Targeting a common genetic mutation in T-cell acute
lymphoblastic leukemia patients

Technology #cu13051

Mutated sequences in NT5C2 include sites suitable for gene inhibition therapy

Currently, T-ALL is treated using nucleoside analogs such as cytarabine, but the efficacy of this treatment is reduced in relapsed patients. This may be due to mutations in the NT5C2 gene code that inhibits these nucleoside analogs, causing the relapses seen in up to 50% of patients. The authors sequenced the mutated NT5C2 region in relapsed T-ALL patients, and found multiple sites that can potentially be targeted using inhibitors to ameliorate the deleterious effects of mutations in this gene and hinder the progression of cancer.

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Applications:
• Treatment for relapsed T-ALL patients with mutations in the NT5C2 gene.
• Treatment for other deleterious conditions that develop resistance to nucleoside analogs because NT5C2 gene mutations. Examples could include myeloid leukemia, non-Hodgkins lymphoma, and hepatitis B and C.
• Developing diagnostic for predicting resistance to nucleoside therapies.
• Drug development for NT5C2 inhibitors to overcome nucleoside analog resistance.

Advantages:
• Common shared mutation allows large populations of patients to benefit from treatments developed from this technology.
• Assist physicians in developing chemotherapy treatment plans in T-ALL patients.

Patent information: Patent pending
Licensing Status:
Available for licensing and sponsored research support
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Related Publications:


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