP214 fusion gene-positive acute leukemia tends to develop extramedullary infiltration, which impairs treatment and prognosis [8].

4.2. Laboratory examination indicators

4.2.1. Routine blood test

Patients usually have abnormal white blood cell counts, which can be elevated or decreased. Relevant studies report a median white blood cell count of 5.8 (1.6–135.4) $\times 10^9$/L at disease onset. Meanwhile, hemoglobin and platelet counts are generally reduced, reflecting anemia and thrombocytopenia [9].

4.2.2. Bone marrow morphology

A significantly elevated proportion of blasts in bone marrow is an important characteristic of acute leukemia [10]. Patients with SET-NUP214 fusion gene-positive acute leukemia have a median bone marrow blast proportion of 0.740 (0.568–0.912). These blasts feature abnormal morphology and function, which form the pathological basis of leukemia.

4.2.3. Immunophenotyping

Immunophenotyping is vital to clarify the cellular origin and subtype of leukemia. Immunophenotyping of patients with SET-NUP214 fusion gene-positive acute leukemia often shows expression of myeloid markers such as CD33. Relevant studies confirm that all patients express CD34 and CD7, and T-ALL patients co-express the myeloid marker CD33. This immunophenotypic feature implies that leukemic cells may possess bipotent differentiation potential toward myeloid and lymphoid lineages, increasing disease heterogeneity.

4.3. Karyotype and gene mutations

4.3.1. Karyotype analysis

Conventional karyotype analysis often fails to detect obvious abnormalities in patients with SET-NUP214 fusion gene-positive acute leukemia. In relevant studies, 4 out of 8 patients who received karyotype detection presented normal karyotypes. This may be attributed to subtle chromosomal microaberrations underlying SET-NUP214 fusion formation, which cannot be identified by conventional karyotyping. Nevertheless, some patients may carry other chromosomal abnormalities such as complex karyotypes, which are potentially related to disease progression and prognosis.

4.3.2. Gene mutations

Patients with SET-NUP214 fusion gene-positive acute leukemia are often accompanied by other gene mutations. In relevant studies, among 10 patients who underwent gene mutation detection, 2 carried PHF6 mutations, 2 carried NOTCH1 mutations, and 2 carried JAK3 mutations. PHF6 gene mutations may relate to cell growth regulation and differentiation; NOTCH1 mutations are common in T-ALL and participate in T-cell development and differentiation; JAK3 mutations may interfere with cellular signal transduction pathways. The coexistence of these gene mutations may synergistically promote the initiation and progression of

leukemia, and also provide potential therapeutic targets for the disease.

5. Analysis of rare cases with SET-NUP214 fusion gene-positive leukemia

5.1. Case 1

5.1.1. Basic information

A 28-year-old male patient presented with fever and fatigue. Routine blood test showed elevated white blood cell count, decreased hemoglobin and platelet counts. Bone marrow puncture indicated acute leukemia, and subsequent fusion gene test confirmed SET-NUP214 fusion gene positivity.

5.1.2. Clinical characteristics

The patient suffered from irregular fever with a maximum temperature of 39 ℃, accompanied by respiratory infection symptoms such as cough and expectoration. Mild hepatosplenomegaly was observed, while no obvious lymphadenopathy was palpated. Immunophenotyping revealed expression of CD34, CD7, CD33 and other antigens, consistent with the characteristics of SET-NUP214 fusion gene-positive T-cell acute lymphoblastic leukemia.

5.1.3. Treatment and prognosis

The patient received standard induction chemotherapy, but developed severe infection during induction therapy and eventually died due to ineffective treatment. This suggests that patients with SET-NUP214 fusion gene-positive acute leukemia may have poor tolerance to chemotherapy, be prone to complications, and have an unfavorable prognosis.

5.2. Case 2

5.2.1. Basic information

A 35-year-old female patient visited the hospital for extensive skin petechiae and ecchymosis. Routine blood test showed significantly reduced platelets, with normal white blood cell count and hemoglobin level. Bone marrow puncture revealed increased abnormal promyelocytes. Subsequent tests excluded PML-RARα fusion gene positivity but detected SET-NUP214 fusion gene positivity, leading to a diagnosis of variant acute promyelocytic leukemia.

5.2.2. Clinical characteristics

The patient had widespread skin petechiae and ecchymosis complicated by gingival bleeding. Chest CT showed a small amount of pulmonary exudate, suggesting potential pulmonary infection. Immunophenotyping demonstrated myeloid features of leukemic cells with partial expression of lymphoid antigens.

5.2.3. Treatment and prognosis

The patient initially received induction therapy with all-trans retinoic acid (ATRA) combined with arsenic trioxide (ATO), which yielded unsatisfactory efficacy. The regimen was then switched to combined chemotherapy, yet the induction effect remained poor. Allogeneic hematopoietic stem cell transplantation was performed afterward. Mild graft-versus-host disease (GVHD) occurred after transplantation and was

controlled by corresponding treatment. The patient currently receives regular follow-up examinations and has resumed normal life and study. It can be seen that allogeneic hematopoietic stem cell transplantation may provide a chance of cure for a small subset of patients with SET-NUP214 fusion gene-positive acute leukemia, helping them recover and return to daily life.

6. Conclusion

SET-NUP214 fusion gene-positive acute leukemia mostly occurs in young and middle-aged males, lacking specific myeloid and T-cell differentiation markers, often accompanied by chromosomal karyotype abnormalities and other gene mutations. This disease is insensitive to chemotherapy, frequently complicated by various complications and associated with an extremely poor prognosis, while allogeneic hematopoietic stem cell transplantation may cure some patients. In the future, systematic research on the correlation between SET-NUP214 fusion gene and the initiation and progression of acute leukemia based on larger sample sizes is required to discover specific targeted drugs, optimize treatment regimens, and improve patients' survival rate and quality of life. Meanwhile, active research on rare fusion gene-positive leukemia contributes to understanding the pathogenesis of leukemia, and further explores new approaches for precise treatment of leukemia.

Disclosure statement

The author declares no conflict of interest.

References

[1] Wang J, Zhan Q, Lu X, et al., 2022, The Characteristics and Prognostic Significance of the SET-CAN/NUP214 Fusion Gene in Hematological Malignancies: A Systematic Review. Medicine, 101(30): e29294.

[2] Chen S, Song W, Qin Y, et al., 2021, Analysis of the Clinical Characteristics of 24 Cases of Hematological Malignancies with SET-NUP214 Fusion Gene. Zhonghua Xue Ye Xue Za Zhi, 42(6): 459–465.

[3] Yang Q, Qian H, Jin Z, et al., 2020, SET-CAN Fusion Gene as Poor Prognosis Predictor in Adult T-Cell Acute Lymphoblastic Leukemia. Leukemia & Lymphoma, 61(1): 217–220.

[4] Zhu H, Zhao X, Qin Y, et al., 2016, B-Cell Acute Lymphoblastic Leukemia Associated with SET-NUP214 Rearrangement: A Case Report and Review of the Literature. Oncology Letters, 11(4): 2644–2650.

[5] Chen Y, Wang Q, Cen J, et al., 2023, Blast Phase of Chronic Myeloid Leukemia with Concurrent BCR::ABL1 and SET::NUP214: A Report of Two Cases. Molecular Carcinogenesis, 62(2): 117–121.

[6] Zhang H, Zhang L, Yan L, et al., 2020, SET-CAN Fusion Gene in Acute Leukemia and Myeloid Neoplasms: Report of Three Cases and a Literature Review. OncoTargets and Therapy, 13: 7665–7681.

[7] Gorello P, La Starza R, Di Giacomo D, et al., 2010, SQSTM1-NUP214: A New Gene Fusion in Adult T-Cell Acute Lymphoblastic Leukemia. Haematologica, 95(12): 2161–2163.

[8] Kau T, Way J, Silver P, 2004, Nuclear Transport and Cancer: From Mechanism to Intervention. Nature Reviews Cancer, 4(2): 106–117.

[9] Strambio-De-Castillia C, Niepel M, Rout M, 2010, The Nuclear Pore Complex: Bridging Nuclear Transport and Gene Regulation. Nature Reviews Molecular Cell Biology, 11(7): 490–501.

[10] Kim J, Lee S, Song J, et al., 2010, Molecular Characterization of Alternative SET-NUP214 Fusion Transcripts in a Case of Acute Undifferentiated Leukemia. Cancer Genetics and Cytogenetics, 201(2): 73–80.