Brief report

Deletion of the α-globin gene cluster as a cause of acquired α-thalassemia in myelodysplastic syndrome

David P. Steensma, Vip Viprakasit, Alex Hendrick, David K. Goff, Joanne Leach, Richard J. Gibbons, and Douglas R. Higgs

Rarely, myelodysplastic syndrome (MDS) is complicated by an acquired form of α-thalassemia (α-thalassemia in myelodysplastic syndrome [ATMDS]) characterized by hypochromic, microcytic, anisopikilocytic red blood cells with hemoglobin H (HbH) inclusions. Acquired mutations in ATRX, a chromatin remodeling gene, have recently been found in 12 patients with typical features of ATMDS, though they have not been detected in MDS patients with similar red blood cell findings but little HbH. The α-globin genes themselves have appeared normal in all ATMDS patients studied to date. Here we characterize the molecular defect in a unique MDS patient with rare HbH inclusions in which an abnormal clone lost a greater than 1.9-Mb segment of the telomeric region of chromosome 16, including both α-globin genes. Red blood cell changes associated with this acquired somatic genotype (−/αα) are surprisingly severe, demonstrating that a minor globin chain imbalance may be unexpectedly deleterious during the abnormal erythropoiesis that occurs in the context of MDS. (Blood. 2004;103:1518-1520)

© 2004 by The American Society of Hematology

Study design

A 72-year-old white British man had microcytic, hypochromic anemia (hemoglobin count, 10.4 g/dL; mean corpuscular volume, 64 fl; mean corpuscular hemoglobin level, 21.7 pg) and neutropenia (leukocyte count, 10.9 × 10⁹/L with 14.7% neutrophils). Two years earlier, he had undergone partial pneumonectomy for localized lung carcinoma; at that time complete blood count findings were normal. The patient had no Mediterranean or Asian ancestors, there was no family history of a hematologic disorder, and iron study results were unremarkable.

From the Medical Research Council Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, John Radcliffe Hospital, University of Oxford, United Kingdom; Division of Hematology, Department of Medicine, Mayo Clinic, Rochester, MN; Department of Pediatrics Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, Thailand; Departments of Clinical and Laboratory Haematology, City Hospitals Sunderland NHS Trust, Tyne and Wear, United Kingdom.


V.V., J.L., R.J.G., and D.R.H. are supported by the Medical Research Council.

D.P.S. is a Mayo Foundation Research Scholar supported by the Mayo Foundation.

Reprints: David P. Steensma, MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, John Radcliffe Hospital, University of Oxford, Headington Oxford OX3 9DU, United Kingdom; e-mail: david.steensma@imrn.ox.ac.uk; steensma.david@mayo.edu.

The publication costs of this article were defrayed in part by page charge payment. Therefore, and solely to indicate this fact, this article is hereby marked “advertisement” in accordance with 18 U.S.C. section 1734.

© 2004 by The American Society of Hematology
Peripheral blood smears demonstrated a dimorphic red cell picture with striking anisopoikilocytosis, microcytosis, and severely hypochromic “ghost” erythrocytes (Figure 1A). A bone marrow aspirate was hypercellular, with marked erythroid hyperplasia, trilineage dysplasia, rare ringed sideroblasts, and no excess of myeloblasts (MDS subtype, refractory anemia with excess blasts, non–hemoglobin H disease). 3 Severe microcytosis and hypochromia is unusual in MDS in the absence of iron deficiency but is typical of ATMDS. 3 In the present case, severe microcytosis and hypochromia was seen, with a mean corpuscular volume of 78 fl and a mean corpuscular hemoglobin concentration of 29 g/dL. Blood smear abnormalities included ghost cells (Figure 1B), nucleated red cells, and hypersegmented neutrophils (Figure 1A). One finding worthy of note was the presence of red blood cells with HbH inclusions (Figure 1B), a finding that is not usually observed in MDS. 3 The patient had an elevated reticulocyte count of 10% red cell precursors, with an HbH content of 2.0% and 10% HbH-containing red blood cells. 3 A supravital stain for HbH inclusions was positive, confirming the presence of HbH inclusions in the patient’s red blood cells.

Globin chain synthesis was measured by labeling an enriched reticulocyte preparation derived from fresh heparinized marrow with 3H leucine, precipitating globin chains, and measuring radioactivity on a liquid scintillation counter, as previously described. 20 Conventional G-banded cytogenetic analysis of unstimulated bone marrow was followed by fluorescence in situ hybridization (FISH) studies of metaphase spreads and interphase nuclei using standard hybridization protocols with cosmid probes specific for the telomeric region of the short arm of chromosome 16, including CRA36, GG1,415C1, and 439A6 (the most proximal of the 4 cosmids, mapping 1.9 Mb from the telomere).

Peripheral blood was separated into granulocyte-enriched and mononuclear cell–enriched fractions by double-density Ficoll-Hypaque (Sigma, St Louis, MO) centrifugation, and DNA was extracted from each fraction using the phenol-chloroform method. For analysis of the α-globin 3′ hypervariable region (an array of 17-bp tandem repeats with high interallelic variability located 8 kb downstream of the α-globin gene complex15), DNA was digested with HindIII restriction endonuclease, and the fragments were electrophoresed through a 1% agarose gel and identified by blot hybridization using a 32P-labeled 4.0-kb HindIII fragment as a probe and autoradiographed. The 5′ hypervariable region (100 kb upstream of the α-globin genes13) was analyzed in similar fashion after DNA digestion with AluI. To probe the α and κ genes directly, DNA was digested with BamHI and BglII and was hybridized on separate blots with radiolabeled 0.5-kb HindIII PstI α-globin probe and κ-globin probe and then autoradiographed.

Haplotyping analysis of the β-globin gene cluster was performed on unfractionated blood and granulocyte and mononuclear cell fractions as previously described, 14 with the addition of the XmnI restriction site at position −158. The remaining α-globin genes were sequenced to exclude point mutations15 using the BigDye (ABI, Foster City, CA) technique.

Results and discussion

Severe microcytosis and hypochromia is unusual in MDS in the absence of iron deficiency but is typical of ATMDS. 3 In the present case, a hypochromic microcytic blood film (Figure 1A) prompted further study to elucidate the underlying molecular defect. In contrast to most previously reported cases of ATMDS in which patients who have not undergone transfusion have had more than 10% HbH-containing red blood cells, here supravital staining demonstrated only 0.11% erythrocytes containing HbH inclusions (Figure 1B). Hemoglobin electrophoresis showed 2.0% hemoglobin A2 and 1.4% hemoglobin F; no clear peak corresponding to
HbH was observed. The patient’s βα/β α globin chain synthesis ratio was reduced to 0.81 (normal, 0.90-1.20), a value typical of heterozygous α-thalassemia (genotypes −α/αα or −/−αα).

The patient’s marrow karyotype was complex and included a rearrangement of the telomeric region of the short arm of chromosome 16: 45, X, −Y, add(3)(q25), del(3)(q25)del(3)(q25), del(4)(p15), del(5)(q21)del(5)(p14), del(6)(p21), −7, del (11)add(q11)del(11q23), del(13)(13;21)(p11;q11), del(16)add(p13)add(q22), −18, −20, −21, +4mar[cp10]/46, XY[1]. FISH studies with the 4 cosmids probes demonstrated signals on the normal chromosome 16 only, indicating that the deletion extended at least 1.9 Mb from the 16p telomere (Figure 1C).

Southern blot analysis of DNA from the patient’s unfractionated blood with 16p-specific polymorphic markers demonstrated moderately reduced intensity of 1 of the 2 bands corresponding to the closely linked αα-globin alleles when compared with healthy controls (Figure 1D). Using DNA isolated from the patient’s purified granulocytes, the band corresponding to the abnormal allele was almost absent, consistent with deletion of 1 of 2 α-globin clusters, but the band was preserved in the mononuclear cells (Figure 1D). In MDS, involvement of myeloid lineages, including granulocytes, in the neoplastic clone is more common than involvement of lymphocytes, and it is likely that the granulocyte fraction in this patient was enriched for the chromosomal abnormality compared with unfractionated blood and the mononuclear cell fraction. Southern blots using probes for the α and ζ genes also demonstrated reduced band intensity compared with healthy controls (data not shown), consistent with the loss of 1 copy of the entire α-globin cluster in myeloid cells. Therefore, the MDS clone exhibited a thalassemic (−/−αα) genotype despite a normal (αα/αα) constitutional haplotype. Haplotypic analysis of the β-globin gene cluster was unremarkable, demonstrating no loss of heterozygosity, the remaining α1 and α2 genes in granulocyte DNA was also normal (data not shown).

Genomic instability in MDS is well recognized, though the underlying etiology remains unclear.17,18 It is probable that the clonal chromosomal loss in the present MDS patient was a random genetic event, manifest as a dramatic red blood cell phenotype as a consequence of loss of 2 α-globin genes; 16p13 is not a common breakpoint in MDS.19 Other examples of acquired red blood cell abnormalities associated with MDS include loss of glycosylphosphatidylinositol (GPI)–anchored proteins including CD55 and CD59,20 enzymeopathies (especially pyruvate kinase deficiency),21 membrane defects including elliptocytosis,22 and blood group isotype changes including exposure of cryptantigens.23,24

To our knowledge this is the first report of a patient with ATMDS in whom an acquired α-globin deletion was demonstrable. This case illustrates that the loss of a single α-globin cluster can cause a dramatic acquired thalassemic phenotype in MDS. It is unclear why the red blood cell changes in this patient are more severe than one would normally see associated with the loss of only 2 of 4 α genes (−/−αα); this may reflect an interaction between minor globin chain imbalance and the already markedly disordered hematopoiesis in MDS. Further molecular characterization of ATMDS patients will help define the mechanisms responsible for this interesting association and may explain the unexpectedly severe red blood cell phenotype.

Acknowledgments

We thank Helena Ayyub for technical assistance and Veronica J. Buckle for comments on the manuscript.

References


Deletion of the $\alpha$-globin gene cluster as a cause of acquired $\alpha$-thalassemia in myelodysplastic syndrome

David P. Steensma, Vip Viprakasit, Alex Hendrick, David K. Goff, Joanne Leach, Richard J. Gibbons and Douglas R. Higgs