To the editor:

Two cases of cyclic neutropenia with acquired CSF3R mutations, with 1 developing AML

Maksim Klimiankou,1,* Sabine Mellor-Heineke,2,* Olga Klimenkova,1 Elisa Reinel,1 Murat Uenalan,3 Siarhei Kandabarau,2 Julia Skokowa,1 Karl Welte,4,† and Cornelia Zeidler2,†

1Department of Hematology, Oncology, Immunology, Rheumatology, and Pulmonology, University Hospital Tuebingen, Tuebingen, Germany; 2Department of Molecular Hematopoiesis and Severe Chronic Neutropenia International Registry, and 3Department of Experimental Hematology, Hannover Medical School, Hannover, Germany; and 4Department of Pediatrics, University Hospital Tuebingen, Tuebingen, Germany

Congenital neutropenia (CN) and cyclic neutropenia (CyN) are rare genetic disorders of hematopoiesis predominantly caused by ELANE mutations.1,3 Due to overlaps in their genetic profiles, CyN can be distinguished from CN by cycling neutrophil counts, usually at 21-day intervals, in the former. In contrast to CN, CyN is also characterized by cycling of platelets, monocytes, and reticulocytes.4,5 Infectious episodes are usually less severe in patients with CyN vs CN. Although CSF3R mutations are frequent in patients with CN and these patients are at increased risk of leukemic transformation, CSF3R mutations and transformation to acute myeloid leukemia (AML) have not been reported to date in patients with CyN.6–11

This report describes a 17-year-old female with CyN who developed AML (French-American-British classification M2). She was first diagnosed with severe neutropenia at age 4 weeks while experiencing Pseudomonas septicemia; at that time, serial blood counts were not collected. Treatment with granulocyte colony-stimulating factor (G-CSF), at a dose of 5.7 μg/kg per day, was initiated at age 2 years. The amount of G-CSF administered was not adjusted for increasing body weight, resulting in a dose of 1.7 μg/kg per day at age 13 years. After a liver abscess at age 14 years, she was referred to our center. She presented with large variations in absolute neutrophil count within our European branch of the Severe Chronic Neutropenia International Registry, with all 3 harboring an ELANE mutation p.Gln739X and an allele frequency of 10%.

To determine whether other CyN patients harbor CSF3R mutations, we performed deep sequencing of DNA from this patient’s BM MNCs obtained 3 years before the diagnosis of AML, all 22 CFU-blast colonies sequenced. Of the BM MNCs isolated at the time of overt AML, 80% were abnormal CFU-blasts, 16% were CFU-G colonies, and 4% were CFU-GM colonies (Figure 2B). All 22 CFU-blast colonies sequenced were positive for the RUNX1 mutation p.Asp171Asn present at an allele frequency of 10%.

Additionally, this CyN-AML patient was found to harbor 2 ELANE mutations, p.Ala233Pro and p.Val235TrpfsX (NP_001963.1), both located at 1 allele (Figure 1C). The ELANE fragment spanning c.697G>C and c.703delG was cloned from genomic DNA isolated from this patient’s peripheral blood MNCs. Sequencing of 20 individual bacterial clones showed that all clones carried both ELANE mutations (Figure 1C). Sequencing of DNA isolated from peripheral blood MNCs of both parents revealed no ELANE mutations (Figure 1C). Moreover, neither parent has shown signs of neutropenia or episodes of bacterial infections. Interestingly, the levels of expression of ELANE protein were much lower in BM polymorphonuclear cells of this CyN-AML patient as compared with healthy controls (Figure 1D).

CN is a preleukemic condition, with >20% of patients developing leukemia after 20 years.6–11 Approximately 80% of CN patients who develop AML are heterozygous for CSF3R mutations, suggesting the involvement of these mutations in leukemogenesis.6–12 To date, CSF3R mutations have never been reported in patients with CyN.7 Deep sequencing of DNA from this patient’s BM MNCs obtained 3 years before the diagnosis of AML revealed a clone with the acquired CSF3R mutation p.Gln741X at a 3% allele frequency (Figure 2A). Two years later, or 1 year before AML diagnosis, the CSF3R mutant allele frequency in this patient’s BM MNCs was 8%. At the time of AML diagnosis, all CSF3R-expressing BM MNCs (predominantly leukemic blasts) were positive for the p.Gln741X mutation (Figure 2A). Because cooperative RUNX1 and CSF3R mutations are present in >65% of CN-AML/MDS patients,12 we tested the patient’s BM MNCs, obtained at the time of leukemia development, for RUNX1 mutations, finding that the RUNX1 mutation p.Asp171Asn was present at an allele frequency of 10%.

A CFU assay was performed to determine the stage of myeloid differentiation at which CSF3R mutations occurred in this CyN-AML patient. Of the BM MNCs isolated at the time of overt AML, 80% were abnormal CFU-blasts, 16% were CFU-G colonies, and 4% were CFU-GM colonies (Figure 2B). All 22 CFU-blast colonies sequenced were positive for the CSF3R p.Gln741X and RUNX1 p.Asp171Asn mutations (Figure 2C).
To our knowledge, this is the first report of acquired CSF3R mutations in CyN patients, with 1 patient subsequently developing AML. The diagnosis of CyN in the first patient was verified through 2 independent courses of neutrophil counts, with this patient also showing cycling of platelets and monocytes. The second patient, with inherited CyN, was positive for an acquired CSF3R mutation, but has no signs of AML or MDS. Long-term data of the SCNIR have shown no risks of acquisition of CSF3R mutations and of myeloid transformation in patients with CyN to date.7,8 The risk of malignant transformation in patients who acquired CSF3R mutations, however, has been documented in patients with CN. In our recent analyses using the same deep-sequencing technology as has been used for the 2 CyN patients, we searched for the presence of CSF3R mutations in 45 patients with ELANE-positive CN. Sixteen of the 45 patients (35.5%) harbored CSF3R mutations; 8 of them (18%) had developed AML. The incidence of CSF3R mutations in CN suggests that clonal populations with CSF3R mutations can expand in CN patients and never evolve into malignant hematopoiesis. This finding may have parallels with recent studies showing that clonal populations with mutations in AML-associated genes are common in older adults and much more common than the frequency of AML.13 Because we have identified only 2 CyN patients with CSF3R mutations, with 1 developing AML and the other without malignant transformation to date, the clinical importance of annual CSF3R mutational analysis to identify CyN patients at high risk of developing leukemia remains unanswered. The CyN-AML patient we identified differs from other patients with CyN in that she required doses of G-CSF that were high (but still within the treatment range of CyN patients in our SCNIR). Genotype–phenotype correlations indicate that the same ELANE mutation can result in either CN or CyN, depending on the genetic background.10,14 The second CyN patient described here had typical familial CyN, inheriting from her father the ELANE p.Val190_Phe199del mutation, which is common in both CyN and CN. She responded to a very low dose (1.5 μg/kg per day) G-CSF therapy. Although CN and CyN are closely related disorders with overlapping molecular and clinical phenotypes,7 platelet cycling was not reported in CN patients in the SCNIR,1 suggesting that both...
patients described in this report had classical CyN, not masked CN. Haurie et al reported that in CyN, the available evidence indicates a broad involvement of the entire hematopoietic system, because cycling is typically observed in more than 1 of the mature hematopoietic cell types. This characterization is in agreement with our definition of CyN. In our opinion, the clinician has to decide on the clinical and molecular data available to classify a patient as CyN or CN, and prognostic counseling is based on this clinical classification.

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Correspondence: Karl Welte, University Children’s Hospital, Hoppe-Seyler-Strasse 1, 72076 Tübingen, Germany; e-mail: karl.welte@med.uni-tuebingen.de.

REFERENCES


Neutrophils are unusual in their reliance on glycolysis to maintain their energy requirements despite the presence of mitochondria and tricarboxylic acid (TCA) cycle intermediaries. This metabolic adaptation is thought in part to underpin their survival and antimicrobial function in tissues that are typically hypoxic. Despite their unique metabolism, little is known about the importance of flux between metabolic pathways in determining neutrophil survival responses. Recent work has demonstrated the importance of the hypoxia-inducible factor (HIF)/prolyl hydroxylase domain (PHD)–containing enzyme oxygen-sensing pathway in this regard, identifying both HIF-1α and PHD3 as critical regulators of neutrophil survival in hypoxia with the extended survival of neutrophils in hypoxia being dependent on HIF-1α expression. In parallel, an expanding body of work has addressed the role of HIF-1α in coordinating macrophage functional responses to proinflammatory mediators. This work led to the observation that, in macrophages, lipopolysaccharide (LPS) causes an intracellular increase in succinate levels, resulting in HIF-1α stabilization and enhanced interleukin-1β signaling. Subsequently, the metabolic rewiring of antimicrobial (M1) and tissue repair (M2) macrophages has been elucidated, with important consequences of TCA cycle activity and integrity for regulation of nitric oxide and N-glycosylation signaling, respectively. Whether TCA cycle activity and succinate accumulation regulates HIF-1α and hypoxic survival in neutrophils is unknown.

Patients with rare germ line mutations in genes encoding the TCA cycle enzyme succinate dehydrogenase (SDH) allow us to directly question the role of the TCA cycle and mitochondrial respiratory chain in neutrophil survival responses. SDH oxidizes succinate to fumarate in the TCA cycle and is a ubiquinone oxidoreductase, also functioning in complex II of the respiratory chain. SDH comprises four subunits (A-D), with inherited mutations of each of the subunits linked to the development of pheochromocytoma (PHEO) and paraganglioma (PGL) after somatic inactivation of the wild-type allele and loss of heterozygosity.

We questioned whether heterozygous germ line mutations in SDHB (SDHBx) would reduce SDH activity in the peripheral blood neutrophils of these patients, leading to accumulation of intracellular succinate. HIF-1α stabilization, and a pseudohypoxic survival phenotype, given the importance of the B subunit for SDH catalytic function and its high prevalence within PHEO/PGL patient populations.

To determine whether succinate is implicated in regulating neutrophil survival responses, we isolated peripheral blood neutrophils from patients with heterozygous germ line SDHBx mutations in whom an increase in intracellular succinate would be predicted. In total, 20 individuals with frameshift, splice, missense, or nonsense mutations were studied (supplemental Table 1, available on the Blood Web site). Although all but 1 patient displayed plasma succinate levels within the normal range, a significantly higher plasma succinate level was observed in patients with SDHBx (Figure 1A). To confirm the consequence of SDHB mutations on intracellular succinate and to measure other TCA cycle and glycolytic intermediaries, peripheral blood neutrophils were isolated from 3 individuals with SDHBx and 3 healthy controls, and relative metabolite abundance was determined by gas chromatography–mass spectrometry (Figure 1B).

Succinate was significantly more abundant in neutrophils isolated from patients with SDHBx than from controls. This finding was paralleled by increases in lactic acid and citric acid, but no changes in other TCA cycle intermediaries (α-ketoglutaric acid, fumaric acid, or malic acid) were observed. Thus, neutrophils heterozygous for mutant SDHB gene expression display the predicted elevation in intracellular succinate, but with no decrease in downstream TCA cycle intermediaries. Citric acid levels were increased, which may reflect an increase in biosynthetic requirements outside the TCA cycle. In keeping with the increased succinate in SDHBx neutrophils, a detectable increase in protein succinylation was also observed (Figure 1C).

To the editor:

Mutations in succinate dehydrogenase B (SDHB) enhance neutrophil survival independent of HIF-1α expression

Robert Jones, Kate E. McDonald, Joseph A. Willson, Bart Ghesquièreme, David Sammut, Eleni Daniel, Pranvera Sadiku, Brian G. Keevil, Peter Carmeliet, Moira K. B. Whyte, John Newell-Price, and Sarah R. Walmsley

1Department of Infection, Immunity, and Cardiovascular Disease and 2Department of Oncology and Metabolism, University of Sheffield, Sheffield, United Kingdom; 3Medical Research Council/University of Edinburgh Centre for Inflammation Research, Queen’s Medical Research Institute, University of Edinburgh, Edinburgh, United Kingdom; 4Laboratory of Angiogenesis and Vascular Metabolism, Vesalius Research Center, VIB, Leuven, Belgium; 5Department of Oncology, KU Leuven, Leuven, Belgium; and 6School of Medicine, University of Manchester, Manchester, United Kingdom


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