



Lymphohematopoietic Cancers Induced by Chemicals and Other Agents: Overview and Implications for Risk Assessment

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ABSTRACT

The objective of this report is to provide an overview of the types and mechanisms underlying the lymphohematopoietic cancers induced by chemical agents and radiation in humans, with a primary emphasis on leukemia and leukemia-inducing agents. Following a brief discussion of hematopoiesis and leukemogenesis, a review of the major classes of leukemia-inducing agents—radiation, chemotherapeutic alkylating agents, and topoisomerase II inhibitors—is presented along with information on the mechanisms by which these leukemias occur. This information is then compared with similar information for selected environmental and occupational leukemia-inducing agents. The last section focuses on how mechanistic information on human leukemia-inducing agents can be used to better inform risk assessment decisions. It is evident that there are different types of leukemia-inducing agents that act through different mechanisms. Even though most have a mutagenic mode of action, leukemia-inducing agents have different potencies and associated risks, which appear to be significantly influenced by the specific mechanisms involved in leukemogenesis. Identifying the specific types of cancer-causing agents with their associated mechanisms and using this information to inform key steps in the risk assessment process remains one of the ongoing challenges for research and regulatory scientists.

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CONTENTS

LIST OF TABLES	v
LIST OF FIGURES	vi
LIST OF ABBREVIATIONS.....	vii
PREFACE.....	viii
AUTHORS, CONTRIBUTORS, AND REVIEWERS	ix
EXECUTIVE SUMMARY	xi
1. INTRODUCTION TO LYMPHOHEMATOPOIETIC CANCERS.....	1
1.1. OVERALL INCIDENCE AND TRENDS	3
2. HEMATOPOIESIS	5
3. ORIGINS OF LYMPHOHEMATOPOIETIC NEOPLASIA	8
4. LEUKEMIA- AND LYMPHOMA-INDUCING AGENTS	11
5. OVERVIEW OF THE MAJOR CLASSES OF LEUKEMIA-INDUCING AGENTS	13
5.1. IONIZING RADIATION	13
5.2. CHEMOTHERAPEUTIC AGENTS	14
5.2.1. Alkylating Agent-Related Leukemias	15
5.2.2. Topoisomerase II Inhibitor-Related Leukemias	16
5.2.3. Other Likely Leukemia-Inducing Therapeutic Agents	19
6. MECHANISMS INVOLVED IN t-AML	21
7. FACTORS CONFERRING AN INCREASED RISK OF INDUCED LEUKEMIA	24
7.1. MYELOSUPPRESSION AND IMMUNOTOXICITY	24
7.2. GENETIC POLYMORPHISMS	25
8. EXAMPLES OF SPECIFIC LEUKEMIA-INDUCING CHEMICALS.....	29
8.1. MELPHALAN.....	29
8.2. ETHYLENE OXIDE	30
8.3. 1,3-BUTADIENE	32
8.4. FORMALDEHYDE	35
9. RISK ASSESSMENT IMPLICATIONS	37
9.1. HAZARD IDENTIFICATION.....	37
9.1.1. Utility of Short-Term Genotoxicity Tests.....	38
9.1.2. Usefulness of Animal Bioassays.....	39
9.1.3. Combining Different Types of Lymphohematopoietic Cancers for Analysis...	40

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CONTENTS (continued)

9.1.4. Potential Influence of Latency Period in Identifying Leukemogens 42
9.1.5. Metabolism and Bioactive Dose at the Target Organ..... 43
9.1.6. DNA-Adduct Type, Metabolism, and Repair 44
9.1.7. Individual Susceptibility 45
9.1.8. Summary 46
REFERENCES 70

This document is a draft for review purposes only and does not constitute Agency policy.

LIST OF TABLES

Table 1.	Simplified classification of the major lymphohematopoietic neoplastic diseases in humans based largely on the French-American-British (FAB) classification	47
Table 2.	WHO classification of myeloid and related neoplasms	49
Table 3.	WHO classification of lymphoid neoplasms.....	51
Table 4.	Cytogenetic comparisons of <i>de novo</i> leukemias and t-AML	54
Table 5.	Frequency of molecular mutations in <i>de novo</i> AML and t-MDS/t-AML	56
Table 6.	Gene mutations observed in the Copenhagen series of 140 patients with t-MDS (<i>n</i> = 89) or t-AML (<i>n</i> = 51).....	57
Table 7.	Characteristics of selected known and probable human leukemia- and lymphoma-inducing agents.....	58
Table 8.	Likely mechanisms involved in the carcinogenesis of selected known and probable human leukemia- and lymphoma-inducing agents.....	61
Table 9.	General characteristics of human leukemias and related neoplasms induced by recognized leukemia-inducing agents	66

LIST OF FIGURES

Figure 1. Simplified model of hematopoiesis showing lineages of major types of hematopoietic cells..... 67

Figure 2. Hierarchical stem cell origins of leukemia and related cancers 68

Figure 3. Genetic pathways of t-MDS and t-AML based on 140 cases from the Copenhagen study group..... 69

LIST OF ABBREVIATIONS

ALL	acute lymphoblastic leukemia
AML	acute myeloid leukemia
ANLL	acute nonlymphocytic leukemias
BEIR	Biological Effects of Ionizing Radiation
CLL	chronic lymphocytic leukemia
CML	chronic myeloid leukemia
EMS	ethyl methane sulfonate
ENU	<i>N</i> -nitroso- <i>N</i> -ethylurea
FAB	French-American-British
IARC	International Agency for Research on Cancer
MDS	myelodysplastic syndromes
MM	multiple myeloma
NCI	National Cancer Institute
NHL	non-Hodgkin lymphoma
NK	natural killer
NQO1	NADPH quinone oxidoreductase 1
SCE	sister chromatid exchange
SEER	Surveillance Epidemiology and End Results
t-AML	karyotypes of patients who have developed leukemia following therapy
TMPT	thiopurine methyltransferase
UNSCEAR	United Nations Scientific Committee on the Effects of Atomic Radiation
WHO	World Health Organization

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PREFACE

This report represents the update and expansion of two earlier U.S. Environmental Protection Agency (EPA) documents entitled “Chemical and Radiation Leukemogenesis in Humans and Rodents and the Value of Rodent Models for Assessing Risks of Lymphohematopoietic Cancers” (EPA/600/R-97/090, May 1997). This report provides an overview of chemically-induced leukemias and lymphomas and is intended to provide insights into how mechanistic information on leukemia-inducing agents can be used to assess risks from leukemia-inducing agents.

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EXECUTIVE SUMMARY

Lymphohematopoietic neoplasias represent a heterogeneous group of clonal hematopoietic and lymphoid cell disorders and are one of the most common types of cancer induced by environmental and therapeutic agents. The objective of this report is to provide an overview of the types and mechanisms underlying the lymphohematopoietic cancers induced by chemical agents and radiation in humans, with a primary emphasis on leukemia and leukemia-inducing agents. Following a brief discussion of hematopoiesis and leukemogenesis, a review of the major classes of leukemia-inducing agents—radiation, chemotherapeutic alkylating agents, and topoisomerase II inhibitors—is presented along with information on the mechanisms by which these leukemias occur. This information is then compared with similar information for selected environmental and occupational leukemia-inducing agents. The last section focuses on how mechanistic information on human leukemia-inducing agents can be used to better inform risk assessment decisions. A brief overview of the major points in the report is presented below.

It is widely recognized that lymphohematopoietic neoplasms originate through multi-step processes involving a series of genetic and epigenetic alterations that transform a normal hematopoietic or lymphoid cell into a malignant tumor. The various lymphohematopoietic cancers are believed to originate in specific types of pluripotent or lineage restricted cells at different stages in hematopoiesis and immune cell development. Current evidence indicates that the acute and chronic myeloid leukemias (CMLs) as well as precursor lymphomas, the acute lymphoblastic leukemias (ALL) – B lymphoblastic leukemia/lymphoma and T lymphoblastic leukemia/lymphoma originate in hematopoietic stem or progenitor cells; whereas, other lymphomas and chronic lymphocytic leukemia (CLL) have their origins in mature lymphoid cells. This information on the origin of these cancers as well as morphologic, cytochemical and immunophenotypic features of the neoplastic cells provide valuable information for grouping various lymphohematopoietic cancers and for identifying the cell types targeted by carcinogenic agents.

Lymphohematopoietic neoplasia represents one of the most common cancers induced by chemical, physical, and infectious agents. To date, the International Agency for Research on Cancer (IARC) has identified over 100 agents as human carcinogens. Of these, approximately 25% have been shown to induce either leukemias or lymphomas in humans. Many of these are antineoplastic drugs, but

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a variety of other agents including industrial chemicals, various forms of radiation, immunosuppressive drugs, and infectious agents have also been shown to induce lymphohematopoietic cancers in humans. In evaluating the different types of induced leukemias and lymphomas, a number of general patterns become apparent. Leukemias are the primary type of cancer induced by chemical agents. Most of these are acute nonlymphocytic leukemias (ANLLs, synonymous with acute myeloid leukemia [AML]) with relatively short median latency periods and are formed through the induction of mutations affecting critical cancer-related genes. Radiation, which is also thought to act through a mutagenic mode of action, is frequently associated with ANLL as well as CML and ALL.

Exposure to a variety of infectious agents is causally related to the formation of lymphoid neoplasms. The induced lymphomas identified to date appear to be primarily associated with chronic infection with either viruses or *Helicobacter* bacteria, agents that are immunomodulating, and/or specifically target lymphoid cells. Two chemical agents, cyclosporine and azathioprine, which are associated with the development of non-Hodgkin lymphoma (NHL) are also strongly immunosuppressive, and this immunosuppression is believed to play a critical role in the development of the associated lymphomas.

Among the induced leukemias, different subtypes with particular characteristics have shown to be induced by different classes of agents. For example, the alkylating agent class of chemotherapeutic agents typically induces acute myeloblastic leukemias that are often preceded by a myelodysplastic phase and are characterized by loss of all or part of chromosomes 5 or 7. These leukemias generally develop with a median latency period of 5–7 years from the beginning of treatment. In contrast, the leukemias induced by the epipodophyllotoxin class of topoisomerase II inhibitors develop much sooner with a median latency period of 2–3 years. These leukemias are typically characterized as monocytic or myelomonocytic subtypes and exhibit reciprocal translocations involving a specific region on the long arm of chromosome 11 (11q23). While much less is known about leukemias and lymphomas induced by environmental agents such as ethylene oxide and 1,3-butadiene, the types of neoplasms causally associated with these agents appear to differ substantially from those described above and suggest that these agents belong to a separate class of carcinogenic agent.

The last section of the report discusses how mechanistic information on human leukemia-inducing agents can be used to better assess the risks from exposure to environmental chemicals. A range of topics is considered including brief discussions on the usefulness of short-term and

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animal bioassays, the combining of various tumor types for analysis, the impact of latency periods on the detection of leukemias, and the modifying influences of metabolism, pharmacokinetics, DNA-adduct type and repair, as well as individual susceptibility factors in assessing the risks associated with leukemia-inducing agents

In conclusion, it is evident that there are different types of leukemia-inducing agents that act through different mechanisms. Even though most have a mutagenic mode of action, leukemia-inducing agents have different potencies and associated risks, which appear to be significantly influenced by the specific mechanisms involved in leukemogenesis. Identifying the specific types of cancer-causing agents with their associated mechanisms and using this information to inform key steps in the risk assessment process remains one of the ongoing challenges for research and regulatory scientists. For the alkylating agent class of carcinogens, an approach such as that described by Vogel and colleagues (Vogel et al., 1998) supplemented with more recent genomic, proteomic, and biomarker information would appear to present a reasonable and scientifically valid step towards this objective.

1 **1. INTRODUCTION TO LYMPHOHEMATOPOIETIC CANCERS**

2
3
4 Lymphohematopoietic neoplasia can be described as an uncontrolled proliferation or
5 expansion of hematopoietic and lymphoid cells that are unable to differentiate normally to form
6 mature blood cells (Sawyers et al., 1991). These neoplasms represent clonal expansions of
7 hematopoietic cells, almost always within either the myeloid or lymphoid lineage (Nowell, 1991;
8 WHO, 2008). Infrequently, some leukemias exhibit both myeloid and lymphoid characteristics
9 and are known as biphenotypic leukemias (Russell, 1997). The myeloid clones are designated as
10 chronic or acute leukemias, depending upon the rate of clonal expansion and the stage of
11 differentiation that dominates the leukemic clone. Lymphoid neoplasms typically manifest
12 themselves in the blood as chronic or acute lymphoblastic leukemias or remain confined to
13 lymphoid proliferative sites such as the lymph nodes or spleen and are designated as lymphomas
14 (Nowell, 1991). Acute leukemias tend to have a rapid onset with a predominance of immature
15 cells whereas chronic leukemias have a more insidious onset and progress over a period of
16 months or years to a blast or acute leukemic phase.

17 Using this basic classification, leukemias can be described as one of four major types—
18 acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphoblastic
19 leukemia (CLL), and chronic myeloid leukemia (CML). Similarly, lymphomas are broadly
20 classified as Hodgkin or non-Hodgkin lymphomas (NHL) depending upon the appearance of a
21 specific cancer cell type, the Reed-Sternberg cell, which is found in Hodgkin lymphomas (ACS,
22 2009). Within these larger groupings, there are numerous subtypes involving specific cells that
23 have unique characteristics, origins, and increasingly recognized clinical significance. These
24 subtypes are generally classified according to morphologic, cytogenetic, immunophenotypic, and
25 more recently, molecular characteristics according to the French-American-British (FAB) or
26 World Health Organization (WHO) classification systems (Head and Pui, 1999; WHO, 2001,
27 2008; Haferlatch et al., 2005). For convenience, a simplified classification scheme for the
28 leukemias and lymphomas based largely on the FAB classification system (shown in Table 1
29 [Sullivan, 1993]) will be the basis for most descriptions used in this document. A more thorough
30 and complicated classification of the primary types and subtypes of lymphohematopoietic
31 diseases based on the most recent WHO classification (WHO, 2008; Vardiman et al., 2009) is
32 shown in Tables 2 and 3 for myeloid and lymphoid neoplasms, respectively. It should be noted

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1 that in the more recent WHO classifications (IARC, 2008c), lymphocytic leukemias and
2 lymphomas are no longer considered to be different diseases and should be evaluated
3 accordingly. However, for simplicity and due to the difficulties involved in reclassifying
4 neoplasms based on studies that were conducted many years ago, the classifications used in the
5 original studies or in the IARC monographs will be used in this document. It should be
6 recognized, however, that considerable heterogeneity exists among NHL subtypes as classified
7 according to older classification systems (Morton et al., 2007). In addition, the older schemes do
8 not consider temporal changes in classifying distinct variants of NHL. For example, lymphomas
9 of mucosa-associated lymphoid tissues (MALT) and mantle cell lymphoma as classified by
10 WHO (2008), were previously considered as either pseudolymphomas or benign lymphoid
11 disorders. Similarly, some forms of T-cell lymphomas and aplastic large-cell lymphomas were
12 earlier classified as Hodgkin's disease (Banks, 1992)

13 Among the leukemias, the two major diagnostic categories, ALL and AML, can be
14 further classified based upon cellular features. ALL is subdivided by FAB morphology (L1, L2,
15 and L3) and by immunophenotype (B-cell, early pre-B, pre-B, and T-cell) (Bhatia et al., 1999).
16 AML is classified primarily by morphological characteristics into eight different FAB subgroups
17 (M0–M7) based upon the myeloid lineage and degree of maturation involved. Similarly, the
18 myelodysplastic syndromes (MDSs), a series of blood disorders characterized by maturation
19 defects resulting in ineffective hematopoiesis, have also been classified by the FAB and WHO
20 systems (see Tables 1 and 2, respectively). These are commonly considered to be preleukemic
21 because a variable, but significant, proportion (1 to 33%) of the various disorders progress to
22 frank leukemia (Wright, 1995; WHO, 2001, 2008; Hasle et al., 2003).

23 The objective of this article is to provide an overview of the types of
24 lymphohematopoietic neoplasia induced by chemical agents and radiation in humans, and to
25 summarize current information on the mechanisms of chemical leukemogenesis. Much of the
26 discussion focuses on myeloid neoplasms due to the evolving knowledge of lymphomas that is
27 only now integrated into ongoing epidemiological and clinical studies. An overview of the major
28 classes of leukemia-inducing agents—radiation, the alkylating agents, and topoisomerase II
29 inhibitors—will then be presented followed by examples of environmental and occupational
30 leukemia-inducing agents and a brief discussion of factors influencing chemical leukemogenesis.
31 Lastly, the article will end with a discussion of how mechanistic information on human

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1 leukemia-inducing agents can be used to better assess the risks from exposure to environmental
2 chemicals.

3

4 **1.1. OVERALL INCIDENCE AND TRENDS**

5 Lymphohematopoietic neoplasms are an uncommon, yet significant, cause of cancer-
6 related deaths. In 2009, it was estimated that leukemia would be diagnosed in 44,790 people in
7 the United States (ACS, 2009). Slightly over half of these will be chronic leukemias (20,540)
8 with the remainder being acute leukemias (18,570) and others that have not been clearly
9 identified (5,680). Because of the limitations of current therapies, leukemia represents the 5th
10 leading cause of cancer deaths among males in the United States and the 7th leading cause among
11 females (ACS, 2009). Furthermore, it was estimated that 74,490 new cases of lymphoma would
12 be diagnosed in the United States in 2009 (ACS, 2009). Of these, 89% (65,980 cases) were
13 estimated to have been NHL and 11% Hodgkin lymphoma (8,510 cases). NHL represents the 9th
14 leading cause of cancer-related deaths in males and the 6th in females. It should be noted that
15 more recent cancer incidence and mortality data can be obtained from the National Cancer
16 Institute (NCI)'s Surveillance Epidemiology and End Results (SEER) Web site
17 (<http://seer.cancer.gov/statistics/>).

18 While leukemia occurs much more commonly in adults than in children, childhood
19 leukemia still accounts for approximately 30% of all childhood cancers in the United States and
20 is a leading cause of disease-related death among children (Smith et al., 2005; ACS, 2006). The
21 incidence of leukemia in children (36 per million) is similar to that seen in young to middle-aged
22 adults (ages 20–44) but roughly one-tenth of that of adults aged 45 years and older, where the
23 annual incidences increase with age from 144 to 545 per million (Xie et al., 2003; ACS, 2006).
24 In adults, roughly 85% of the leukemias are myeloid in origin with the remainder being
25 lymphoid (Greaves, 1999). In children, the opposite occurs with 80% of the leukemias
26 originating from lymphoid cells. Moreover, the incidence trends for adult and pediatric
27 leukemias differ substantially. While the overall trend for adult leukemia has generally declined
28 with time, the incidence of childhood leukemias has increased noticeably in recent years, largely
29 due to an increase of ALL and AML in children that has increased by 1.1 and 0.5% per year,
30 respectively (Xie et al., 2003). Similar increases have been seen across Europe and in other
31 developed countries (Hrusaket et al., 2002; Steliarova-Foucher et al., 2004). Fortunately, there has

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1 been significant progress in treating childhood leukemias so that the 5-year survival rate for the
2 affected children is now approximately 80% (ACS, 2006). The survival rate for adult leukemias
3 varies by type with 5-year survival rates of 22% for AML patients, 66% for ALL patients, and
4 76% for CLL patients (ACS, 2009).

5

2. HEMATOPOIESIS

Hematopoiesis is the process by which the cells of the blood are formed. The development of the hematopoietic system begins in several mesodermal lineages in the mammalian conceptus with cells migrating from the primitive streak to three blood-forming tissues: the yolk sac, the para-aortic splanchnopleura/aorta-gonadal-mesonephros region, and the chorio-allantoic placenta (for review, see Dzierzak and Speck [2008]). Hematopoietic stem cells capable of conferring complete long-term and multi-lineage repopulation of hematopoiesis in irradiated adult recipient mice appear in the aorta-gonadal-mesonephros and other tissues during the middle of embryogenesis (Embryonic Day 10.5 in the mouse). These cells proceed to colonize the liver, then the thymus, spleen, and bone marrow (by Embryonic Day 15 in the mouse) where hematopoiesis primarily occurs after birth.

The formation of blood cells originates with the hematopoietic stem cell. As described by Wilson and Trumpp (2008), stem cells are functionally defined as cells that can both self-renew (maintain their numbers at a constant level) and give rise to all mature cells in the tissue in which they reside. The formation of blood cells is supported by a small population of pluripotent stem cells that exhibit the capacity to self-renew and are capable of extensive proliferation. These cells can also reconstitute all hematopoietic lineages and are capable of long-term reconstitution of the hematopoietic system of recipient animals. The primitive pluripotent stem cells are estimated to comprise 1 in 100,000 bone marrow cells and give rise to multipotent and committed progenitor cells, which represent approximately 2–5 per 1,000 marrow cells (Mihich and Metcalf, 1995). Each of these progenitor cells can generate 100,000 or more maturing progeny. The process of proliferation and differentiation is regulated by more than 25 growth factors, cytokines, and other regulators that may act directly upon one or more of the major lineages of blood cells or interact to influence cell growth (Mihich and Metcalf, 1995). A diagram illustrating the relationships between the major cell types involved in hematopoiesis is shown in Figure 1.

With the exception of lymphocytes where maturation also continues in the thymus, spleen and peripheral tissues, the formation of blood cells in normal human adults occurs almost exclusively in the bone marrow. All mature circulating blood cells have a finite life with the majority of cells being terminally differentiated and unable to replicate (Bagby, 1994). In order

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1 to maintain steady-state levels, the formation of cells in the marrow must equal the rate of
2 cellular senescence and elimination. As a result, the hematopoietic system has a tremendous
3 proliferative capacity with estimates of cell turnover ranging from 130 to 500 billion cells per
4 day in a 70-kg man (Jandl, 1996; Bryder et al., 2006). In addition, the hematopoietic system in
5 the central bone marrow helps respond to a variety of environmental stresses and infection by
6 increasing the blood cell counts of specific lineages when needed (Bagby, 1994; Jaiswal and
7 Weissman, 2009). For example, upon exposure to a hypoxic environment, erythrocyte
8 production will increase without a change in the production of neutrophils. Similar lineage-
9 specific responses are required following exposure to myelotoxic agents. To maintain steady-
10 state blood cell levels and to respond to environmental pressures, hematopoiesis, of necessity,
11 must be a highly regulated process. Historically, the responses to infection and environmental
12 stresses were believed to occur exclusively within the bone marrow. However, as described
13 below, it has recently been shown that an immune response to infection can occur at
14 extramedullary sites due to the homing, proliferation, and differentiation of hematopoietic stem
15 and progenitor cells at these ecotopic sites within the body (Jaiswal and Weissman, 2009;
16 Schulzet et al., 2009).

17 As indicated above, the hematopoietic stem cells normally reside within the bone
18 marrow, a tissue with specialized vasculature and shielding that provides an excellent
19 environment for the development of blood cells (Papayannopoulou and Scadden, 2008). In
20 addition to their ability to self-renew, primitive pluripotent hematopoietic stem cells give rise to
21 a number of multipotent progenitor cells, which, in turn, give rise to oligopotent progenitor cells
22 (see Figure 1 and Bryder et al. [2006]). Among these, the committed lymphoid progenitors give
23 rise to mature B lymphocytes, T lymphocytes, and natural killer (NK) cells whereas the common
24 myeloid progenitors give rise to granulocyte-macrophage progenitors (which differentiate into
25 monocytes/macrophages and granulocytes), and megakaryocyte/erythrocyte progenitors (which
26 differentiate into megakaryocytes/platelets and erythrocytes). Both the myeloid and lymphoid
27 progenitor cells have also been proposed to form dendritic cells, which play a role in regulating
28 the immune system. In addition to these major types of blood cells, a number of the cell types,
29 for example, the granulocytes can further differentiate into more specialized blood cells such as
30 neutrophils, eosinophils, and basophils. As a result, the number of unique cell types derived

1 from the hematopoietic stem cell is quite large and, as indicated above, the total number of
2 individual cells formed per day numbers in the hundreds of billions.

3 Hematopoietic stem and progenitor cells are commonly identified based on the presence
4 or absence of lineage markers or antigen expression on the cell surface or in the cytoplasm. As
5 presented by Bryder and associates, the most primitive hematopoietic stem cell identified to date
6 in humans exhibits the cell surface markers, $\text{Lin}^- \text{CD90}^+ \text{CD38}^- \text{CD34}^+$ meaning that it is negative
7 for the lineage differentiation surface antigen Lin, namely $\text{B}^- \text{G}^- \text{M}^- \text{T}^-$ (B220 for B cells, Gr-1 for
8 granulocytes, Mac-1 for myelomonocytic cells, and CD4 and CD8 for T cells), negative for the
9 surface antigen CD38 and positive for the surface antigens CD90 and CD34 (Bryder et al., 2006;
10 Li and Li, 2006). As described by Iwasaki and Akashi (2007) and (Bryder et al., 2006), the
11 lineage markers and differentiation pathways differ in notable ways between the mouse and the
12 human.

13 While hematopoietic stem and progenitor cells normally reside in specialized niches in
14 the bone marrow, they can be mobilized into the peripheral blood either at low levels
15 spontaneously or in large numbers as a result of cytokine or chemical treatment (Levesque et al.,
16 2007; Schulzet et al., 2009). These mobilized cells remain in circulation for only short periods of
17 time (minutes to hours) before homing to another peripheral tissue or returning to the bone
18 marrow. As a result, there appears to be a constitutive recirculation of hematopoietic stem and
19 progenitor cells between the bone marrow, extramedullary tissues, and the lymphoid
20 compartments (Schulzet et al., 2009). Consequently, it is theoretically possible for DNA damage
21 or other types of potentially leukemogenic alterations to affect hematopoietic stem cells while
22 they circulate in the blood and extramedullary spaces. Upon exposure to mobilizing agents such
23 as specific chemokines, toxicants, antibodies, or growth factors, or under conditions of stress or
24 myelosuppression, large numbers of these stem and progenitor cells can be released into the
25 peripheral blood (Levesque et al., 2007). Clinically, these mobilized cells can be harvested for
26 use in bone marrow transplantation. The natural role of mobilization is not fully known, but
27 there is evidence that the circulating hematopoietic stem and progenitor cells may help replenish
28 tissue-residing myeloid cells such as specific monocytes, macrophages, and dendritic cells or
29 help in rapidly responding to tissue injury and infection (Jaiswal and Weissman, 2009; Schulzet
30 et al., 2009).

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3. ORIGINS OF LYMPHOHEMATOPOIETIC NEOPLASIA

As with other cancers, leukemogenesis and lymphomagenesis are multi-step processes involving a series of genetic and epigenetic alterations involved in the transformation of a normal cell into a malignant cell. The various lymphohematopoietic cancers are believed to originate in specific types of pluripotent or lineage-restricted cells at different stages in hematopoiesis (see Figure 2; Greaves, 1999). As illustrated in the figure, leukemias and lymphomas can originate within many types of hematopoietic or hematopoietic-forming cells. With a few rare exceptions, most leukemias and lymphomas originate at the hematopoietic stem cell stage or at later progenitor or lineage-restricted stages. For example, most adult leukemias of myeloid origin (AML, MDS, and CML) as well as adult ALL are believed to originate at the pluripotent stem or progenitor cell stage whereas childhood leukemias are believed to originate during a subsequent stage of differentiation at either the lineage-restricted lymphoid or myeloid stem cell stage. For most types of adult AML, the key leukemic transformations appear to occur in hematopoietic stem cells (Warner et al., 2004). However, for APL, the key transformative event may occur at the committed myeloid progenitor stage (Passegue et al., 2003; Warner et al., 2004). For a few others, such as those possessing the MLL-ENL fusion gene, the transformative event can occur either at the pluripotent or the committed stem cell stage (Cozzio et al., 2003). In contrast, many lymphomas (NHL, Hodgkin lymphoma, Burkitt lymphoma) and all myelomas, as well as, several rare leukemias/lymphomas (adult T-cell leukemia, prolymphocytic leukemia, hairy cell leukemia) and one common (CLL) leukemia are believed to originate in mature lymphoid cells (Greaves, 1999; Harris et al., 2001). An understanding of the origin of these cancers can be useful for grouping various lymphohematopoietic cancers and can provide insight into the cell types targeted by carcinogenic agents.

Consistent with the multi-step nature of leukemogenesis, over 300 different genetic alterations and mutations have been identified (Kelly and Gilliland, 2002). Indeed, a recent examination of alterations affecting the MLL gene, a cancer-related gene located at band 11q23, in pediatric and adult leukemias, identified a total of 87 different rearrangements, primarily translocations, involving this one gene (Meyer et al., 2006). While most of the detected alterations are rare, certain translocations and genes are more prevalent and are typically associated with specific leukemic subtypes (Bhatia et al., 1999; Greaves and Wiemels, 2003).

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1 Many of these genetic alterations can only be detected at the molecular level. However, others
2 have been detected using cytogenetic, molecular cytogenetic and genomic approaches.
3 Nonrandom chromosomal alterations are detected in the neoplastic cells of a majority of patients
4 with leukemias or lymphomas, and the identification of genes involved in these alterations has
5 provided valuable insights into leukemogenesis and lymphomagenesis in humans (Chen and
6 Sandberg, 2002; Mrozek et al., 2004; Pedersen-Bjergaard et al., 2006; Qian et al., 2009). Because
7 of their importance, an overview of genetic changes in the development of leukemia is described
8 below.

9 Common clonal cytogenetic changes seen in leukemias include alterations in
10 chromosome number such as loss or gain of one or more chromosomes (e.g., monosomy 7 and
11 trisomy 8, respectively), balanced and unbalanced chromosome translocations, deletions, or
12 inversions involving specific chromosomal regions as well as complex arrangements involving
13 combinations of the above. In some cases, these are a reflection of the genetic instability that is
14 common in many types of cancers. However in many cases, these are highly specific involving
15 genes that are directly involved in the cancer process. For example, the translocation between
16 chromosomes 15 and 17, (t(15;17)(q22;q12-21)) that is characteristic of the promyelocytic form
17 of AML (FAB M3), results in a fusion gene involving the PML gene on chromosome 15 and the
18 retinoic acid receptor *alpha* (RAR α) gene on chromosome 17. This hybrid gene blocks
19 differentiation of the developing myeloid cells at the promyelocytic stage (Downing, 1999), a
20 characteristic feature of the disease. As seen in Table 4, significant differences have been seen in
21 the karyotypes of patients who have developed leukemia following therapy and those who have
22 no history of exposure to chemotherapy or other leukemogenic agents. The former are called
23 t-AML and the latter, *de novo* leukemias.

24 In addition to these microscopically visible chromosomal alterations, mutations at the
25 molecular level affecting specific cancer-related genes such as RAS, FLT3, GATA1, and TP53
26 have also been seen in t-AML and *de novo* leukemias at varying frequencies (see Table 5). For
27 example, mutations in genes of the receptor tyrosine kinase/RAS-BRAF signal transduction
28 pathway are reported to be present in over 50% of *de novo* AML (Christiansen et al., 2005).
29 These occur through many mechanisms including base pair substitutions, frame shifts, internal
30 tandem duplications, gene fusions, and splicing errors (for examples in AML1, see [Roumier et
31 al., 2003]). In addition, epigenetic alterations such as changes in the methylation patterns in

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1 leukemia-related genes or their promoter regions have also been seen in many types of leukemia,
2 including t-AML (Zhenget al., 2004; Pedersen-Bjergaard et al., 2006; Nerviet al., 2008).

3 In recent years, researchers have begun to identify patterns among the myriad of
4 translocations, gene arrangements, and point mutations involved in myeloid leukemias and have
5 created a model for leukemogenesis (Deguchi and Gilliland, 2002; Kelly and Gilliland, 2002).
6 According to the model proposed by (Kelly and Gilliland, 2002)

7
8 AML is the consequence of collaboration between at least two broad classes of
9 mutations. Class I mutations, exemplified by constitutively activated tyrosine
10 kinases or their down stream effectors, such as BCR/ABL, TEL/PDGFR, β ,
11 N-RAS, or K-RAS mutants, or constitutively activated FLT3, confer a
12 proliferative or survival advantage to hematopoietic cells. When expressed alone,
13 these mutant genes confer a CML-like disease characterized by leukocytosis with
14 normal maturation and function of cells. Class II mutations result in loss of
15 function of transcription factors that are important for normal hematopoietic
16 differentiation and include the AML1/ETO, CBF β /SMMHC, PML/RAR α , and
17 NUP98/HOXA9 fusions as well as point mutations in hematopoietic transcription
18 factors such as AML1 and C/EBP α . These mutations would also be predicted to
19 impair subsequent apoptosis in cells that do not undergo terminal differentiation.
20 When expressed alone, these mutations may confer a phenotype like most MDS.
21 Regardless of the timing or order of acquisition of mutations, individuals who
22 accrue both Class I and Class II mutations have a clinical phenotype of AML
23 characterized by a proliferative and/or survival advantage to cells and by impaired
24 hematopoietic differentiation.

25
26 A list of the gene mutations seen in patients with t-MDS or t-AML separated into these two
27 mutation classes is shown in Table 6.

28 More recently, additional interrelationships between new and previously identified
29 genetic alterations, leukemogenic agents, and types of leukemia have been reported
30 (Christiansen et al., 2001, 2004; Harada et al., 2003; Zhenget al., 2004; Klymenko et al., 2005;
31 Rege-Cambrinet al., 2005; Wiemels et al., 2005). As illustrated by (Pedersen-Bjergaard et al.,
32 2008), the interactions between these various genes can become quite complicated, and the
33 outcome of these interactions is not fully understood. It should also be noted that some genes
34 such as TP53 do not easily fit within this classification scheme, which suggests that other types
35 of genetic changes are likely to be necessary for the conversion of a normal hematopoietic stem
36 or progenitor cell into a fully transformed leukemic cell (Pedersen-Bjergaard et al., 2008).

37

4. LEUKEMIA- AND LYMPHOMA-INDUCING AGENTS

While most leukemias occur in individuals with no obvious exposure to radiation or chemical carcinogens (*de novo* leukemias), a significant number, known as secondary leukemias develop in individuals who have previously been exposed to radiation, industrial chemicals, or chemotherapeutic agents. Approximately 40 years ago, the IARC began evaluating chemicals (and later other types of agents) for their ability to induce cancer in humans. Since 1971, IARC has evaluated more than 900 agents (including exposure circumstances) and identified more than 100 as being carcinogenic to humans (classified as Group 1: *Carcinogenic to Humans*[IARC, 2010]). Another 66 have been classified in Group 2A, which indicates agents that are *Probably Carcinogenic to Humans*. Among the 100+ agents in Group 1, approximately 25% have been established as causing a lymphohematopoietic cancer (see Table 7). These include eight therapeutic drugs or mixtures, five industrial chemicals or contaminants, two immunosuppressive drugs, six forms of radiation, two occupational or lifestyle exposures, and six infectious agents. Thus, leukemias and lymphomas represent one of the most common types of cancer induced by a wide variety of carcinogens. In addition, three other Group 1 carcinogens (see Table 7), which induce cancer at other sites, are also thought to be likely to induce either a leukemia or lymphoma. Of the 66 Group 2A agents, there is evidence based either on human studies, animal bioassays, or structural similarities that at least 10 of these chemicals are also likely to cause leukemia in humans. Table 7 lists the Group 1 and 2A agents that have been established, or are likely to cause leukemia or lymphoma, as well some of their characteristics. The same list of agents with key information related to the likely mechanisms responsible for the lymphohematopoietic cancers is shown in Table 8.

In examining the information in Tables 7 and 8, a number of general patterns become apparent. Leukemias are the primary type of cancer induced by the chemical agents, and most of these are ANLLs (synonymous with AML). These were almost always induced by agents that are either directly DNA-reactive or that can be metabolized (or otherwise converted) into DNA-reactive species. Many of the leukemogens are bifunctional alkylating agents; chemicals that form adducts on DNA bases involved in base-pairing such as the O⁶ of guanine or induce chromosomal damage through the inhibition of topoisomerase II. The primary mode of action for these agents is through the induction of mutations, either gene mutations or chromosomal

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1 mutations. Consistent with their proposed mutagenic mode of action, most of the leukemia-
2 inducing agents have been reported to induce structural chromosome aberrations in the
3 peripheral blood of exposed humans. Myelotoxicity is also commonly seen in humans (and
4 animals) exposed to these leukemogenic agents. Exposure to radiation in various forms was
5 frequently associated with ALL and CML, in addition to ANLL. These are also likely due to the
6 effects of ionizing radiation on DNA, either directly or indirectly, and are believed to occur
7 through a mutagenic mode of action.

8 In contrast to these DNA-damaging agents, exposure to a variety of infectious agents is
9 causally related to the formation of lymphoid neoplasms. The induced lymphomas appear to be
10 primarily associated with chronic infection with either viruses or *Helicobacter* bacteria that are
11 immunomodulating and/or specifically target lymphoid cells. The two chemical agents,
12 cyclosporine and azathioprine, which also induce NHL, are also strongly immunosuppressive. In
13 addition, TCDD, which may induce NHL, is also immunosuppressive, so this could be the
14 mechanism underlying its lymphoma-inducing effects. Although not reviewed by IARC and,
15 hence, not presented in Tables 7 and 8, autoimmune disorders and other diseases associated with
16 immune stimulation and inflammation are increasingly recognized from large consortia studies as
17 risk factors for lymphoma (Vajdic et al., 2009, Ekstrom Smedby et al., 2008; Cocco et al., 2008;
18 Nieters et al., 2006).

19 Similar to the Group 1 agents, the Group 2A leukemogens are associated with the
20 induction of ANLL. For chemicals for which information is available, these agents are also
21 myelotoxic and clastogenic and are believed to most likely induce their leukemogenic effects
22 through a mutagenic mechanism.

23 In summary, the vast majority of the leukemia-inducing agents are believed to act
24 through a mutagenic mode of action whereas the lymphoma-inducing agents most likely act
25 through immunomodulation and related effects. An overview of the major classes of leukemia-
26 inducing agents is presented below.

27

1 **5. OVERVIEW OF THE MAJOR CLASSES OF LEUKEMIA-INDUCING AGENTS**

2
3
4 **5.1. IONIZING RADIATION**

5 As a result of its widespread medical, military, and energy-related uses, large numbers of
6 people have been exposed to ionizing radiation, and its adverse effects have been extensively
7 documented (IARC, 2000b, 2001; UNSCEAR, 2000a, b; Ron, 2003; NRC, 2006). Exposure to
8 ionizing radiation has been shown to result in numerous types of cancer including several types
9 of leukemia as well as adverse effects that are likely to be involved in leukemogenesis including
10 myelotoxicity, immune suppression, and genetic damage leading to chromosomal and gene
11 mutations. The earliest association between radiation and cancer was seen for leukemia, and it
12 has been repeatedly seen in numerous population studies including those exposed through
13 medical, military, and environmental exposures (IARC, 2000b, 2001; UNSCEAR, 2000b; Ron,
14 2003; NRC, 2006). It should be noted that there are a variety of types of radiation and radioactive
15 materials. Most of the studies that have been conducted have investigated the effects of ionizing
16 radiation, which for simplicity, will be considered as one individual agent in this section.

17 Assessing the risks associated with radiation exposure is challenging and is influenced by the
18 type of radiation, the tissue dose, the proportion of the body exposed, the extent of cell killing,
19 and the DNA-repair capacity of the individual or tissue (Curtis et al., 1994). Host factors such as
20 age, sex, genetic composition, and health of the exposed individuals can also influence the risk of
21 radiation-induced leukemia.

22 All age groups are affected, but children, in particular, have been shown to be at an
23 elevated risk for radiation-induced leukemia as seen in the Life Span Study of the atomic bomb
24 survivors in Hiroshima and Nagasaki. Among the survivors who were exposed to both *gamma*,
25 and to a lesser extent, neutron radiation, the highest leukemia risks were seen in children
26 (Preston et al., 1994, 2004). Significant dose-related increases were seen for ALL, AML, and
27 CML, with the excess risks for ALL and CML being approximately 100% higher in the exposed
28 males than in the females. When the leukemias were reclassified using the FAB classification
29 scheme, all AML subtypes were present with a predominance of myeloblastic leukemias with
30 and without maturation (M1 and M2) (Matsuo et al., 1988). Among the ALL cases, most cases
31 exhibited the L2 subtype, but a significant portion also showed the L1 subtype. Latency periods
32 were shorter for those under 15 years of age with a leukemia peak at 5–7 years post exposure as

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1 compared to later peaks for those exposed at later ages (Kamada and Tanaka, 1983). The
2 leukemia risk also decreased more rapidly in children as compared to those in older age groups.
3 Overall, the risks to children were highest during the period from 1950 to 1965 and returned to
4 near background levels thereafter (Prestonet al., 1994).

5 Similarly, the use of radiation for medical purposes has been associated with increases in
6 leukemia. Increased risk of leukemia has been reported following the use of radiation for
7 diagnostic tests, for the treatment of benign diseases, and following radiotherapy for cancer
8 (Ron, 1998, 2003). For hematopoietic and lymphoid tissues that are diffuse, a significant portion
9 of the tissue must be irradiated to increase the incidence of neoplasia (Storeret al., 1982). The
10 leukemia risks from medical irradiation appear to have diminished in recent years due to a use of
11 lower and more restricted doses as well as changes in therapeutic strategy in which high doses
12 are applied within limited fields. High radiation doses (above 3–4 Gray) result in extensive
13 killing of marrow-containing progenitor cells and have been associated with a reduced risk of
14 developing leukemia (Boiceet al., 1987; NRC, 1990; Curtiset al., 1994).

15

16 **5.2. CHEMOTHERAPEUTIC AGENTS**

17 Following the initiation of intensive chemotherapy with genotoxic agents, increases in
18 therapy-related leukemias began to appear (Seiber and Adamson, 1975; Kantarjian and Keating,
19 1987; Levine and Bloomfield, 1992; Leoneet al., 1999). These leukemias, also known as
20 treatment-related or secondary leukemias, consisted primarily of AML, although a small increase
21 in therapy-related ALL has also been seen (Hungeret al., 1992; Andersenet al., 2001). With
22 increased periods of follow-up, increases in other types of solid tumors have also been observed
23 (Tuckeret al., 1988; Loescheret al., 1989; Boffetta and Kaldor, 1994; van Leeuwenet al., 1994;
24 Vega-Stromberg, 2003; Traviset al., 2005; Hodgsonet al., 2007).

25 Over time as new agents and therapeutic strategies have been employed, additional
26 agents have been recognized as inducing leukemia in humans. Indeed as seen in Table 7,
27 chemotherapeutic drugs comprise the largest group of agents generally recognized as human
28 leukemia-inducing agents. Currently, therapy-related leukemias constitute 10 to 20% of the
29 leukemia cases seen at major medical institutions (Deschler and Lubbert, 2006;
30 Pedersen-Bjergaardet al., 2007).

1 The identification of specific agents involved in leukemogenesis and the interpretation of
2 many of the studies can be challenging due to the use of multiple therapeutic agents, varying
3 dosing regimens, concurrent use of radiotherapy, and variable periods of patient follow-up. Over
4 time, two main classes of leukemogenic therapeutic drugs have been identified—alkylating
5 agents and topoisomerase II inhibitors (Pedersen-Bjergaard and Philip, 1991; Pedersen-Bjergaard
6 and Rowley, 1994; Pedersen-Bjergaard et al., 2006). An overview of the leukemias (including
7 myelodysplastic syndromes) induced by these two classes of chemotherapeutic drugs will be
8 briefly discussed in the following sections.

10 **5.2.1. Alkylating Agent-Related Leukemias**

11 A large number of studies have demonstrated that patients treated with alkylating agent-
12 based chemotherapy are at an increased risk of MDS and AML (Levine and Bloomfield, 1992;
13 Pedersen-Bjergaard and Rowley, 1994; Smith et al., 1994). These risks have been seen for both
14 children and adults and are strongly related to the cumulative dose of the alkylating agent
15 (Pedersen-Bjergaard and Philip, 1987; Tucker et al., 1987; Hunger et al., 1992;
16 Pedersen-Bjergaard et al., 2000; Pyatt et al., 2005). The administered agents also exhibit varying
17 degrees of hematopoietic toxicity, immunotoxicity, and genotoxicity, which can also be affected
18 by the agent, dose, and route of administration (Gale, 1988; Ferguson and Pearson, 1996;
19 Sanderson and Shield, 1996). The incidence of treatment-related MDS and AML
20 (t-MDS/t-AML) in adults treated with antineoplastic drugs has been reported to range from 1%
21 to >20% (Felix, 1998; Leone et al., 2001). The increases in this type of therapy-related leukemia
22 generally appear 1 to 2 years after treatment and may remain elevated for 8 or more years
23 following the completion of chemotherapy (Pedersen-Bjergaard and Philip, 1987;
24 Pedersen-Bjergaard and Philip, 1991; Davies, 2000; Schonfeld et al., 2006).

25 In adults, leukemias induced by alkylating agents exhibit characteristics that generally
26 allow them to be distinguished from *de novo* leukemias and those induced by topoisomerase II
27 inhibitors (Pedersen-Bjergaard and Rowley, 1994; Eastmond et al., 2005). These leukemias are
28 typically myeloblastic with or without maturation (FAB M1 and M2 subtypes) and are
29 characterized by trilineage dysplasia and clonal unbalanced chromosome aberrations, most
30 commonly involving loss of the entire chromosome or part of the long arms of chromosomes
31 5 and 7 (–7, 7q–, –5, 5q–). These t-AML have a modal latency of 4–7 years, and the onset of

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1 the actual leukemia is often preceded by myelodysplasia. It should be noted that AML induced
2 by ionizing radiation tends to exhibit similar features (MDS, clonal unbalanced chromosomal
3 aberrations, etc.) although the range of the FAB subtypes induced by radiation tends to be
4 broader (Matsuo et al., 1988; Philip and Pedersen-Bjergaard, 1988; Gundestrup et al., 2000).

5 Using structure-activity relationships as well as other predictive approaches with in vivo
6 rodent and *Drosophila* data, Voegelé et al. (1998) were able to identify three major categories of
7 DNA-reactive chemical and therapeutic agents. As described by the authors, Category 1
8 consisted of mono-functional alkylating agents such as ethylene oxide and methyl methane
9 sulfonate, which primarily react at the N7 and N3 moieties of purines in DNA. Efficient DNA
10 repair was the major protective mechanism against the relatively weak genotoxic effects of these
11 agents, which might not be detectable in repair-competent cells. High doses were generally
12 needed for the induction of tumors in rodents. A strong target site specificity for the adverse
13 effects was seen, and this appeared to be related to DNA repair capacity. Category 2 agents such
14 as procarbazine and *N*-nitroso-*N*-ethylurea (ENU) induce both *O*-alkyl adducts and *N*-alkyl
15 adducts in DNA. In general, the induced *O*-alkyl adducts appeared to be slowly repaired, or not
16 repaired, which made these agents potent carcinogens and germ cell mutagens. The inefficient
17 repair of the *O*-alkyl-pyrimidines, in particular, was responsible for their potent mutagenic
18 activity. Category 3 agents such as melphalan and busulfan induced structural aberrations
19 through their ability to cross-link DNA, and this was the major factor contributing to their high
20 genotoxic potency, which appeared to be related to the number of DNA crosslinks per target
21 dose unit that were induced. The genotoxic effects for the Category 3 agents occurred at, or
22 near, toxic levels. For all three categories of genotoxic agents, strong correlations were observed
23 between their carcinogenic potency, acute toxicity, and germ-cell specificity.

24 25 **5.2.2. Topoisomerase II Inhibitor-Related Leukemias**

26 In the late 1980s, a new type of therapy-related leukemia was recognized that exhibited
27 unusual features that differed from those previously seen following treatment with alkylating
28 agents and radiation (Pui et al., 1989; Pui and Relling, 2000). The affected patients had been
29 treated with etoposide or teniposide, two of a newly developed epipodophyllotoxin class of
30 chemotherapeutic agents (Pedersen-Bjergaard and Philip, 1991). In the ensuing years, these
31 epipodophyllotoxins have become widely used, especially for treating childhood cancers, and a

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1 large number of studies have been published establishing an association between treatment with
2 these drugs and the subsequent development of leukemia (Haupt et al., 1993; Smith et al., 1994;
3 Pedersen-Bjergaard et al., 1995; Pui and Relling, 2000; Leone et al., 2001; Hijiyama et al., 2009).

4 The leukemia risk following epipodophyllotoxin therapy was reported to be very high in
5 early studies, with cumulative incidences approaching 19% in some treatment groups (Pui et al.,
6 1989). Interestingly, in some cases, the risk of a secondary cancer appeared to be more closely
7 related to the treatment regimen than to total dose (Pui et al., 1991; Pui and Relling, 2000).
8 Patients receiving epipodophyllotoxins on a weekly or twice-weekly basis had much higher
9 cumulative risks (12.4%) than those receiving the drugs on a biweekly schedule (1.6%). Similar
10 results have been seen in more recent studies (Smith et al., 1999) although others have seen a
11 correlation between cumulative dose and epipodophyllotoxin-induced t-AML (Neglia et al.,
12 2001; Le Deley et al., 2003). With implementation of newer treatment protocols, the risk of
13 t-AML has been reduced substantially and is now within the range of that seen with alkylating
14 chemotherapeutic agents (Smith et al., 1993; Pui and Relling, 2000). There is also evidence that
15 the combined treatment of topoisomerase II inhibitors with alkylating agents (or cisplatin)
16 confers a greater risk of t-AML than seen with either type of chemotherapeutic agent alone
17 (Sandoval et al., 1993; Smith et al., 1994; Blatt, 1995). In most reported cases, the incidence of
18 t-AML induced by these drugs is estimated to range from 2 to 12% (Felix, 1998; Leone et al.,
19 2001).

20 The epipodophyllotoxins exhibit moderate myelosuppression, identifiable chromosomal
21 damage, and their leukemogenic effects by inhibiting topoisomerase II through a process that
22 involves stabilization of the DNA-enzyme complex (Smith et al., 1994; Ferguson and Pearson,
23 1996). Topoisomerase II is a nuclear enzyme involved in a wide variety of cellular functions,
24 including DNA replication, transcription, and chromosome segregation (Anderson and Berger,
25 1994; Nitiss, 2009). Leukemias induced following treatment with epipodophyllotoxin-type
26 topoisomerase inhibitors appear from 10 months to 8 years following the initiation of
27 chemotherapy, with a median latency of 2 to 3 years (Smith et al., 1994; Leone et al., 2001). The
28 induced AMLs are primarily of the monocytic or myelomonocytic subtypes (M4 and M5) and
29 are rarely preceded by a myelodysplastic phase, a pattern that differs significantly from
30 alkylating agent or radiation-induced leukemias (Pedersen-Bjergaard and Rowley, 1994; Smith et
31 al., 1994; Leone et al., 2001; Pedersen-Bjergaard et al., 2006).

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1 Infrequently, ALL has been reported in patients following treatment with both alkylating
2 agents and topoisomerase II-inhibiting drugs (Hungeret al., 1992; Andersen et al., 2001; Hijjiya et
3 al., 2009). Although t-ALLs occur infrequently, they seem to be more common in children
4 under the age of 15 who have previously been treated with a topoisomerase II inhibitor
5 (Andersen et al., 2001).

6 One of the unique features of t-AML, and to a lesser extent t-ALL, induced by the
7 epipodophyllotoxin-type of topoisomerase II inhibitors, is the presence of clonal-balanced
8 translocations involving the MLL gene (also known as ALL-1, HRX, and HTRX-1) located on
9 the long arm of chromosome 11 (11q23) in the leukemic cells. Cytogenetic studies of patients
10 with leukemias induced by these agents have shown that in over 50% of the cases, the leukemic
11 clone involved a balanced translocation affecting the 11q23 region and another chromosomal
12 partner, usually t(6;11), t(9;11), and t(11;19) (Pedersen-Bjergaard and Rowley, 1994; Smith et al.,
13 1994; Canaaniet al., 1995). In children previously treated with topoisomerase inhibitors, up to
14 90% of the secondary leukemias have an 11q23 alteration (Canaaniet al., 1995). As indicated
15 previously, to date, 87 rearrangements involving the MLL gene have been identified, and 51 of
16 the translocation partner genes have been characterized at the molecular level (Meyer et al.,
17 2006). The four most common MLL translocation partner genes (AF4, AF9, ENL, and AF10)
18 encode nuclear proteins that are part of a protein network involved in histone H3K79
19 methylation (Meyer et al., 2006) indicating an important role for this pathway in
20 epipodophyllotoxin leukemogenesis.

21 Numerous lines of evidence indicate that topoisomerase II as well as DNA-repair
22 enzymes such as those involved in non-homologous end joining play an important role in the
23 formation of the 11q23 translocations. These have been summarized in series of reviews
24 (Greaves and Wiemels, 2003; Aplan, 2006; Felix et al., 2006; Zhang and Rowley, 2006). The
25 presence of topoisomerase II recognition sites has been found in proximity to the translocation
26 breakpoints as have recombinase recognition sites, Alu sequences, DNase hypersensitive sites,
27 and scaffold attachment regions and suggest that multiple types of damage and repair probably
28 contribute to the generation of the observed translocations (Pui and Relling, 2000; Felix et al.,
29 2006; Zhang and Rowley, 2006). Interestingly, in a recent report, Le et al., (2009) reported that
30 the translocation breakpoints within the MLL gene occurred in a highly specific fashion at the
31 base of a secondary DNA structure formed from a palindrome. A stringent topoisomerase II

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1 consensus binding site was located at the apex of the secondary DNA structure. The authors
2 proposed a model in which topoisomerase II facilitates the formation of a secondary structure
3 that results in site-specific DNA strand breakage that is efficiently processed into translocations
4 (Leet al., 2009). This processing most likely occurs through a mechanism involving
5 nonhomologous end joining (Greaves and Wiemels, 2003; Zhang and Rowley, 2006). It should
6 also be noted that the MLL gene has been shown to be prone to breakage during apoptosis, and it
7 has been proposed that the observed translocations occur in hematopoietic cells rescued at an
8 early, reversible stage during the apoptotic process (Stanulla et al., 1997; Bettiet al., 2005;
9 Vaughan et al., 2005; Basecke et al., 2006). A role for apoptosis has also been proposed in the
10 formation of other leukemia-related translocations (Eguchi-Ishimae et al., 2001).

11

12 **5.2.3. Other Likely Leukemia-Inducing Therapeutic Agents**

13 In recent years, evidence has accumulated that other inhibitors of topoisomerase II, such
14 as the anthracycline, anthracenedione, and bisdioxopiperazine derivatives, can also induce
15 secondary leukemias (Xue et al., 1992; Zhan et al., 1993; Blatt, 1995; Andersen et al., 1998;
16 Le Deley et al., 2003; Mistry et al., 2005; May et al., 2010). The leukemias induced by these
17 agents are similar to the epipodophyllotoxins in that they have short latency periods and are
18 infrequently preceded by myelodysplasia. However, they typically exhibit different types of
19 clonal-balanced rearrangements (e.g., t(8;21), t(15;17), and inv(16)) and different FAB subtypes
20 (M2 and M3).

21 Although azathioprine, 6-thioguanine, and 6-mercaptopurine are primarily associated
22 with immunosuppression and the induction of NHL, a number of studies have suggested that
23 patients treated with these 6-thioguanosine monophosphate-producing drugs are at an increased
24 risk of developing ANLL (Boet et al., 1999; Karran, 2006; Yenson et al., 2008). It has been
25 suggested that the risks are higher in patients with low thiopurine S-methyltransferase activity
26 and may involve aberrant mismatch repair and microsatellite instability (Boet et al., 1999; Karran,
27 2006). Interestingly, the leukemias of many of these patients also show loss of chromosome 7 or
28 part of chromosomes 5 or 7 (5q- or 7q-) (Yenson et al., 2008).

29 A summary of the types of leukemia and related lymphoid neoplasms as well as key
30 characteristics of the leukemias induced by different types of leukemia-inducing agents is
31 presented in Table 9. Information on leukemias induced by the bisdioxopiperazine class of

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1 topoisomerase II inhibitors has also been added to facilitate comparisons with benzene. There is
2 recent evidence to suggest that one mechanism by which benzene induces leukemia is through
3 inhibition of topoisomerase II by a mechanism that may be similar to that of the
4 bisdioxopiperazine class of topoisomerase II inhibitors (Mondrala and Eastmond, 2009).
5

1 **6. MECHANISMS INVOLVED IN t-AML**

2
3
4 For more than 20 years, Pedersen-Bjergaard and colleagues have collected information
5 on patients with t-AML and t-MDS who have been treated at their clinic in Copenhagen,
6 Denmark. Based on the genetic alterations seen in this cohort of 140 patients as well as
7 information in the literature, they have identified eight separate pathways that appear to lead
8 either directly to t-AML or lead to t-MDS and then to t-AML. These pathways are illustrated in
9 Figure 3 (from [Pedersen-Bjergaard et al., 2006]). The pathways have been classified into three
10 groups largely based upon the therapeutic agent that was likely responsible for the leukemia.
11 Each of the pathways is described below based on descriptions extracted from their 2006 article
12 (i.e., Pedersen-Bjergaard et al., 2006).

13 Pathway I in the figure was characterized by patients who developed t-MDS prior to
14 t-AML and exhibited either loss of chromosome 7 or part of the long arm of that chromosome
15 (7q-). These patients also did not exhibit the recurrent balanced translocations that are
16 associated with AML. Most of these patients (35/39) had been treated with alkylating agents,
17 and most (35/39) presented with t-MDS prior to t-AML. Methylation of the p15 promoter,
18 considered a late event in leukemogenesis, was seen in 84% of the patients. In addition to the
19 chromosome 7 changes, the leukemias of a significant portion (15/39 or 38%) of these patients
20 had point mutations in the AML1 (also known as RUNX1) gene. A number of these patients
21 also had mutations in either the TP53 tumor suppressor gene or an activating mutation in the
22 RAS oncogene.

23 Pathway II predominated in patients that exhibited loss of all (-5) or part of the long arm
24 of chromosome 5 (5q-). Approximately half of the patients in this group also had -7 or 7q-
25 alterations. As with Pathway I, onset of this disease is closely related to the use of alkylating
26 agent chemotherapy (27/34) and an initial presentation as t-MDS (26/34). Seventy-seven percent
27 of these patients exhibited mutations in TP53. The patients also often present with a complex
28 karyotype, loss of part of the short arm of chromosome 17 (17p-), or showed an amplification or
29 duplication of chromosome bands 11q23 or 21q22. Methylation of the p15 promoter occurred in
30 80-90% of the patients of this group.

31 Pathway III was characterized by balanced translocations involving the 11q23
32 chromosome band and one of many partner chromosomes. These translocations frequently

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1 occurred in patients who had been previously treated with topoisomerase II inhibitors and
2 exhibited AML of the FAB subtypes M4 or M5. Three of the 11 patients in this group had a
3 RAS mutation, and another 3 had a BRAF mutation. Methylation of the p15 promoter was seen
4 in 50% of the patients.

5 Pathway IV occurred in patients with balanced translocations involving chromosome
6 bands 21q22 or 16q22 leading to chimeric rearrangements involving the core binding factor
7 genes AML1 or CBFβ. These chromosomal changes are generally associated with previous
8 treatment with topoisomerase II inhibitors, most commonly of the anthracycline class. While
9 patients in this group with a t(3;21)(q26;q22) often present as t-MDS, most of the others present
10 directly with t-AML. Chromosome 7 alterations were also seen in five of nine patients with
11 21q22 translocations. Point mutations in c-Kit and PTPN11 were seen in a few patients.
12 Methylation of the p15 promoter was seen in 83% of the patients.

13 Pathway V occurred in only two patients and is characterized by a translocation between
14 chromosomes 15 and 17 involving the PML and RARA genes. Therapy-related promyelocytic
15 leukemia (M3) that exhibits the characteristic t(15;17) has been reported to occur in patients
16 treated with doxorubicin or mitoxantrone. One of the patients in this group also had a mutation
17 due to FLT3 internal tandem duplication.

18 Pathway VI is an uncommon pathway in which t-AML patients exhibit balanced
19 translocations involving the NU98 gene at chromosome band 11p15. None of the 140 patients in
20 the Copenhagen series exhibited this pattern.

21 Pathway VII exhibits a normal karyotype, and most often presents directly as t-AML.
22 Approximately 17% of the patients in the Copenhagen series fell within this group and have not
23 been consistently associated with any previous type of chemotherapy. The mutations seen are
24 also commonly seen in *de novo* leukemias suggesting that these may represent sporadic cases of
25 *de novo* leukemia occurring in these patients. Methylation of the p15 promoter was only seen in
26 50% of these patients.

27 Pathway VIII is composed of patients that exhibit unique or unusual chromosome
28 alterations and represents 14% of the Copenhagen cohort. These cases do not show an
29 association to any specific type of previous therapy and may also represent cases of *de novo*
30 leukemia. Methylation of the p15 promoter was also uncommon occurring in 40% of the cases.

1 Consistent with the description presented above, patients with t-AML with leukemic cells
2 exhibiting loss of all or part of chromosomes 5 or 7, frequently present initially with t-MDS and
3 have often been previously treated with alkylating agent chemotherapeutic drugs. In contrast,
4 t-AML exhibiting certain specific reciprocal translocations such as t(11q23) and t(21q22) occur
5 in patients that were previously treated with a topoisomerase II-containing chemotherapeutic
6 regimen and develop without a preceding MDS.

7

1 **7. FACTORS CONFERRING AN INCREASED RISK OF INDUCED LEUKEMIA**

2
3
4 **7.1. MYELOSUPPRESSION AND IMMUNOTOXICITY**

5 Myelosuppression and immunotoxicity frequently accompany exposure to leukemia-
6 inducing agents, particularly those such as the chemotherapeutic drugs, ionizing radiation, and
7 benzene, for which leukemogenicity has been clearly established (Ferguson and Pearson, 1996;
8 Eastmond, 1997). The number of individuals affected and the magnitude of toxicity are
9 influenced by the agent and dose-related factors such as total dose, dose per treatment, schedule,
10 and route of administration as well as individual host factors (genetic susceptibility, prior
11 therapy, health status, etc.) (Gale, 1988). A brief overview of the myelosuppressive effects of
12 cancer therapeutic drugs has been written by Gale (1988) and is the basis for the following
13 description. The severity of myelotoxicity induced by antineoplastic drugs varies considerably
14 by chemical class. For drugs associated with t-AML, moderate-to-severe effects are generally
15 seen. The epipodophyllotoxins, cisplatin, and procarbazine typically produce more moderate
16 toxicity whereas severe effects are more common for the alkylating agents, the anthracyclines,
17 and the nitrosoureas.

18 The period between dosing and the onset or appearance of the myelosuppression is also
19 related to the class of agent. For some agents such as ionizing radiation, the onset of
20 myelotoxicity occurs within 0 to 48 hours after exposure. For others, longer periods are
21 required. The onset of myelosuppression by the alkylating agents and anthracyclines occurs 1 to
22 3 weeks following exposure and is believed to be due to the effect of these agents on immature
23 hematopoietic cells that becomes more evident as the more mature blood cells die and require
24 replacement. Myelosuppression induced by the nitrosoureas and mitomycin C is less frequent
25 and occurs 4 to 8 weeks after treatment. This delayed effect is believed to be due to a relatively
26 selective effect on immature stem cells. However, the onset of this delayed effect is dose-
27 dependent. A two- to three-fold increase in dose reduces the onset of myelotoxicity to 1 week.
28 For some drugs such as busulfan, the manifestation of the myelotoxic effects is considered to be
29 latent and may only be manifested under stress-related conditions.

30 In most cases, the induced myelotoxicity is transient with the blood cell counts returning
31 to normal following the cessation of treatment or exposure (Hendry and Feng-Tong, 1995;
32 Ironset al., 2005). However, in some cases, the induced myelosuppression can be more

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1 persistent and progress to pancytopenia or infrequently to aplastic anemia, a condition that
2 confers a much greater risk of developing leukemia (~10%) (Aksoyet al., 1984; Jandl, 1987;
3 Oharaet al., 1997; Imashukuet al., 2003). Increased risks have also been seen for those who have
4 previously exhibited less severe forms of bone marrow toxicity. Studies of benzene-exposed
5 workers have shown that the leukemia mortality rate was much higher for workers who had
6 previously been diagnosed with bone marrow poisoning (700 per 10⁶ person-years) as compared
7 to those exposed to, but not poisoned by, benzene (14 per 10⁶ person-years), and particularly as
8 compared to the general population (2 per 10⁶ person-years) (Yin and Li, 1994). In one report,
9 36% of the benzene leukemia cases had a history of benzene poisoning with leukopenia or
10 pancytopenia (Yinet al., 1994). However, this also indicates that for most cases, clinically
11 detectable myelotoxicity may not be observed. It should also be noted that at lower exposure
12 levels, the decreases in cell counts occurring in exposed groups may fall within what is
13 considered the normal clinical range (Quet al., 2002; Lanet al., 2004). This highlights one of the
14 challenges in using myelotoxicity as a biomarker, as the normal range varies considerably in
15 adults. For example, the mean white blood cell count in adults is $7,200 \times 10^3/\mu\text{L}$ with a 95%
16 range from 3,900 to $10,900 \times 10^3/\mu\text{L}$ (Jandl, 1996).

17

18 **7.2. GENETIC POLYMORPHISMS**

19 Inherited polymorphisms in genes involved in xenobiotic metabolism and other cellular
20 processes have been associated with increased risks of myelotoxicity or leukemia in numerous
21 studies of patients or workers exposed to leukemogenic agents. In some instances, similar
22 associations have been seen in follow-up studies by other investigators. However, in a
23 significant number of cases, the results have either not been repeated or have not been
24 reproducible. Consequently, it is difficult to make firm conclusions about many of the reported
25 polymorphisms. Several recent reviews on polymorphisms and leukemia have been published
26 that the reader may want to refer to for further details (Cheok and Evans, 2006; Cheoket al.,
27 2006; Sinnettet al., 2006; Seedhouse and Russell, 2007). The following is a brief overview of
28 some of the genetic polymorphisms involved in DNA metabolism, repair, and xenobiotic
29 metabolism that have been repeatedly associated with altered risks of developing leukemia,
30 particularly induced leukemias.

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1 Since most leukemogens are genotoxic and exert their effects by damaging DNA, the
2 DNA repair capacity of the bone marrow is likely to have a significant influence on the risk of
3 t-AML. Indeed, individuals with congenital deficiencies in enzymes that are involved in DNA
4 repair such as ataxia telangiectasia, Bloom syndrome, and Fanconi anemia are at significantly
5 higher risk for developing leukemia and other lymphohematopoietic cancers (Segel and
6 Lichtman, 2004). Individuals with these and other uncommon genetic syndromes such as
7 neurofibromatosis 1 are also at an increased risk of t-AML following treatment with radiation,
8 alkylating agents, and/or topoisomerase II inhibitors (Mariset al., 1997; Seedhouse and Russell,
9 2007).

10 Genetic polymorphisms in DNA repair genes that occur more frequently in the
11 population can also confer an increased risk of t-AML. Defective mismatch repair is often
12 manifested by microsatellite instability in the cancer cells. Microsatellite instability is frequently
13 seen in leukemias, particularly in t-AML, where it has been reported to occur in ~50% of the
14 cases (Karran et al., 2003; Seedhouse and Russell, 2007). In contrast, less than 5% of *de novo*
15 leukemias exhibit microsatellite instability. While the basis for this instability is still unknown,
16 factors that may contribute are deficiencies in DNA-mismatch repair enzymes. In a fairly recent
17 report, the hMSH2 mismatch repair variant was shown to be significantly overrepresented in
18 t-AML patients that had previously been treated with O⁶-guanine-forming alkylating agents
19 including cyclophosphamide and procarbazine, as compared with controls (Worrillow et al.,
20 2003). Similarly, polymorphisms in genes involved in DNA repair (e.g., WRN, TP53, hOGG1,
21 XRCC1, ERCC3, and BRCA2) have been reported by a number of investigators to be associated
22 with a decrease in white blood cell counts or an increase in chromosomal damage in benzene-
23 exposed workers or workers previously poisoned by benzene (Shenet al., 2006; Kimet al., 2008;
24 Wuet al., 2008; Hosgood et al., 2009; Sunet al., 2009).

25 Polymorphisms affecting DNA metabolism have also been reported to confer an
26 increased risk of t-AML. Thiopurine methyltransferase (TMPT) catalyzes the S-methylation of
27 thiopurine medications such as 6-mercaptopurine and 6-thioguanine, which are commonly used
28 as chemotherapeutic agents. As summarized from Cheok and Evans (2006), the thiopurine
29 methyltransferase pathway is the primary mechanism for inactivation of thiopurines in
30 hematopoietic tissues. The link between thiopurine methyltransferase polymorphisms and
31 mercaptopurine toxicity has been extensively investigated, and studies have shown a strong

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1 relationship between thiopurine methyltransferase deficiency polymorphisms and hematopoietic
2 toxicity. Three variant alleles are responsible for >95% of the cases with low or intermediate
3 thiopurine methyltransferase activity. Patients homozygous or heterozygous for the low activity
4 alleles are inefficient at detoxifying the mercaptopurines and accumulate high concentrations in
5 their hematopoietic tissues. If their administered doses are not modified, they are at high risk for
6 severe hematopoietic toxicity. Inherited thiopurine methyltransferase deficiency has also been
7 associated with a higher risk of t-AML, particularly in ALL patients treated with topoisomerase
8 II inhibitors (Thomsenet al., 1999; Gadneret al., 2006). It has been postulated that the increased
9 risk may be due to an interference of 6-thioguanine or methylated 6-mercaptopurine with DNA
10 repair after DNA damage has been induced by other chemotherapeutic agents.

11 The influence of polymorphisms in other xenobiotic metabolizing genes on the incidence
12 of leukemia has been the subject of many investigations (Cheoket al., 2006; Leoneet al., 2007;
13 Seedhouse and Russell, 2007; Guillem and Tormo, 2008; Leoneet al., 2010). In many cases,
14 there was no difference between the frequencies seen in t-AML patients as compared to *de novo*
15 leukemia patients or a control cohort. A number of studies have indicated that individuals with
16 genes coding for nonfunctional or less active copies of various glutathione-S-transferases,
17 CYP3A4, and NADPH-quinone-oxidoreductase 1 (NQO1) have an increased risk for developing
18 t-AML following chemotherapy. However, these results have not consistently been seen. The
19 relationship between NQO1 and leukemia is presented below as an example.

20 Polymorphisms in NQO1, an enzyme involved with the reduction of quinones and
21 protection against oxidative stress, have been repeatedly associated with the development of
22 leukemia. Studies have reported that an inactivating polymorphism in NQO1 (the C609T slow
23 variant) was overrepresented in patients with t-AML (Larsonet al., 1999), in those with *de novo*
24 AML (particularly those with translocations or an inv (16) clonal aberration [Smithet al., 2001]),
25 and in infant leukemias with a 11q23 karyotype, and infants and children with the t(4;11) form of
26 ALL (Wiemelset al., 1999; Smithet al., 2002). While these initial studies indicated a consistent
27 association with a number of different leukemia types, more recent studies have been less
28 consistent with many not showing an association (Blancoet al., 2002; Sirmaet al., 2004;
29 Eguchi-Ishimaeet al., 2005; Maliket al., 2006).

30 Genetic polymorphisms affecting NQO1 have also been associated with increased
31 myelotoxicity and may confer an increased risk of leukemia. For example, benzene-exposed

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1 individuals who were rapid CYP2E1 metabolizers and had the C609T slow variant for NQO1
2 had a 7.6-fold increased risk of benzene poisoning as compared to exposed individuals with the
3 slow metabolizer phenotype who had one or two of the wild type NQO1 alleles (Rothman et al.,
4 1997). In another study by this research group, different NQO1 polymorphisms, as well as a
5 polymorphism in myeloperoxidase, an enzyme implicated in the bioactivation of benzene's
6 quinone metabolites in the bone marrow, were associated with lower blood cell counts in
7 benzene-exposed workers (Lan et al., 2004). A similar association between NQO1 and
8 chromosomal damage in the peripheral blood lymphocytes of benzene-exposed was also recently
9 reported by another research group (Kim et al., 2008).

10

11

8. EXAMPLES OF SPECIFIC LEUKEMIA-INDUCING CHEMICALS

The information on the mechanisms of action of the various leukemia-inducing agents presented in the following section has been extracted and summarized from the respective IARC monographs.

8.1. MELPHALAN

A modified version of the section below will be published in a forthcoming issue of the IARC monographs.

The antineoplastic drug melphalan is a direct-acting, bifunctional alkylating agent that binds to cellular macromolecules including DNA, RNA, and proteins (Osborne et al., 1995). As a phenylalanine derivative of nitrogen mustard, it is capable of producing a variety of DNA adducts including monoadducts at the N7 of guanine and the N3 of adenine as well as interstrand crosslinks - premutagenic lesions that are believed to play a critical role in its toxic and carcinogenic effects (Povirk and Shuker, 1994; Lawley and Phillips, 1996; GlaxoSmithKline, 2007). In the classification scheme of Vogel et al., 1998, melphalan is a Category 3 agent that would be expected to be a potent mutagen and carcinogen.

Melphalan has been tested for genotoxicity in an assortment of short-term tests, with positive results seen in a wide variety of assays both in vitro and in vivo (IARC, 1987a, b). Increased frequencies of chromosomal aberrations and sister chromatid exchanges (SCEs) occurring in the peripheral blood lymphocytes have also been reported in multiple studies of patients treated therapeutically with melphalan (IARC, 1987a; Raposa and Varkonyi, 1987; Mamuriset al., 1989, 1990; Poppet al., 1992; Amielet al., 2004). Patients treated with this anticancer agent have also exhibited hematotoxicity and immunosuppression (Goldfrank et al., 2002; GlaxoSmithKline, 2007).

As indicated in the most recent IARC evaluation, patients treated with melphalan are at a significantly elevated risk of developing ANLL (Grosse et al., 2009) (see Table 7). Leukemias that have developed in patients previously treated with melphalan (often in combination with other agents) have shown the alterations involving chromosomes 5 and 7 that, as described above, are characteristic of t-AML induced by alkylating agents (Rodjeret et al., 1990). While there is some evidence that melphalan may directly induce damage targeting chromosomes 5 or 7

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1 (cf. Mamuriset al. [1989, 1990] and Amielet al. [2004]), this drug has also been reported to
2 induce nonspecific chromosomal alterations in a variety of experimental models and in the
3 lymphocytes of treated patients as indicated earlier. The detection of elevated levels of
4 chromosome aberrations in the peripheral blood lymphocytes of the treated patients is of
5 particular note, as multiple prospective studies have now shown that individuals with increased
6 levels of chromosome aberrations or micronuclei in these cells are at increased risk of
7 developing cancer later in life (Hagmaret al., 1998; Liouet al., 1999; Smerhovskyyet al., 2001;
8 Hagmaret al., 2004; Boffettaet al., 2007).

10 **8.2. ETHYLENE OXIDE** (largely summarized from IARC, 2008b)

11 Ethylene oxide is a direct-acting alkylating agent that has been shown to bind to DNA,
12 RNA, and protein. The major DNA adduct recovered *in vivo* is *N*7-(hydroxyethyl) guanine, an
13 adduct that is not considered to be particularly mutagenic. Additional adducts such as
14 3-(2-hydroxyethyl)-adenine and *O*⁶-(2-hydroxyethyl)guanine, which would be expected to be
15 more mutagenic, are either not detected or are detected at very low levels (Walker et al., 1992).
16 Ethylene oxide is readily metabolized to non-DNA reactive products by glutathione-
17 *S*-transferases and epoxide hydrolases, and this is likely to reduce the concentrations of ethylene
18 oxide that are able to reach the DNA. In the classification scheme of Voget al., 1998, ethylene
19 oxide is a Category 1 agent that would be expected to be a relatively weak mutagen and
20 carcinogen *in vivo* as compared to other, primarily antineoplastic, alkylating agents.

21 Ethylene oxide has been shown to be genotoxic and mutagenic in numerous assays in
22 both somatic and germ cells, and in both prokaryotic and eukaryotic organisms (IARC, 1994,
23 2008b). It is highly active in *in vitro* systems, with lesser activity being seen *in vivo*. Numerous
24 studies have shown that ethylene oxide can induce point mutations in both reporter genes and
25 cancer genes of multiple tissues in mice and rats. Based on these studies, however, ethylene
26 oxide was considered to be a relatively weak point mutagen *in vivo*. Ethylene oxide was shown
27 to induce chromosomal damage in rodents, but observable damage occurred only at high
28 concentrations indicating that it is also a relatively weak clastogen in experimental animals.
29 Somewhat surprisingly, increased frequencies of chromosomal aberrations have been seen in the
30 peripheral blood lymphocytes of ethylene oxide-exposed workers in 18 of 24 studies that were
31 evaluated (IARC, 2008b). As indicated above, individuals with elevated frequencies of

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1 chromosomal aberrations in their peripheral blood are at an elevated risk of developing cancer.
2 Ethylene oxide induced lymphohematopoietic cancers in female mice (lymphomas) and male
3 and female rats (mononuclear cell leukemia) in chronic bioassays. In contrast to most other
4 leukemia-inducing agents, exposure to ethylene oxide has not been associated with myelotoxicity
5 in humans.

6 In two fairly recent studies, an elevated frequency of mutations or a change in mutational
7 spectra was seen in the tumors of ethylene oxide-treated mice (Houleet al., 2006; Honget al.,
8 2007). High frequencies of *K-Ras* mutations were detected in the lung, Harderian gland, and
9 uterine tumors of the ethylene oxide-treated animals. A minor increase in mutation frequency
10 and a major change in the mutational spectrum of *Tp53* mutations were also seen in mammary
11 gland tumors of ethylene-oxide treated mice (Houleet al., 2006). The high frequencies of
12 mutations present in these genes, particularly mutations in the critical codons of *K-Ras* and
13 inactivation of *Tp53*, indicate that mutations are induced in the tumors of ethylene oxide-treated
14 mice, and that the changes likely play an important role in ethylene oxide-induced tumorigenesis
15 in these tissues.

16 There is little known about the mechanisms underlying ethylene oxide-induced tumors in
17 humans. However, activating mutations in the *RAS* family of oncogenes and inactivation of
18 *TP53* have been shown to play critical roles in the development of both spontaneous and
19 chemically induced cancers (Pedersen-Bjergaard et al., 2006; Zarbl, 2006). Of note, activating
20 mutations in *RAS* genes have been shown to occur in up to 30% of AML cases (Byrne and
21 Marshall, 1998). In most cases, it is N-*RAS* that is activated although activation of K-*RAS* is
22 occasionally seen (Byrne and Marshall, 1998; Bowen et al., 2005). The mutations typically occur
23 in codons 12, 13, and 61, sites that are critical for the normal regulation of *RAS* activity. The
24 activating mutations lead to the generation of constitutively activated *RAS* proteins that cannot be
25 switched off and inappropriately generate proliferative signals within the cell (Byrne and
26 Marshall, 1998). While *RAS* mutations occur frequently in *de novo* AML, they are generally
27 less commonly seen in t-MDS/t-AML. As shown in Table 6, they were only seen in 14 of the
28 140 patients in the Copenhagen cohort (Christiansen et al., 2005; Pedersen-Bjergaard et al., 2008).
29 Some patients that lack *RAS* mutations still exhibit an overexpression of *RAS* genes, and this has
30 been considered as further evidence for the involvement of dysregulated *RAS* signaling in
31 leukemogenesis (Byrne and Marshall, 1998). Interestingly, an elevated expression of the N-*RAS*

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1 oncogene (as well as the *TP53* tumor suppressor gene) was reported in the lymphocytes of two
2 small groups of ethylene oxide-exposed hospital nurses (Emberet al., 1998a, b).

3 Mutations in the *TP53* tumor suppressor gene have also been detected in a subset of
4 t-MDS/t-AML patients. For example, 34 of the 140 patients in the Copenhagen cohort exhibited
5 *TP53* mutations (Pedersen-Bjergaard et al., 2008). These were typically seen in patients whose
6 leukemia cells exhibited a loss of all or part of chromosomes 5 and 7.

7 In its recent evaluation (Baan et al., 2009; IARC, 2009), the IARC working group
8 indicated that “there is *limited evidence* in humans for a causal association of ethylene oxide with
9 lymphatic and haematopoietic cancers (specifically lymphoid tumors, i.e., non-Hodgkin
10 lymphoma, multiple myeloma, and chronic lymphocytic lymphoma)...” It should be noted that
11 ANLL was not one of the lymphohematopoietic cancers that was considered by the IARC
12 working group to be associated with ethylene-oxide exposure. As a result, the information on
13 t-AML presented above, while valid for other types of alkylating agents, may not be relevant in
14 this case. As seen in Table 7, the three lymphohematopoietic cancers mentioned by IARC have
15 generally not been associated with other alkylating agents with the exception of butadiene, which
16 has been associated with CLL and NHL (described below). It should also be noted that the three
17 types of neoplasm listed by IARC originate in mature B lymphoid cells, which is also somewhat
18 unusual for alkylating agent-related cancers.

19 20 **8.3. 1,3-BUTADIENE** (summarized largely from IARC, 1999, 2008a)

21 Butadiene is a widely used industrial chemical that has been shown to induce cancer in
22 mice, rats, and humans. Butadiene is metabolized to a number of epoxide metabolites
23 (stereoisomers of epoxybutene, epoxybutanediol, and diepoxybutane) that can react directly with
24 DNA. The most common DNA adduct detected in mice and rats is the *N7*-guanine adduct
25 (*N7*-trihydroxybutylguanine), which is derived from either epoxybutanediol or diepoxybutane.
26 Other adducts at base-pairing sites that can be formed from the epoxide metabolites of butadiene
27 include adducts at the *N3*-cytosine, *N1*-adenine, *N6*-adenine, *N1*-guanine, and *N2*-guanine.
28 Crosslinks between *N7*-guanines have been detected in the liver and lungs of butadiene-treated
29 mice. The butadiene epoxide metabolites can also be metabolized to non-DNA reactive products
30 by glutathione-*S*-transferases and epoxide hydrolases. In the classification scheme in Vogelet
31 al., 1998, butadiene through its diepoxybutane metabolite was considered a Category 3 agent,

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1 which would be expected to be a potent mutagen and carcinogen. However, it was suggested by
2 Vogel et al. (1998) that because the DNA crosslinks formed by diepoxybutane are primarily
3 intrastrand crosslinks that are more readily repaired, diepoxybutane is a much weaker mutagen
4 and carcinogen than other Category 3 agents. Metabolic factors are also likely to contribute to
5 butadiene's reduced potency in rats (and probably humans). However, it should be noted that
6 butadiene is readily bioactivated in mice and is a potent carcinogen in that species.

7 Butadiene and its epoxide metabolites have been shown to be genotoxic and mutagenic in
8 most experimental systems both in vitro (with metabolic activation for butadiene) and in vivo.
9 Butadiene exhibited clastogenic effects in mice inducing chromosomal aberrations, micronuclei,
10 and SCEs. Similar effects were not seen in rats, and this is believed to be due to metabolic
11 differences between the two species. Butadiene has also been shown to induce mutations with
12 bioactivation in mammalian cells and in vivo in mice. It should be noted that considerably fewer
13 studies of the genotoxicity of butadiene have been conducted in rats as compared to mice. The
14 genotoxicity of the epoxide metabolites has also been extensively studied. Not surprisingly
15 given its bifunctional nature, the diepoxybutane is the most potent of the three metabolites. For
16 example, when monoepoxybutene, diepoxybutane, and 3,4-epoxy-1,2-butanediol were tested for
17 mutagenicity at *HPRT* and *TK* loci in the TK6 human lymphoblastoid cells (Cochrane and
18 Skopek, 1993; Cochrane and Skopek, 1994), all three epoxides were mutagenic, but the
19 mutagenicity of the diepoxybutane was much greater than that seen for the other two epoxides.
20 However, as noted by IARC (2008a), while genotoxicity studies have indicated that
21 diepoxybutane is the most genotoxic of the epoxides formed from butadiene, the relative
22 contribution of the various epoxide metabolites to the mutagenicity and carcinogenicity of
23 butadiene is not known as the monoepoxybutene metabolite is likely to be formed in greater
24 quantities.

25 Using either conventional techniques or new molecular cytogenetic techniques such as
26 fluorescence in situ hybridization with DNA probes, increased frequencies of chromosomal
27 aberrations have not generally been seen in the peripheral blood lymphocytes of butadiene-
28 exposed workers. Exposure to butadiene has also not been associated with myelotoxicity in
29 exposed humans.

30 Mutations in the cancer-related *K-Ras*, *H-Ras*, *Tp53*, *p16/p15*, and *b-catenin* genes have
31 been detected in tumors of mice exposed to butadiene. *K-Ras* mutations, frequently a G-to-C

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1 transversion at codon 13, have been seen in hemangiosarcomas, lymphomas, and cancers of the
2 lung, forestomach, and mammary tumors of butadiene-treated mice. Mutations in the *Tp53*
3 tumor-suppressor gene have been detected in mouse lymphomas, brain tumors, and mammary
4 gland tumors. Similarly, mutations in the *p15* and *p16* tumor suppressor genes were seen in
5 induced lymphomas, and mutations in *b-catenin* were seen in the mammary gland tumors. The
6 prevalence of mutations in these cancer-related genes provides strong evidence for a mutagenic
7 mechanism in butadiene carcinogenesis. As indicated above, mutations in the *RAS* and *TP53*
8 genes have been seen in *de novo* leukemias and t-AMLs seen in humans.

9 In its 2008 evaluation (IARC, 2008a), IARC concluded

10
11 Overall, the epidemiological studies provide evidence that exposure to butadiene
12 causes cancer in humans. ... This conclusion is primarily based on the evidence
13 for a significant exposure–response relationship between exposure to butadiene
14 and mortality from leukaemia in the University of Alabama in Birmingham study,
15 which appears to be independent of other potentially confounding exposures. It is
16 also supported by elevated relative risks for non-Hodgkin lymphoma in other
17 studies, particularly in the butadiene monomer production industry. The Working
18 Group was unable to determine the strength of the evidence for particular
19 histological subtypes of lymphatic and haematopoietic neoplasms because of the
20 changes in coding and diagnostic practices for these neoplasms that have occurred
21 during the course of the epidemiological investigations. However, the Working
22 Group considered that there was compelling evidence that exposure to butadiene
23 is associated with an increased risk for leukaemias.

24
25 The most recent IARC evaluation (Baanet al., 2009; IARC, 2009) did not provide additional
26 clarification on the histological subtypes, stating that “there is sufficient evidence in humans for
27 the carcinogenicity of 1,3-butadiene” and that “butadiene causes cancer of the haematolymphatic
28 organs.” Assuming that the earlier diagnoses were correct, the types of leukemias in the
29 University of Alabama study that showed significant dose-related associations with butadiene
30 exposure were CLL and CML. Increases in other NHLs such as reticulosarcoma and
31 endothelioma seen in other studies were also provided as supportive evidence. Neither of these
32 two types of leukemia has been commonly seen in leukemias induced by most other alkylating
33 agents (see Table 7). It should be noted that increases in CLL and NHL have been reported with
34 ethylene oxide exposure.

35
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1 **8.4. FORMALDEHYDE** (summarized primarily from IARC, 2006, unless otherwise
2 indicated)

3 Formaldehyde is a common industrial chemical, an environmental contaminant, and an
4 endogenous metabolite. It has been shown to induce cancer in rats and humans. Formaldehyde
5 is a reactive chemical that primarily binds to sulfhydryl and amine groups in polypeptides and
6 proteins. However, it can also form DNA-protein crosslinks, which have been shown to be
7 associated with its cytotoxic and genotoxic effects. It has also been shown to bind weakly to
8 DNA forming monoadducts and DNA-DNA crosslinks (Lu et al., 2010). Formaldehyde also
9 binds readily to reduced glutathione, forming a hemithioacetal that can be converted to formate
10 by formaldehyde dehydrogenase.

11 Formaldehyde has exhibited genotoxic and mutagenic effects in a large number of
12 experimental systems. *In vitro*, it has been shown to induce mutations in bacteria and
13 mammalian cells, DNA-protein crosslinks and strand breaks, and chromosomal aberrations. In
14 rodent models, it has been shown to induce DNA adducts, DNA-DNA and DNA-protein
15 crosslinks, chromosome aberrations, and micronuclei, primarily at the site of exposure. Genetic
16 damage has not typically been seen in the bone marrow or other locations distal from the site of
17 exposure. Occasional reports of systemic effects are found in the literature, but these have not
18 been seen in most studies.

19 One of the tumor types induced by formaldehyde in rats is squamous-cell nasal
20 carcinoma. *Tp53* mutations were seen in 5 of 11 carcinomas isolated from the formaldehyde-
21 exposed rats. However, because the types of mutation seen in the nasal tumors differed from
22 those seen in other model systems, the principal author of the study suggested that the observed
23 mutations may have been due to an indirect effect, possibly occurring as a result of inflammation
24 and regenerative cell proliferation in the nasal passages of the exposed rats (Recio, 1997).

25 Formaldehyde-exposed workers have been reported to exhibit increased frequencies of
26 DNA-protein crosslinks in their peripheral blood lymphocytes. Increased frequencies of
27 micronuclei were reported to occur in the nasal and oral mucosa of formaldehyde-exposed
28 workers but were not seen in the oral mucosal cells of volunteers exposed to variable levels of
29 formaldehyde under controlled exposure conditions (Speitet al., 2007). Similarly, while negative
30 results were reported in some studies, others have reported that formaldehyde-exposed workers
31 had increased frequencies of structural chromosome aberrations and SCEs in their peripheral

1 blood lymphocytes (IARC, 2006; Zhanget al., 2009). Formaldehyde exposure has not typically
2 been associated with hematotoxicity in humans (or animals). The mixed results seen in the
3 various studies may be explained, in part, by differences in exposure levels. Recently, a
4 biomonitoring study was conducted on a group of Chinese workers with particularly high
5 formaldehyde exposures (median 8-hour time weighted average exposure level of 1.28 ppm
6 [Zhanget al., 2010]). The researchers found that the exposed workers had lower blood cell
7 counts and that peripheral stem/progenitor cells obtained from the workers exhibited elevated
8 frequencies of monosomy for chromosome 7 and trisomy for chromosome 8—cytogenetic
9 alterations commonly seen in human leukemias.

10 In its 2006 evaluation of formaldehyde (IARC, 2006), the working group concluded that
11 “there is *sufficient evidence* in humans for the carcinogenicity of formaldehyde” based on the
12 occurrence of nasopharyngeal cancer. With regards to leukemia, the working group concluded
13 that “there is strong but not sufficient evidence for a causal association between leukaemia and
14 occupational exposure to formaldehyde.” They felt at that time that it was “not possible to
15 identify a mechanism for the induction of myeloid leukaemia in humans by formaldehyde.” In
16 the more recent 2009 evaluation (Baanet al., 2009; IARC, 2009), the new working group
17 concluded that “the epidemiological evidence on leukaemia has become stronger, and new
18 mechanistic studies support a conclusion of *sufficient evidence* in humans. This highlights the
19 value of mechanistic studies, which in only 5 years, have replaced previous assertions of
20 biological implausibility with new evidence that formaldehyde can cause blood-cell
21 abnormalities that are characteristic of leukaemia development.” However, it should be noted
22 that this conclusion was controversial as the working group was almost evenly split on the
23 evaluation, with a slight majority seeing the evidence as *sufficient* for carcinogenicity, and the
24 minority viewing the evidence as *limited*. A recent compilation and meta-analysis of
25 formaldehyde-induced leukemia studies have indicated that formaldehyde exposure is most
26 closely associated with myeloid leukemias, primarily AML (Zhanget al., 2009).

27

1 **9. RISK ASSESSMENT IMPLICATIONS**

2
3
4 As indicated above, approximately 25% of the agents established by IARC as human
5 carcinogens induce lymphohematopoietic cancers, and approximately 22% are associated with
6 the induction of leukemia, primarily AML. These agents have a wide variety of uses, and given
7 their established carcinogenic effects, they have been the focus of many risk assessments and
8 safety evaluations. For some of these carcinogens such as benzene or ionizing radiation, these
9 assessments and their refinements have been ongoing for decades and involve large amounts of
10 information. The sections below focus on how mechanistic information on these carcinogenic
11 agents can be used to inform risk assessment decisions. The following discussion is not intended
12 to be comprehensive but rather will focus on some key issues related to contemporary risk
13 assessment discussions. .

14
15 **9.1. HAZARD IDENTIFICATION**

16 Hazard identification is the process by which hazardous substances—carcinogenic agents
17 in this case—are identified and characterized. According to the IARC Preamble (IARC, 2008d),
18 which describes the IARC groupings and the weight-of-evidence decision-making process, the
19 Group I category “is used when there is *Sufficient Evidence of Carcinogenicity* in humans.
20 Exceptionally, an agent may be placed in this category when evidence of carcinogenicity in
21 humans is less than *sufficient* but there is *Sufficient Evidence of Carcinogenicity* in experimental
22 animals and strong evidence in exposed humans that the agent acts through a relevant
23 mechanism of carcinogenicity.” Ethylene oxide represents one of the exceptional agents, which
24 was classified based on less than sufficient evidence in humans but with sufficient evidence in
25 animals.

26 The Group 2A agents represent chemicals that are probable human carcinogens for which
27 there “is *Limited Evidence of Carcinogenicity* in humans and *Sufficient Evidence of*
28 *Carcinogenicity* in experimental animals. In some cases, an agent may be classified in this
29 category when there is *Inadequate Evidence of Carcinogenicity* in humans and *Sufficient*
30 *Evidence of Carcinogenicity* in experimental animals and strong evidence that the carcinogenesis
31 is mediated by a mechanism that also operates in humans. Exceptionally, an agent may be
32 classified in this category solely on the basis of *Limited Evidence of Carcinogenicity* in humans.

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1 An agent may be assigned to this category if it clearly belongs, based on mechanistic
2 considerations, to a class of agents for which one or more members have been classified in
3 Group 1 or Group 2A.” Most of the Group 2A agents listed in Table 8 have mechanisms of
4 action such as mutagenicity that are commonly associated with carcinogenesis. However, they
5 have not been adequately studied in humans, or for many of the chemotherapeutic agents, they
6 were administered in combination therapy often with other carcinogenic agents so that the
7 carcinogenic effects for the agent being investigated cannot be separately identified.

8 For most of the evaluations, studies of cancer in humans and animals have played the
9 primary role in the IARC classification. Information on the mechanism of action has typically
10 only played a supportive role. As a result, it is reasonable to examine information on the
11 mechanisms of action of the Group 1 and 2A carcinogens to help identify carcinogens and
12 improve the hazard identification process. Below are several observations about how
13 mechanistic information has and may be used in hazard identification for leukemia-inducing
14 agents.

16 **9.1.1. Utility of Short-Term Genotoxicity Tests**

17 As seen in Table 8, most of the agents identified by IARC as human carcinogens are
18 likely to act through a mutagenic mode of action. The majority of the Group 1 and 2A
19 carcinogens are alkylating agents, but other classes of genotoxic agents such as topoisomerase II
20 inhibitors or nucleotide analogs are also present. The majority of the Group 1 and 2A leukemia-
21 and lymphoma-inducing agents are active in short-term tests both in vitro (with metabolic
22 activation as needed) and in vivo (IARC, 1987a). This is not surprising given their mechanisms
23 of action. The exceptions to this tend to be the infectious agents and the immunosuppressive
24 agents that act through nongenotoxic or indirect genotoxic mechanisms of action.

25 As also shown in Table 7, most of the leukemia-inducing agents have been shown to
26 induce chromosomal aberrations or micronuclei in the peripheral blood lymphocytes of exposed
27 humans (and animals). In addition, at commonly used and frequently high doses, these agents
28 also cause significant bone marrow toxicity with noticeable decreases in blood cell counts of the
29 exposed individuals. There are a few Group 1 agents that are exceptions and do not manifest
30 these particular patterns. Ethylene oxide and butadiene have not been reported to induce
31 hematotoxicity in humans, and butadiene has not been shown to induce structural chromosome

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1 aberrations in exposed workers. These two are also somewhat unusual in that the types of
2 cancers associated with their exposure are CLL and NHL, neoplasms that originate in mature B
3 lymphoid cells.

4 5 **9.1.2. Usefulness of Animal Bioassays**

6 There is substantial evidence to indicate that chronic animal bioassays are effective in
7 detecting human carcinogens. As described in the IARC Preamble (IARC, 2008d), “all known
8 human carcinogens that have been studied adequately for carcinogenicity in experimental
9 animals have produced positive results in one or more animal species.” However, as further
10 noted in the Preamble, “although this association cannot establish that all agents that cause
11 cancer in experimental animals also cause cancer in humans, it is biologically plausible that
12 agents for which there are *Sufficient Evidence of Carcinogenicity* in experimental animals also
13 present a carcinogenic hazard to humans.” Accordingly, the vast majority of the Group 1
14 leukemia- and lymphoma-inducing agents shown in Table 7 have been reported previously to be
15 carcinogenic in rodent bioassays (Eastmond, 1997). Indeed, many of them have been shown to
16 induce leukemias or lymphomas in mice and in rats. Most of these have been shown to occur in
17 mice and were T-cell leukemias or lymphomas, rather than the ANLL, which is prevalent in
18 humans. As a result, there appears to be fundamental differences between the types of
19 lymphohematopoietic tumors induced in humans and rodents. The reason for this remains
20 unknown but may be related to species differences in hematopoiesis and/or immune surveillance
21 (Eastmond, 1997).

22 The good correlation seen for animals and humans mentioned above was based primarily
23 on the results for chemical carcinogens and probably does not hold for many of the infectious
24 agents, which are likely to only infect humans and closely related species. In addition, it is not
25 clear at this point if this correlation will hold true for the topoisomerase II inhibitors, as most of
26 them have not been adequately tested in experimental animals. While the fusion gene products
27 have clearly been shown to affect hematopoiesis and can cause leukemias in mice (Corralet al.,
28 1996; Dobson et al., 1999; Lavauet al., 2000; Forster et al., 2003; Soet al., 2003), it is not certain
29 if the genes are located in regions in the rodents that will allow the same chimeric genes to be
30 formed. It should also be noted that the Group 2A carcinogens are also positive in rodent

1 bioassays; however, this is to be expected, as this characteristic is one of the primary reasons that
2 the chemicals have been listed.

3

4 **9.1.3. Combining Different Types of Lymphohematopoietic Cancers for Analysis**

5 In evaluating epidemiological studies, a decision has to be made about which specific
6 types of disease should be combined for the analysis. Often the reporting of leukemias has been
7 grouped into the four common categories of AML, CML, ALL, and CLL. Similarly, the
8 lymphomas and myelomas have been grouped into NHL (lymphosarcoma, reticulosarcoma, and
9 other malignant neoplasms of lymphoid and histocytic tissue), Hodgkin's disease, and multiple
10 myeloma (MM). More recent case-control studies of lymphoma have expanded the NHL
11 grouping to include CLL, or to group lymphomas by cell type or by specific International
12 Classification of Disease-Oncology category (e.g., diffuse lymphatic B-cell lymphoma, follicular
13 lymphoma, etc.). However, many different types of groupings have been used in analyzing
14 epidemiological data, primarily reflecting the classification system in use at the time of diagnosis
15 or cause of death. An illustration of the various types of groupings used for studies of benzene
16 has been described by (Savitz and Andrews, 1997). In addition, evaluations of the induction of
17 lymphohematopoietic diseases by an agent over time can be challenging due to changes in
18 diagnosis, the names of diseases, and classification schemes, as well as lack of detailed case and
19 exposure information. Other issues such as misclassification errors and insufficient information
20 on death certificates can also influence the outcome of the studies. The decision about how to
21 analyze the data can also have a significant influence on the outcome of the analysis and the
22 conclusions of the study.

23 As illustrated in Tables 1–3, there are a large number of distinct lymphohematopoietic
24 cancers. By analyzing each separately, a study would only have the power to detect cancers that
25 were very strongly associated with exposure to an agent if detection was even possible. In
26 addition, the large number of comparisons could lead to some associations being labeled as
27 significant due simply to random chance. As a result, it is common to combine specific
28 lymphohematopoietic cancers for analysis. The key question, which has not fully been
29 answered, is which categories of specific cancer should be combined for analysis. The value of
30 combining uncommon lymphohematopoietic cancers has been demonstrated by Savitz and
31 Andrews for benzene (Savitz and Andrews, 1996; Savitz and Andrews, 1997). Benzene

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1 exposure is strongly associated with ANLL. However, its association with lymphoid cancers has
2 been a source of ongoing discussion. Savitz and Andrews showed that by analyzing non-AML
3 cancers together, a significant association between benzene exposure and these cancers could
4 also be shown. IARC, in its most recent evaluation, has given more credence to an association
5 between benzene and other lymphohematopoietic cancers as it concluded that there was
6 evidence, albeit limited, for an association between benzene and ALL, CLL, NHL, and multiple
7 myeloma (Baanet al., 2009; IARC, 2009). These results suggest that benzene can target the
8 hematopoietic stem and progenitor cells as well as more mature lymphoid cells.

9 In addition to combining specific types of cancers for analysis during individual studies,
10 it may be informative to see how various authoritative bodies such as IARC, the National
11 Academies of Science Biological Effects of Ionizing Radiation (BEIR) committee, and the
12 United Nations Scientific Committee on the Effects of Atomic Radiation (UNSCEAR) have
13 combined the lymphohematopoietic cancers in making decisions about risk or for weight-of-
14 evidence determinations for various leukemogenic agents. As indicated above for benzene,
15 IARC chose to evaluate the major types of cancer separately. However, it is likely that the
16 association between benzene and one type of cancer provided supportive evidence that benzene
17 could be associated with another type of lymphohematopoietic cancer. This type of supporting
18 evidence appears to have played an important role in the evaluations of butadiene where
19 associations with CML, CLL, and to some degree, NHL, were combined in concluding that
20 butadiene exposure caused cancer of the “haematolymphatic organs.” Similarly, information on
21 associations with different types of lymphohematopoietic cancers contributed to the recent IARC
22 evaluation on formaldehyde (AML and CML) and ethylene oxide (NHL, MM, and CLL). It
23 should be noted that for butadiene and probably benzene, supportive evidence came from
24 associations with both myeloid and lymphoid tumors.

25 In recent evaluations of ionizing radiation, it has been common to use all leukemias or
26 combine the results for ALL, AML, and CML in modeling the data and assessing cancer risks
27 (UNSCEAR, 2000a,b; NRC, 2006 and references therein). Increases in CLL have not been seen
28 in radiation-exposed study groups. When presenting the study results, the radiation-induced
29 leukemias are frequently described in various documents as simply leukemias or non-CLL
30 leukemias.

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1 Thus, as illustrated in the evaluation of the various cancer-inducing agents, there is no
2 strict consensus on how specific lymphohematopoietic cancers should be combined for analysis
3 and weight-of-evidence determinations. As discussed above, a variety of combinations including
4 those combining acute and chronic myeloid neoplasms as well as lymphoid and myeloid
5 neoplasms have been used in recent evaluations.

6 7 **9.1.4. Potential Influence of Latency Period in Identifying Leukemogens**

8 The period between the initial exposure to a carcinogenic agent and the onset of cancer is
9 known as the latency period. Latency periods for leukemias tend to be much shorter than those
10 seen for other induced cancers such as lung cancer induced by tobacco smoke, which has a
11 median latency period of approximately 30 years (Weiss, 1997). As indicated above, the latency
12 period for topoisomerase II inhibitors is quite short with median latency periods of 2–3 years.
13 For radiation and chemical chemotherapy agents, the induced leukemias first appear 1–2 years
14 after the beginning of treatment. The median incidence peaks at about 4–7 years, and by 10–15
15 years after the beginning of treatment, the incidence has frequently declined to control or near
16 control levels (Casciato and Scott, 1979; Pedersen-Bjergaard et al., 1987; Kaldoret al., 1990;
17 Davies, 2000; Schonfeldt et al., 2006). This indicates that for leukemogens such as the
18 chemotherapeutic alkylating agents, the risk of developing t-AML will most likely peak at ~4–7
19 years after the beginning of exposure and will begin to decline with additional follow-up.
20 Continuing follow-up beyond 10 to 15 years after treatment would be expected to significantly
21 reduce associations between exposure and leukemia and cause a bias in results towards no effect.
22 Hence, adding person-years after exposure ends or is substantially reduced, as sometimes occurs
23 in occupational studies, may significantly weaken true associations between exposure and the
24 incidence of leukemia. The influence of latency or time since first exposure has been clearly
25 demonstrated for benzene (Rinskyet al., 2002; Silveret al., 2002) and has been postulated to have
26 had an influence on recent formaldehyde results (Beane Freemanet al., 2009). Failure to account
27 for latency period for weak carcinogens or under conditions of modest exposure for potent
28 carcinogens could reduce the association so that the agent or exposure would no longer be
29 considered carcinogenic. One note of caution is that the described latency periods have typically
30 been seen with high doses of the leukemia-inducing agents. There is evidence that the latency

1 period can be significantly influenced by the administered dose with higher doses producing
2 shorter latency periods and lower doses producing longer latency periods (Cadman et al., 1977).

4 **9.1.5. Metabolism and Bioactive Dose at the Target Organ**

5 One of the fundamental principles of toxicology is that the toxicological response is
6 related to the dose of the bioactive agent in the target tissue. However, the tissue dose of the
7 bioactive agent may differ significantly from the external exposure dose. For many carcinogens,
8 even if exposure occurs, the chemical may not arrive at the target organ in a form that enables it
9 to exert a toxic or mutagenic effect due to pharmacokinetic or metabolic reasons. In fact, this is
10 a fundamental difference between the risk assessment of ionizing radiation and chemical
11 leukemogens. Because of its ability to directly penetrate tissues, radiation risk estimates are
12 almost always based on the dose of radiation that reaches the bone marrow. In contrast, risks for
13 chemical leukemogens such as benzene, butadiene, or ethylene oxide are typically based on the
14 exposure dose and may not accurately reflect the bioactive dose that reaches the bone marrow.

15 Studies have also shown that pharmacokinetic and metabolic factors can significantly
16 influence the risks from leukemia-inducing agents. For example, the peak plasma concentrations
17 of melphalan have been shown to vary by over 50-fold after oral dosing due to variability in
18 absorption, first pass metabolism, and rapid hydrolysis (GlaxoSmithKline, 2007). Indeed, for a
19 few patients, detectable plasma levels of melphalan were not seen even after the administration
20 of a high dose (1.5 mg/kg) of the drug (Choi et al., 1989). The differences in plasma
21 concentration would undoubtedly have an effect on its efficacy as well as its risk of inducing
22 t-AML.

23 Metabolism has been shown to exert a major effect on the mutagenic and carcinogenic
24 risks of leukemia-inducing agents. For example, as discussed earlier, ethylene oxide is highly
25 genotoxic and mutagenic in vitro. Yet, in vivo, it is a relatively weak mutagen and carcinogen as
26 compared to other alkylating agents (Vogel et al., 1998). It should be noted that most of the
27 alkylating agents used for comparison were antineoplastic drugs designed to be highly toxic.
28 This is likely due to the efficient metabolism of the reactive epoxide by epoxide hydrolases,
29 glutathione transferases, and other detoxification enzymes as well as efficient repair of the
30 induced adducts. Similarly, bioactivation of leukemogens such as butadiene, benzene, and

1 cyclophosphamide to their reactive metabolites has been shown to significantly influence the
2 toxicity and genotoxicity of these agents.

4 **9.1.6. DNA-Adduct Type, Metabolism, and Repair**

5 The type of DNA adducts formed and their repair can have a major impact on the
6 toxicity, mutagenicity, and probably the cancer risk of leukemia-inducing agents. As indicated
7 earlier, three major classes of alkylating agents have been identified that have significantly
8 different mutagenic and carcinogenic potencies (Vogel et al., 1998). Category 1 agents were
9 mono-functional alkylating agents such as ethylene oxide and methyl methane sulfonate, which
10 primarily react at the N7 and N3 moieties of purines in DNA. These adducts are efficiently
11 repaired, and as a result, these agents tend to be relatively weak mutagens and carcinogens with
12 higher doses associated with observed increases in tumors in animals. Category 2 agents such as
13 procarbazine and ENU induce *O*-alkyl adducts and *N*-alkyl adducts in DNA, which are often
14 involved in base pairing and are slowly repaired. These agents are generally potent mutagens
15 and carcinogens. Category 3 agents such as melphalan and busulfan induce DNA breaks and
16 structural aberrations through their ability to cross-link DNA. They are highly toxic, mutagenic,
17 and carcinogenic. As indicated above, butadiene can be metabolized to diepoxybutane, a cross
18 linking agent, so it is classified as a Category 3 agent. However, its potency for rats and
19 probably humans has been reported to be much lower than the other Category 3 agents. This is
20 probably due to the need for metabolism as indicated above as well as the nature of the adducts
21 formed by butadiene. The butadiene crosslinks tend to be intrastrand and are more efficiently
22 repaired. Consistent with this explanation is the fact that diepoxybutane is believed to be the
23 reactive intermediate formed from treosulfan, a chemotherapeutic agent that appears to be
24 somewhat less potent in inducing t-AML in humans than other Category 3 chemotherapeutic
25 agents when considered on a mg/kg-basis (Kaldoret al., 1990). Interestingly, it should be noted
26 that treosulfan administration to humans has been associated with AML whereas occupational
27 exposure to 1,3-butadiene has been associated with CLL and CML. One possible explanation is
28 that the epoxybutene metabolite may play a more important role than diepoxybutane in inducing
29 the butadiene-related leukemias in humans.

1 **9.1.7. Individual Susceptibility**

2 Many factors such as age, sex, genetic composition, and general health status have been
3 shown to influence susceptibility to leukemia-inducing agents. For example, age has been
4 shown to be a factor in susceptibility to radiation-induced leukemia. Studies of the atomic bomb
5 survivors, who were exposed to both *gamma*, and to a lesser extent, neutron radiation, indicated
6 that the highest leukemia risks were seen in children (Prestonet al., 1994, 2004). The leukemia
7 risk also decreased more rapidly in children as compared to those in older age groups (Prestonet
8 al., 1994). Interestingly, a similar increased susceptibility has not been seen for children treated
9 with alkylating agent-based chemotherapy as their leukemia risks do not appear to be greater
10 than those seen in adults, and in some cases, may be less (Levine and Bloomfield, 1992; Pyattet
11 al., 2005, 2007). However, direct comparisons are difficult as in most studies children and adults
12 have been treated with different therapeutic regimens. For the nontherapeutic classes of
13 leukemia-inducing agents, little is known about the relative susceptibility of children to
14 leukemia, as the critical studies have almost always been conducted on adults. However, a
15 number of studies on related biomarkers have indicated that children or adolescents are also
16 susceptible to the toxic and genotoxic effects of these leukemogenic chemicals (Aksoyet al.,
17 1974; Aksoy, 1988; Niazi and Fleming, 1989; Neriet al., 2006).

18 Genetic polymorphisms in genes coding for xenobiotic metabolizing enzymes, DNA-
19 metabolizing or repair enzymes, and drug transporter proteins are other factors that have been
20 implicated as significantly influencing an individual's risk of developing leukemia when exposed
21 to genotoxic agents. A considerable number of studies have been conducted to identify enzymes
22 involved in the bioactivation and the inactivation of carcinogenic agents (for reviews, see
23 Cheoket al. [2006], Leoneet al. [2007, 2010], and Guillem and Tormo [2008]). As discussed
24 above and in the review articles, significant associations have been seen for a number of genes
25 coding for xenobiotic metabolizing enzymes, DNA-metabolizing and repair enzymes, and drug
26 transporters. Individuals with genes coding for nonfunctional or less active copies of various
27 glutathione-*S*-transferases, CYP3A4, and NQO1 have been reported to be at increased risk for
28 developing t-AML following chemotherapy. Similar increased risks have been seen for
29 individuals that lack efficient DNA-metabolizing or repair enzymes such as enzymes involved in
30 nucleotide excision repair or mismatch repair. However, further research in this area is needed
31 as similar associations for the metabolizing enzymes and DNA-repair enzymes have not been

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1 seen in other studies. As discussed by Lutz and colleagues, from a population risk perspective,
2 the increased susceptibility associated with the various genetic polymorphisms can have a
3 significant impact on cancer risks, particularly among those exposed to lower doses (Lutz, 1990,
4 2001).

5
6 **9.1.8. Summary**

7 As evident from Table 8 and from the above discussion, leukemia-inducing agents act
8 through different mechanisms to induce their carcinogenic effects. While most of these are
9 likely to act through a mutagenic mode of action, different leukemogens have different potencies
10 and different associated risks, which appear to be significantly influenced by the specific
11 mechanisms involved. Even among the alkylating agents, different chemicals can have different
12 potencies that are likely due to the nature of the DNA adducts formed and their repair as well as
13 metabolic and pharmacokinetic factors. In addition, polymorphisms in genes related to
14 xenobiotic metabolism and DNA repair can lead to increased susceptibility among groups in the
15 population.

Table 1. Simplified classification of the major lymphohematopoietic neoplastic diseases in humans based largely on the French-American-British (FAB) classification

I.	Neoplasms of multipotent stem cell origin	
	Chronic myelogenous leukemia	CML
II.	Neoplasms possibly originating in the multipotent stem cell	
	Myelodysplastic syndromes	MDS
	Refractory anemia	RA
	Refractory anemia with ring sideroblasts	RARS
	Refractory anemia with excess blasts	RAEB
	Chronic myelomonocytic leukemia	CMML
	Refractory anemia with excess blasts in transformation	RAEB
	Chronic myeloproliferative disorders	
III.	Neoplasms originating in stem cells or myeloid-committed precursors	
	Acute myeloid leukemia or acute nonlymphocytic leukemia	AML/ANLL
	Acute myeloblastic leukemia with minimal differentiation	M0
	Acute myeloblastic leukemia without maturation	M1
	Acute myeloblastic leukemia with maturation	M2
	Acute promyelocytic leukemia	M3
	Acute myelomonocytic leukemia	M4
	Acute monocytic leukemia	M5
	Acute erythroleukemia	M6
	Acute megakaryoblastic leukemia	M7
	Malignant histiocytosis	
IV.	Neoplasms of lymphoid-committed precursors	
	Immature phenotype: Acute lymphoblastic leukemia	ALL, L1,L2
	B-cell lineage	b-ALL
	T-cell lineage	t-ALL
	Intermediate or mature phenotype: non-Hodgkin's lymphoma	NHL
	Nodal/splenic phase	
	Leukemic phase	
	B-cell lineage	
	non-Burkitt's	
	Burkitt's	L3
	T-cell lineage	
	Lymphoblastic lymphoma	
	Adult T-cell leukemia/lymphoma	
	Mature lymphocytic phenotype	
	Prolymphocytic leukemia	
	Chronic lymphocytic leukemia	CLL
	B-cell lineage	
	T-cell lineage	
	Hairy cell leukemia	
	Plasmacytoid phenotype: Marrow-phase predominant	
	Macroglobulinemia	

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Heavy chain diseases
Myeloma
Hodgkin's Lymphoma

Adapted from Sullivan (1993).

Table 2. WHO classification of myeloid and related neoplasms

MYELOPROLIFERATIVE NEOPLASMS (MPNs)

Chronic myelogenous leukemia, *BCR-ABL1*-positive
Chronic neutrophilic leukemia
Polycythemia vera
Primary myelofibrosis
Essential thrombocythemia
Chronic eosinophilic leukemia, not otherwise specified
Mastocytosis
 Cutaneous mastocytosis
 Systemic mastocytosis
 Mast cell leukemia
 Mast cell sarcoma
 Extracutaneous mastocytoma
Myeloproliferative neoplasms, unclassifiable

MYELOID AND LYMPHOID NEOPLASMS ASSOCIATED WITH EOSINOPHILIA AND ABNORMALITIES OF *PDGFRA*, *PDGFRB*, OR *FGFR1*

Myeloid and lymphoid neoplasms with *PDGFRA* rearrangement
Myeloid neoplasms with *PDGFRB* rearrangement
Myeloid and lymphoid neoplasms with *FGFR1* abnormalities

MYELODYSPLASTIC/MYELOPROLIFERATIVE NEOPLASMS (MDS/MPN)

Chronic myelomonocytic leukemia
Atypical chronic myeloid leukemia, *BCR-ABL1*-negative
Juvenile myelomonocytic leukemia
Myelodysplastic/myeloproliferative neoplasm, unclassifiable
Refractory anemia with ring sideroblasts and thrombocytosis (provisional entry)

MYELODYSPLASTIC SYNDROME (MDS)

Refractory cytopenia with unilineage dysplasia
 Refractory anemia
 Refractory neutropenia
 Refractory thrombocytopenia
Refractory anemia with ring sideroblasts
Refractory cytopenia with multilineage dysplasia
Refractory anemia with excess blasts
Myelodysplastic syndrome with isolated del(5q)
Myelodysplastic syndrome, unclassifiable
Childhood myelodysplastic syndrome
Refractory cytopenia of childhood (provisional entry)

ACUTE MYELOID LEUKEMIA AND RELATED NEOPLASMS

Acute myeloid leukemia with recurrent genetic abnormalities
AML with t(8;21)(q22;q22); *RUNX1-RUNX1T1*

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AML with inv(16)(p13.1;q22) or t(16;16)(p13.1;q22); *CBFB-MYH11*
APL with t(15;17)(q22;q12); *PML-RARA*
AML with t(9;11)(p22;q23); *MLLT3-MLL*
AML with t(6;9)(p23;q34); *DEK-NUP214*
AML with inv(3)(q21;q26.2) or t(3;3)(q21;q26.2); *RPNI-EVII*
AML (megakaryoblastic) with t(1;22)(p13;q13); *RBM15-MKLI*
AML with mutated NPM1 (provisional entry)
AML with mutated CEBPA (provisional entry)

Acute myeloid leukemia with myelodysplasia-related changes

Therapy-related myeloid neoplasms

Acute myeloid leukemia, not otherwise specified

AML with minimal differentiation
AML without maturation
AML with maturation
Acute myelomonocytic leukemia
Acute monoblastic/monocytic leukemia
Acute erythroid leukemia
Pure erythroid leukemia
Erythroleukemia, erythroid/myeloid
Acute megakaryoblastic leukemia
Acute basophilic leukemia
Acute panmyelosis with myelofibrosis

Myeloid sarcoma

Myeloid proliferations related to Down syndrome

Transient abnormal myelopoiesis
Myeloid leukemia associated with Down syndrome

Blastic plasmacytoid dendritic cell neoplasm

ACUTE LEUKEMIAS OF AMBIGUOUS LINEAGE

Acute undifferentiated leukemia
Mixed phenotype acute leukemia with t(9;22)(q34;q11.2); *BCR-ABL1*
Mixed phenotype acute leukemia with t(v;11q23); *MLL* rearranged
Mixed phenotype acute leukemia, B-myeloid, NOS
Mixed phenotype acute leukemia, T-myeloid, NOS
Natural killer (NK) cell lymphoblastic leukemia/lymphoma (provisional entry)

Source: WHO (2008).

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Table 3. WHO classification of lymphoid neoplasms

PRECURSOR LYMPHOID NEOPLASMS

B lymphoblastic leukemia/lymphoma

- B lymphoblastic leukemia/lymphoma, NOS
- B lymphoblastic leukemia/lymphoma with recurrent genetic abnormalities
- B lymphoblastic leukemia/lymphoma with t(9;22)(q34;q11.2);*BCR-ABL 1*
- B lymphoblastic leukemia/lymphoma with t(v;11q23);*MLL* rearranged
- B lymphoblastic leukemia/lymphoma with t(12;21)(p13;q22) *TEL-AML1 (ETV6-RUNX1)*
- B lymphoblastic leukemia/lymphoma with hyperdiploidy
- B lymphoblastic leukemia/lymphoma with hypodiploidy
- B lymphoblastic leukemia/lymphoma with t(5;14)(q31;q32) *IL3-IGH*
- B lymphoblastic leukemia/lymphoma with t(1;19)(q23;p13.3);*TCF3-PBX1*

T lymphoblastic leukemia/lymphoma

MATURE B-CELL NEOPLASMS

- Chronic lymphocytic leukemia/small lymphocytic lymphoma
- B-cell prolymphocytic leukemia
- Splenic marginal zone lymphoma
- Hairy cell leukemia
- Splenic B-cell lymphoma/leukemia, unclassifiable (provisional entry)*
- Splenic diffuse red pulp small B-cell lymphoma (provisional entry)*
- Hairy cell leukemia—variant (provisional entry)*
- Lymphoplasmacytic lymphoma
 - Waldenstrom macroglobulinemia
- Heavy chain diseases
 - Alpha-heavy chain disease
 - Gamma-heavy chain disease
 - Mu heavy chain disease
- Plasma cell myeloma
- Solitary plasmacytoma of bone
- Extranasal plasmacytoma
- Extranodal marginal zone B-cell lymphoma of mucosa-associated lymphoid tissue (MALT-lymphoma)
- Nodal marginal zone B-cell lymphoma
 - Pediatric nodal marginal zone lymphoma (provisional entry)*
- Follicular lymphoma
 - Pediatric follicular lymphoma (provisional entry)*
- Primary cutaneous follicle center lymphoma
- Mantle cell lymphoma
- Diffuse large B-cell lymphoma (DLBCL), NOS
 - T-cell/histiocyte-rich large B-cell lymphoma
 - Primary DLBCL of the CNS

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Primary cutaneous DLBCL, leg type
EBV positive DLBCL of the elderly (provisional entry)
DLBCL associated with chronic inflammation
Lymphomatoid granulomatosis
Primary mediastinal (thymic) large B-cell lymphoma
Intravascular large B-cell lymphoma
ALK-positive large B-cell lymphoma
Plasmablastic lymphoma
Large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease
Primary effusion lymphoma
Burkitt lymphoma/leukemia
B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and Burkitt lymphoma
B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and classical Hodgkin lymphoma

MATURE T-CELL AND NK-CELL NEOPLASMS

T-cell prolymphocytic leukemia
T-cell large granular lymphocytic leukemia
Chronic lymphoproliferative disorder of NK cells (provisional entry)
Aggressive NK-cell leukemia
Systemic EBV-positive T-cell lymphoproliferative disease of childhood
Hydroa vacciniforme-like lymphoma
Adult T-cell leukemia/lymphoma
Extranodal NK/T-cell lymphoma, nasal type
Enteropathy-type T-cell lymphoma
Hepatosplenic T-cell lymphoma
Subcutaneous panniculitis-like T-cell lymphoma
Mycosis fungoides
Sézary syndrome
Primary cutaneous CD30-positive anaplastic large cell lymphoma
Lymphomatoid papulosis
Primary cutaneous anaplastic large cell lymphoma
Primary cutaneous gamma-delta T-cell lymphoma
Primary cutaneous CD8 positive aggressive epidermotropic cytotoxic T-cell lymphoma (provisional entry)
Primary cutaneous CD4 positive small/medium T-cell lymphoma
Peripheral T-cell lymphoma, NOS (provisional entry)
Angioimmunoblastic T-cell lymphoma
Anaplastic large cell lymphoma, ALK positive
Anaplastic large cell lymphoma, ALK positive (provisional entry)

HODGKIN LYMPHOMA

Nodular lymphocyte predominant Hodgkin lymphoma
Classical Hodgkin lymphoma
Nodular sclerosis classical Hodgkin lymphoma

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Lymphocyte-rich classical Hodgkin lymphoma
Mixed cellularity classical Hodgkin lymphoma
Lymphocyte-depleted classical Hodgkin lymphoma

HISTIOCYTIC AND DENDRITIC-CELL NEOPLASMS

Histiocytic sarcoma
Langerhans cell histiocytosis
Langerhans cell sarcoma
Interdigitating dendritic cell sarcoma
Follicular dendritic cell sarcoma
Fibroblastic reticular cell tumor
Indeterminate dendritic cell tumor
Disseminated juvenile xanthogranuloma

POST-TRANSPLANT LYMPHOPROLIFERATIVE DISORDERS (PTLD)

Early lesions
 Plasmacytic hyperplasia
 Infectious mononucleosis-like PTLD
Polymorphic PTLD
Monomorphic PTLD (B- and T/NK-cell types)
Classical Hodgkin lymphoma type PTLD

Source: WHO (2008).

Table 4. Cytogenetic comparisons of *de novo* leukemias and t-AML^a

Cytogenetic features	AML	
	<i>de novo</i> n = 3649 (%)	t-AML n = 581 (%)
Number of anomalies		
1 anomaly	2186 (60)	242 (42)
2 anomalies	641 (18)	104 (18)
≥3 anomalies	822 (23)	235 (40)
Ploidy level		
hypodiploid	813 (22)	224 (39)
pseudodiploid	1843 (51)	242 (42)
hyperdiploid	974 (27)	108 (19)
tri-/tetraploid	13 (0.4)	7 (1.2)
unknown ploidy	6 (0.2)	0
Unbalanced anomalies	2734 (75)	491 (85)
3p-	33 (0.9)	17 (2.9)
-5	152 (4.2)	73 (13)
5q-	249 (6.8)	77 (13)
-7	340 (9.3)	167 (29)
-7 (sole)	114 (3.1)	51 (8.8)
7q-	147 (4.0)	36 (6.2)
der(1;7)	8 (0.2)	12 (2.1)
loss of 5 and/or 7	717 (20)	284 (49)
+8	614 (17)	84 (14)
+8 (sole)	269 (7.4)	19 (3.3)
11q-	82 (2.2)	17 (2.9)
der(12p)	153 (4.2)	37 (6.4)
13q-	32 (0.9)	7 (1.2)
-17	172 (4.7)	53 (9.1)
der(17p)	104 (2.9)	36 (6.2)
-18	129 (3.5)	40 (6.9)
20q-	45 (1.2)	13 (2.2)
-21	92 (2.5)	41 (7.1)
Balanced anomalies	1713 (47)	215 (37)
t(1;3)(p36;q21)	2 (0.1)	3 (0.5)
inv(3)(q21q26) ^b	26 (0.7)	1 (0.2)
t(6;11)(q27;q23)	7 (0.2)	2 (0.3)
t(6;9)(p23;q34)	18 (0.5)	1 (0.2)
t(8;16)(p11;p13)	10 (0.3)	2 (0.3)
t(8;21)(q22;q22)	335 (9.2)	11 (1.9)
t(9;11)(p22;q23)	64 (1.8)	35 (6.0)
t(9;22)(q34;q11)	52 (1.4)	0
t(11;19)(q23;p13)	16 (0.4)	14 (2.4)
t(11q23)	144 (3.9)	72 (12)
t(15;17)(q22;q12)	388 (11)	16 (2.8)
inv(16)(p13q22) ^c	144 (3.9)	4 (0.7)
t(21q22)	375 (10)	20 (3.4)

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^aIncludes 'unselected' cases from the Mitelman Database of Chromosome Aberrations in Cancer.

^bIncludes also cases with t(3;3)(q21;q26).

^cIncludes also cases with t(16;16)(p13;q22).

Source: Mauritzson et al. (2002). Reprinted by permission from the Nature Publishing Group.

Table 5. Frequency of molecular mutations in *de novo* AML and t-MDS/t-AML^a

Mutated gene	AML <i>de novo</i>	t-MDS/t-AML
<i>FLT3 (ITD)^b</i>	35%	0%
<i>FLT3 (TKD)^c</i>	9%	<1%
<i>NRAS</i>	10–15%	10%
<i>KITD816</i>	~5%	NA ^d
<i>MLL (ITD)^b</i>	3%	2–3%
<i>RUNX1</i>	10–15%	15–30%
<i>TP53</i>	10%	25–30%
<i>PTPN11</i>	~2%	3%
<i>NPM1</i>	35–50%	4–5%
<i>CEBPA</i>	6–15%	Rare
<i>JAK2V617F</i>	2–5%	2–5%

^aFrom Qian et al. (2009). Reprinted with permission from Elsevier.

^bITD = internal tandem duplication.

^cTKD = tyrosine kinase-domain.

^dNA = not available.

Table 6. Gene mutations observed in the Copenhagen series of 140 patients with t-MDS ($n = 89$) or t-AML ($n = 51$)^a

	t-MDS	t-AML
Class I mutations		
Tyrosine kinases		
FLT3 ITD+ point mutations	1	10
cKIT point mutations	0	2
cFMS point mutations	0	0
JAK2 point mutations	2	0
Genes in the RAS/BRAF pathway		
KRAS or NRAS point mutations	7	7 ^b
BRAF point mutations	0	3 ^b
PTPN11 point mutations	2	2
Class II mutations		
Transcription factors		
AML1/CBFB chimerically rearranged	3	7
AML1 point mutations	20	2
MLL chimerically rearranged	0	11
MLL ITD	1	1
RARA chimerically rearranged	0	2
EVI1 chimerically rearranged	3	1
CEBPA point mutations	0	0
NPM1 point mutations	3	7
Tumor suppressor gene		
TP53 point mutations	25	9
Total 131 mutations observed	67	64

^aFrom Pedersen-Bjergaard et al. (2008) Reprinted with permission from the Nature Publishing Group.

^bOne patient had a mutation of KRAS together with a mutation of BRAF possibly in different subclones.

Table 7. Characteristics of selected known and probable human leukemia- and lymphoma-inducing agents

Agents carcinogenic to humans	CAS	1° Lymphohemato-poietic cancer	2° limited evidence	Myelotoxicity	Chromosomal Aberrations^a	Source(s)
<i>DNA-reactive</i>						
1,3-Butadiene		Lympho-hematopoietic cancers		- ^b	-	IARC, 2008a, 2009; Baanet al., 2009
1,4-Butanediol dimethanesulfonate (Busulfan, Myleran)	55-98-1	ANLL		+	SCA	Grosset al., 2009; IARC, 1987b
Chlorambucil	305-03-3	ANLL		+	SCA	Grosset al., 2009; IARC, 1987b
(1-(2-)Chlorethyl)-3-(4-methylcyclohexyl) nitrosurea (Methyl-CCNU, Semustine)	13909-09-6	ANLL		+	NI ^c	Grosset al., 2009
Cyclophosphamide	50-18-0	ANLL		+	SCA	Grosset al., 2009; IARC, 1987b
Ethylene Oxide	75-21-8		NHL, MM, CLL	-	SCA	IARC, 2009, 2008b; Baanet al., 2009
Formaldehyde	50-00-0	Myeloid leukemias		+/-	+/-	IARC, 2009, 2006
Melphalan	148-82-3	ANLL		+	SCA	Grosset al., 2009; IARC, 1987b
MOPP therapy		ANLL		+	SCA	Grosset al., 2009; IARC, 1987b
Treosulfan	299-75-2	ANLL		+	NI	Grosset al., 2009; IARC, 1987b
Thio-TEPA (tris(1-aziridinyl)-phosphine)	52-24-4	Leukemia		+	SCA	Grosset al., 2009; IARC, 1987b
<i>Topoisomerase II-inhibitor</i>						
Etoposide	33419-42-0	ANLL		+	MN	Grosset al., 2009; IARC, 2000a
<i>Immunosuppressive agents</i>						
Cyclosporine	79217-60-0	NHL		-	SCA	Grosset al., 2009; IARC, 1990c
Azathioprine	446-86-6	NHL		+	SCA	Grosset al., 2009; IARC,

						1987b
<i>Other</i>						
Benzene	71-43-2	ANLL	NHL, ALL, CLL, MM	+	SCA	IARC, 2009; Baanet al., 2009
2,3,7,8-TCDD	1746-01-6		NHL	-	-	IARC, 2009
X- and Gamma-radiation		ANLL, CML, ALL		+	SCA	IARC, 2000b
Neutron radiation			leukemia	NI	SCA	IARC, 2000b
Thorium-232 and its decay products		ANLL, CML, ALL		NI	SCA	El Ghissassiet al., 2009; IARC, 2001
Phosphorus-32, as phosphate		ANLL		+	SCA	IARC, 2001
Fission products including strontium-90		Leukemia (non-CLL)		NI	NI	El Ghissassiet al., 2009; Krestinaet al., 2010
Tobacco smoking and tobacco smoke		ANLL		NI	SCA	IARC, 2004
Tobacco smoking (parental exposure)			Childhood Leukemia (ALL)	NI	NI	Secretanet al., 2009
Rubber manufacturing occupation		Leukemia, Lymphoma		NI	SCA	IARC, 2009
Painting occupation (maternal exposure)			Childhood leukemia	NI	NI	IARC, 2009
<i>Infectious agents</i>						
Epstein-Barr virus		Burkitt's lymphoma, NHL NK/T-cell lymphoma, Hodgkin's lymphoma		-	NI	Bouvardet al., 2009; IARC, 1997
Human immunodeficiency virus Type 1		NHL, Hodgkin's lymphoma		+	NI	Bouvardet al., 2009; IARC, 1996a
Human T-cell lymphotropic virus Type 1		Adult T-cell leukemia and lymphoma		-	NI	Bouvardet al., 2009; IARC, 1996b
Hepatitis C virus		NHL		-	NI	Bouvardet al., 2009
<i>Helicobacter pylori</i>		low-grade B-cell		-	NI	Bouvardet al., 2009

		MALT				
Kaposi's sarcoma herpes virus		1° effusion lymphoma		-	NI	Bouvardet al., 2009
Selected agents probably carcinogenic to humans (IARC Group 2A)						
<i>DNA-reactive</i>						
Bischloroethyl nitrosourea (BCNU; carmustine)	154-93-8		ANLL	+	NI ^d	IARC, 1987b
1-(2-)Chlorethyl-3-cyclohexyl-1-nitrosourea (CCNU; lomustine)	13010-47-4		ANLL	+	NI	IARC, 1987b
N-Ethyl-N-nitrosourea	759-73-9		ANLL?	NI	NI ^d	IARC, 1987b
Cisplatin	15663-27-1		leukemia	+	NI ^d	IARC, 1987b
Nitrogen Mustard (Mechlorethamine)	51-75-2		ANLL	+	SCA	IARC, 1987b
Procarbazine	671-16-9		ANLL	+	NI ^d	IARC, 1987b
Chlorozotocin	54749-90-5		ANLL	+	NI	IARC, 1990b
<i>Topoisomerase II-inhibitor</i>						
Adriamycin	25316-40-9		ANLL	+	SCA	IARC, 1987b
Teniposide	29767-20-2		ANLL	+	NI ^d	IARC, 2000c
<i>Other</i>						
Azacytidine	320-67-2		Leukemia	+	NI ^d	IARC, 1990a
Chloramphenicol	56-75-7		ANLL	+	NI	IARC, 2000c

^aSCA = structural chromosome aberrations, MN = micronuclei.

^bMyelotoxicity is either not seen or infrequently seen.

^cNo information located for humans.

^dIncreases seen in the blood or bone marrow of experimental animals.

Table 8. Likely mechanisms involved in the carcinogenesis of selected known and probable human leukemia- and lymphoma-inducing agents

Agents carcinogenic to humans (IARC Group 1 or similar)						
<u>Agent</u>	Cancer	Class	Activation	1° Mechanism	Other	1° Source
1,3-Butadiene	Various	Industrial chemical	Bioactivated to mono- and bifunctional alkylating agents	Mutation resulting from DNA binding and/or chromosomal alterations	Metabolized into diepoxybutane	IARC, 2008a, 2009; Baanet al., 2009
Busulfan (Myleran; 1,4-Butanediol dimethanesulfonate)	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations		Grosset al., 2009
Chlorambucil	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations		Grosset al., 2009
Semustine (Methyl-CCNU; 1-(2-Chlorethyl)-3-(4-methylcyclohexyl)1-nitrosurea)	ANLL	Therapeutic agent	Degrades to direct-acting alkylating and carbamoylating agents	Mutation resulting from DNA binding and/or chromosomal alterations		Grosset al., 2009
Cyclophosphamide	ANLL	Therapeutic agent	Bioactivated to bifunctional alkylating agent and acrolein	Mutation resulting from DNA binding and/or chromosomal alterations		Grosset al., 2009
Ethylene oxide	Various	Industrial chemical	Direct-acting alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 2008b, 2009; Baanet al., 2009
Formaldehyde	ANLL	Industrial chemical	Direct-acting, forms DNA-protein crosslinks	Unknown, possibly mutation resulting from DNA binding and/or chromosomal alterations		IARC, 2006, 2009; Baanet al., 2009
Melphalan	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations		Grosset al., 2009
MOPP therapy	ANLL	Combination of therapeutic	A direct-acting bifunctional and an	Mutation resulting from DNA binding and/or		Grosset al., 2009

		agents	indirect monofunctional alkylating agent, a microtubule inhibitor, and a glucocorticoid	chromosomal alterations		
Treosulfan	ANLL	Therapeutic agent	Converts to a mono- and bifunctional alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations	Converts into diepoxybutane, an (intrastrand?) crosslinking agent.	Hartley et al., 1999; Grosset al., 2009
Thio-TEPA (tris(1-aziridinyl)-phosphine)	Leukemia	Therapeutic agent	Direct-acting trifunctional alkylating agent. Also, metabolized to monofunctional alkylating agent aziridine.	Mutation resulting from DNA binding and/or chromosomal alterations		Maanen et al., 2000; Grosset al., 2009
Etoposide	ANLL	Therapeutic agent	Topoisomerase II-poison	Mutation resulting from chromosomal breakage and translocations	Results in modified transcription factor	Grosset al., 2009
Cyclosporine	NHL	Therapeutic agent	Inhibition of transcription factors that regulate inducible cytokine expression	Immunosuppression		Grosset al., 2009
Azathioprine	NHL	Therapeutic agent	Metabolized into nucleotide analog	Immunosuppression	Also genotoxic	Grosset al., 2009
Benzene	ANLL	Industrial chemical and environmental agent	Metabolized into reactive protein and DNA-binding species	Unknown, likely mutation resulting from either DNA binding, topoisomerase II-inhibition, and/or oxidative damage	Likely multiple metabolites and modes of action involved	Baanet al., 2009; IARC, 2009
2,3,7,8-TCDD	NHL ^a	Environmental contaminant	Receptor-mediated effects modifying cellular replication and apoptosis	Unknown, likely immunosuppression	Also can lead to DNA damage through oxidative stress	Baanet al., 2009; IARC, 2009; Holsapple et al., 1996

X- and <i>Gamma</i> -radiation	ANLL CML ALL	Therapeutic, energy and military uses	Direct and indirect DNA damage	Mutation resulting from DNA damage and/or chromosomal alterations		IARC, 2000b; El Ghissassiet al., 2009
Alpha and beta particle emitters	ANLL (also CML and ALL for Th- 32)	Therapeutic, energy and military uses	Direct and indirect DNA damage	Mutation resulting from DNA damage and/or chromosomal alterations		IARC, 2001; El Ghissassiet al., 2009
Tobacco smoking and tobacco smoke	ANLL	Lifestyle use	Direct and indirect DNA damage	Unknown, likely mutation resulting from DNA binding and/or chromosomal alterations		IARC, 2004; Secretanet al., 2009
Tobacco smoking (parental)	Childhood ALL	Parental use	Direct and indirect DNA damage	Unknown, assumed mutation resulting from DNA binding and/or chromosomal alterations occurring in germ cells or <i>in utero</i>	Epigenetic changes could also contribute	IARC, 2004; Secretanet al., 2009
Rubber manufacturing occupation	Leukemia Lymphoma	Occupational exposure	Unknown but DNA- reactive chemicals are used	Unknown, assumed to be mutation resulting from DNA binding and/or chromosomal alterations and/or immunosuppression		IARC, 2009
Painting occupation	Childhood leukemia ^a	Occupational exposure	Unknown but DNA- reactive chemicals are used	Unknown, assumed mutation resulting from DNA binding and/or chromosomal alterations occurring in germ cells or <i>in utero</i>	Other mechanisms are also likely.	IARC, 2009
Epstein-Barr virus	Burkitt's lymphoma NHL NK/T-cell lymphoma Hodgkin's	Infectious agent	Viral infection and expression of viral proteins leading to lymphocyte transformation	Alteration in normal B- lymphocyte function leading to cell proliferation, inhibition of apoptosis, genomic instability, and cell		Hjalgrim and Engels, 2008; Bouvardet al., 2009

	lymphoma			migration		
Human immunodeficiency virus Type 1	NHL	Infectious agent	Viral infection and expression of viral proteins leading to loss of CD 4+ T lymphocytes	Immunosuppression (as an indirect effect)		Hjalgrim and Engels, 2008; Bouvardet al., 2009
Human T-cell lymphotropic virus Type 1	Adult T-cell leukemia and lymphoma	Infectious agent	Viral infection and expression leading to lymphocyte transformation	Immortalization and transformation of T cells		Hjalgrim and Engels, 2008; Bouvardet al., 2009
Hepatitis C virus	NHL	Infectious agent	Viral infection and expression of viral proteins leading to chronic immune stimulation	Chronic immune stimulation		Hjalgrim and Engels, 2008; Bouvardet al., 2009
<i>Helicobacter pylori</i>	Low-grade B-cell MALT	Infectious agent	Inflammation leading to cellular alterations	Oxidative stress, altered cellular turnover and gene expression, methylation, and mutation	Chronic immune stimulation.	Hjalgrim and Engels, 2008; Bouvardet al., 2009
Kaposi's sarcoma herpes virus	1° Effusion lymphoma	Infectious agent	Viral infection and expression of viral proteins	Cell proliferation, inhibition of apoptosis, genomic instability, cell migration		Bouvardet al., 2009
Selected agents probably carcinogenic to humans (IARC Group 2A)						
Bischloroethyl nitrosourea (BCNU; carmustine)	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Voget al., 1998
(1-(2-)Chlorethyl)-3-cyclohexyl-1-nitrosourea (CCNU; lomustine)	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Voget al., 1998
<i>N</i> -Ethyl- <i>N</i> -nitrosourea	ANLL?	Experimental reagent	Direct-acting alkylating agent	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Voget al., 1998

Cisplatin	Leukemia	Therapeutic agent	Direct-acting bifunctional DNA binding agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Vogelet al., 1998
Nitrogen Mustard (Mechlorethamine)	Leukemia	Therapeutic agent	Direct-acting bifunctional alkylating agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Vogelet al., 1998
Procarbazine	ANLL	Therapeutic agent	Bioactivated to a monofunctional alkylating agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Vogelet al., 1998
Chlorozotocin	ANLL	Therapeutic agent	Direct-acting bifunctional alkylating agent.	Mutation resulting from DNA binding and/or chromosomal alterations		IARC, 1987b; Vogelet al., 1998
Adriamycin	ANLL	Therapeutic agent	Topoisomerase II-poison and redox-cycling agent	Mutation resulting from chromosomal breakage and translocations		IARC, 1987b
Teniposide	ANLL	Therapeutic agent	Topoisomerase II-poison	Mutation resulting from chromosomal breakage and translocations		IARC, 2000c
Azacytidine	Leukemia	Therapeutic agent	DNA-methyltransferase inhibitor through metabolism and incorporation into DNA.	Alters DNA methylation and gene expression. Is also genotoxic.		NTP, 2005; Stresemann and Lyko, 2008
Chloramphenicol	ANLL	Therapeutic agent	Binds to ribosomal subunit blocking protein synthesis in mitochondria. Metabolite may also induce DNA damage	Unknown, presumed to be mutation resulting from DNA damage and/or chromosomal alterations		NTP, 2005

^aLimited Evidence

Table 9. General characteristics of human leukemias and related neoplasms induced by recognized leukemia-inducing agents

Agent	Disease ^a	FAB ^a	MDS ^b	Typical clonal Chromosome Abnormalities	Latency (yrs) ^c
Ionizing radiation	AML ALL CML	M1–M6 L1–L2	+++	-7, -5, 7q-, 5q- t(9;22)	5–7 8 5
Alkylating agent chemotherapeutic drugs	AML	M1, M2	+++	-7, -5, 7q-, 5q-	~5
Ethylene oxide	{CLL} ^d {NHL} {MM}	?	-	?	?
1,3-Butadiene	{CLL} {CML} {NHL}	?	-	?	?
Epipodophyllotoxin topoisomerase II inhibitors	AML	M4, M5	+/-	t(11q23)	2–3
Dioxopiperazine topoisomerase II inhibitors	AML	M2, M3	+/-	t(8;21) t(15;17)	3
Benzene	AML {ALL} {CLL} {NHL} {MM}	M1, M2, M6 M3	++	Mixed ^e t(8;21), t(15;17)	<12
Formaldehyde	AML {CML}	?	-	?	?

^aSee Figure 3, for abbreviations on the types of lymphohematopoietic neoplasms and the leukemia subtypes classified according to the French-American-British (FAB) system.

^bMDS = myelodysplastic syndrome.

^cApproximate median latency period.

^dNeoplasms in brackets indicate that there is limited evidence that they are induced by the agent.

^eClonal chromosomal abnormalities are present, but the karyotypes reported to date have been inconsistent. Two recent reports have provided additional evidence for the involvement of t(8;21) and t(15;17) (Mondrala and Eastmond, 2009; Wonget al., 2010).

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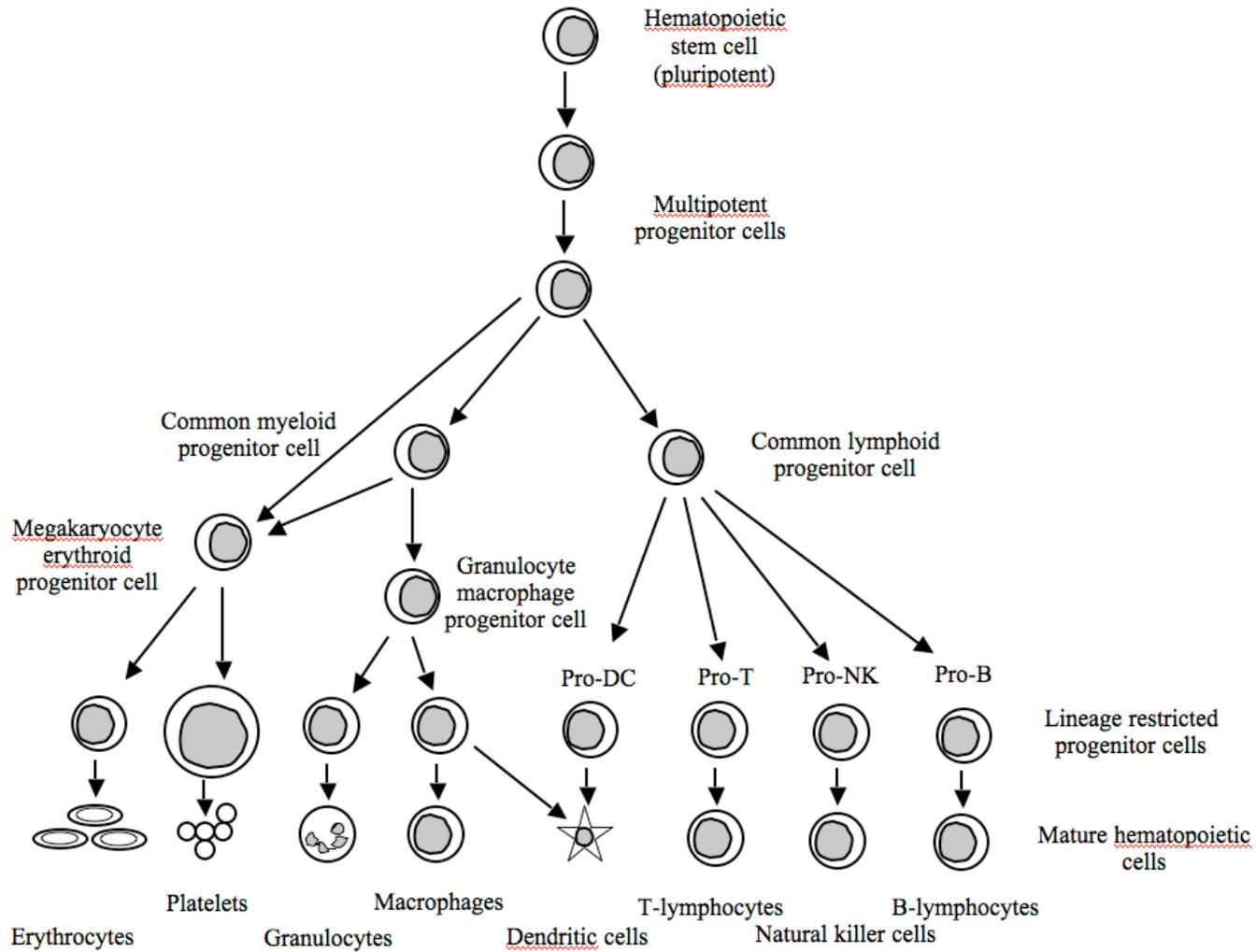


Figure 1. Simplified model of hematopoiesis showing lineages of major types of hematopoietic cells.

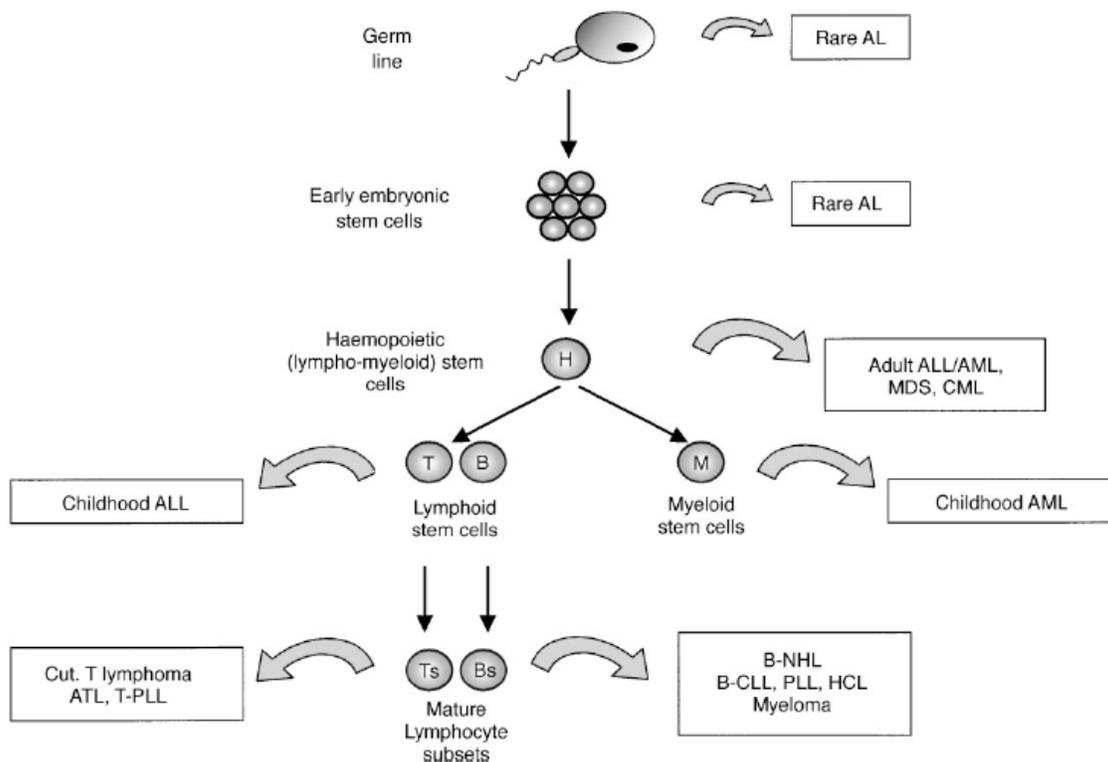


Figure 2. Hierarchical stem cell origins of leukemia and related cancers. The arrows denote the likely level of clonal selection for the majority of the leukemia subtypes listed.

Abbreviations: AL = acute leukemia; Cut. T lymphoma = cutaneous T-cell lymphoma; ATL = adult T-cell leukemia; T-PLL = T-cell prolymphocytic leukemia; B-cell non-Hodgkin lymphoma; PLL = prolymphocytic leukemia; HCL = hairy cell leukemia. For other abbreviations, see Table 1.

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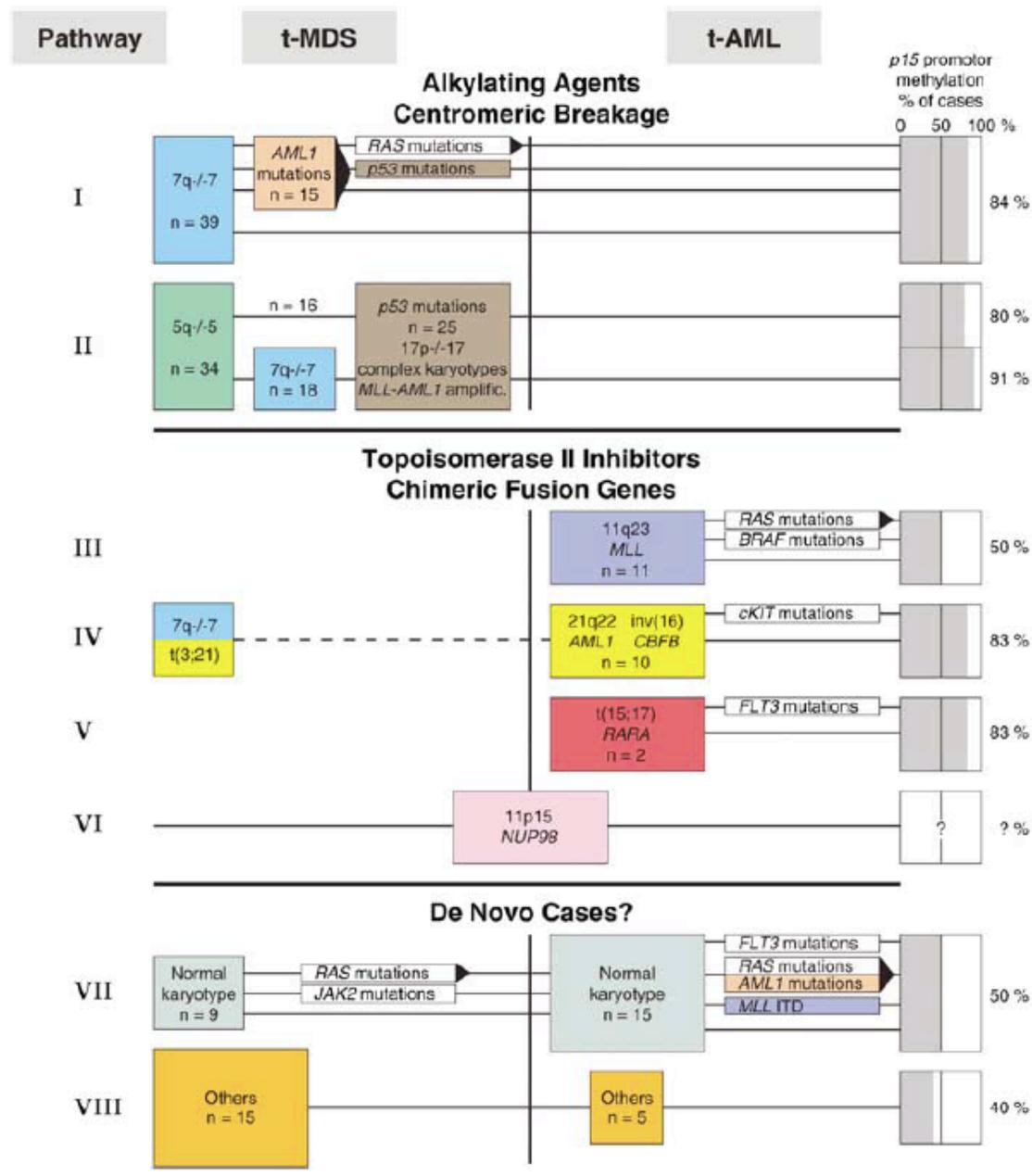


Figure 3. Genetic pathways of t-MDS and t-AML based on 140 cases from the Copenhagen study group. The black triangle indicates significant association with transformations from t-MDS to t-AML.

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