ras Gene Mutations and Clonal Analysis Using RFLPs of X-chromosome Genes in Myelodysplastic Syndromes*

J. W. G. Janssen 1, M. Buschle 1, M. Layton 2, J. Lyons 1, and C. R. Bartram 1

A. Introduction

Myelodysplastic syndromes (MDS) comprise a heterogeneous group of clonal disorders characterized by quantitative and qualitative abnormalities of hematopoiesis [1, 2].

Up to 30% of cases eventually develop into acute nonlymphocytic leukemia (ANLL). Previous observations by us and others have demonstrated a frequent (30%) activation of the N-ras oncogene in ANLL [3-6].

The involvement of the different cell lineages in MDS has been rather controversial. Various approaches such as isoenzyme studies (G-6-PD polymorphisms), cytogenetic analysis (clonal chromosome abnormalities), and autosomal DNA polymorphism as markers of clonality have been employed to study the stem cell origin of MDS. However, these analyses produced conflicting data and have not clearly identified the stem cell origin of MDS [7-12].

Although no accepted effective treatment exists for MDS, some studies have reported response rates of up to 30% to the administration of low-dose cytarabine (LD-AraC) [13, 14], whereas other studies demonstrate a cytotoxic effect of LD-AraC [15, 16].

In this report we address the possible role of ras in MDS, the identification of its stem cell origin, and the biological action of LD-AraC treatment in MDS.

B. Materials and Methods

I. Patients

Eighty-one cases of primary MDS were screened for ras point mutations. The patients were classified according to FAB criteria: there were 19 cases of refractory anemia (RA), nine cases of refractory anemia with ring sideroblasts (RARS), 22 cases of refractory anemia with excess blasts (RAEB), seven cases of refractory anemia with excess blasts in transformation (RAEB-T), and 24 cases of chronic myelomonocytic leukemia (CMMoL). Peripheral blood or bone marrow samples, as well as a skin biopsy from one patient, were obtained with informed consent.

Moreover, seven of these patients were investigated for clonality, including three patients with RA, two with RARS, one patient with RAEB, and one with CM-MoL.

Lymphocyte counts of the samples were between 43% and 52%. Peripheral blood did not contain any blasts except for that of the RAEB patient, who had 1% blasts.

II. Southern Blot Analysis

High-molecular-weight DNA was prepared from bone marrow or peripheral
blood cells by standard techniques. Clonal analyses with the X-linked phosphoglycerate kinase (PGK) probe were performed as described by Vogelstein et al. [17].

III. Detection of ras Gene Mutations

About 150 ng of genomic DNA were amplified for ras sequences by means of the polymerase chain reaction (PCR) [18]. Amplified DNA was spotted onto nylon filters, fixed by UV illumination, and hybridized with an oligomer panel that is able to detect all possible amino acid substitutions at codons 12, 13, and 61 of N-ras, Ki-ras, and H-ras [19].

C. Results

By means of a rapid dot-blot screening procedure based on a combination of in vitro amplification of ras-specific sequences and hybridization to specific oligonucleotide probes, we analyzed 81 cases of MDS for point mutations at codons 12, 13, and 61 in N-ras, Ki-ras, and H-ras. Mutations of Ki-ras and N-ras were detected in four cases. One RAEB showed a Ki-ras mutation, two CMMoLs exhibited N-ras mutations, and one other CMMoL scored positive for a mutation of Ki-ras at codon 12. In all four ras-positive cases, the normal ras allele was also present.

As the positive MDS samples contained less than 5% blasts and our dot-blot technique is able to detect a ras point mutation only if more than 10% of the cells are positive, we conclude that hematopoietic cells characterized by a ras gene mutation have maintained the potential to differentiate in vivo.

In order to determine which cell lineages are involved in MDS we performed cell separation studies of two cases of ras mutation-positive CMMoL. Mononuclear cells and granulocytes were separated by standard Ficoll-Hypaque density gradient centrifugation. T- and B-lymphocytes and monocytes were fractionated by positive selection with immunomagnetic beads [20]. Thus we could show that the ras mutation was present in all four cell fractions, including granulocyte, monocyte, T- and B-lymphocyte lineages ([6]; unpublished results).

Figure 1 shows the analysis of a ras-positive case of MDS, a patient suffering from RAEB who was treated with LD-AraC. The wild-type codon 12 Ki-ras allele (glycine) was present before as well as after treatment. However, the mutated ras allele had disappeared completely after low-dose AraC treatment.

In seven female MDS patients belonging to different FAB types we investigated clonality by X-chromosome inactivation analyses. For this purpose we employed a recently published technique that utilizes the occurrence of DNA polymorphisms at X-linked loci [17]. The active and inactive alleles can be distinguished from each other by a methylation-sensitive endonuclease, as the 5' cytosine methylation pattern of

Fig. 1. Disappearance of mutated Ki-ras sequence after treatment with low-dose AraC. Five nanograms of amplified DNA from a patient with RAEB was spotted onto a nylon filter and hybridized to oligomers representing the Ki-ras wild-type allele (top row) and the Ki-ras mutated allele (bottom row). DNA analysis had shown a mutation of one allele at codon 12, Ki-ras substituting valine (GTT) for glycine (GGT) in peripheral blood cells (a) at presentation. Loss of ras mutation was observed in peripheral blood (b) and bone marrow (c) after a second course of LD-AraC.