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T-Cell Lymphoma Cell Lines (HUT102 and HUT78) Established at the National Cancer Institute: History and Importance to Understanding the Biology, Clinical Features, and Therapy of Cutaneous T-Cell Lymphomas (CTCL) and Adult T-Cell Leukemia-Lymphomas (ATLL)

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Abstract Efforts at the National Cancer Institute to generate continuous in vitro cultures from patients with mycosis fungoides and the Sezary syndrome, neoplasms with a mature T-helper phenotype, led to the establishment of two cell lines, HUT78 and HUT102. Further characterization of these cell lines led to the identification of the first human retrovirus, HTLV-1, in the HUT102 cells, and the clinical description of the syndrome of HTLV-1 associated acute T-cell leukemia/lymphoma; the serum antibody test to screen for this virus was developed from the serum of the patient from whom the cell line was derived. The HUT78 cell line was pivotal in the identification and characterization of the HIV retrovirus in that a subclone, H9, proved to be permissive for replication of HIV in vitro. Propagation of HIV in vitro in H9 cells allowed for the development of immunological reagents to screen blood supplies for the presence of the virus. Further biologic and molecular studies of these lines have led not only to a better understanding of the underlying diseases but also to the development of rational therapeutic approaches.

Key words: CTCL, Sezary, HTLV-I, HIV, IL-2

Mycosis fungoides was originally described as a skin disease in 1806 [1]. During the remainder of the 1800s and early 1900s the clinical manifestations of the disease, its natural history and pathologic features were described [2,3]. The erythrodermic variant of the disease was described during this period and Sezary described a variant with generalized erythroderma and circulating malignant cells in 1939 [4]. The only treatment before the 1950s was radiation therapy which played only a palliative role.

The fact that the underlying cell of origin was a lymphocyte was not recognized until 1970 [5]. Since that time there has been an explosion in our understanding of the biology, pathogenesis, and treatment options for these and other T-cell non-Hodgkins lymphomas. In the early 1970s the National Cancer Institute (NCI) began a systematic study of these disorders which led to much of this increased understanding. Part of these advances were made through a close interaction between clinical and laboratory investigators and the cell lines which they established. This chapter will review the progress made through these collaborations and cell lines.

EARLY CLINICAL STUDIES OF CUTANEOUS T-CELL LYMPHOMAS AT THE NCI

Dr. Marvin Lutzner in the Dermatology Branch of the NCI, studied the morphology of the Sezary syndrome in the early 1970s, describing the cerebriform nature of the nucleus (Fig. 1) [6]. At this time it was just appreciated that these malignant cells were malignant T-cells [5,7] derived from the mature helper subset [8]. Dr. Richard Edelson and coworkers, also from the Dermatology Branch, showed that antithymocyte globulin [9] and leukapheresis [10] could improve both the skin lesions and the

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circulating Sezary cells in these patients. The improvement in skin lesions and lymph nodes after removal of circulating cells by leukophoresis led us to postulate that there was traffic between the malignant cells in various sites and to explore the cell kinetics of the disease and the sites of proliferation of the malignant cells. Dr. Stanley Shackney, Dr. Edelson, and Dr. Bunn conducted a series of studies with ^{3}HTdR which confirmed the trafficking between cells in lymph nodes, peripheral blood, and skin [11,12]. The highest rate of cell proliferation appeared to be in the skin. The challenge of treating these patients led to a formal effort to study the natural history, staging, treatment, and biology of the cutaneous T-cell lymphomas which was undertaken by the NCI-Veterans Administration Medical Oncology Branch and, later, the NCI-Navy Medical Oncology Branch.

Biopsy of lymph nodes, liver, other sites of visceral involvement, and peripheral blood specimens were obtained from all patients as part of their staging assessment [13–15]. These samples were analyzed for the DNA content of the malignant cells [16], their morphology as determined by light and EM microscopy [17–19], and their karyotypes [20,21]. These clinical studies showed that nearly all patients had early evidence of systemic disease, explaining why topical therapies failed to cure patients with disease which appeared to be confined to the skin.

The karyotypic studies showed that chromosomal abnormalities were present in the majority of cases and clonal abnormalities were the rule [20,21]. However, the clonal abnormalities varied between cases. We studied the malignant cells in considerable detail. We originally showed that these cells had the phenotype of helper T-cells by using monoclonal antibodies developed to these antigens [22,23]. We subsequently showed that the cells also had the genotype of T-cells with monoclonal rearrangements of the T-cell receptor gene [24].

CELL CULTURE STUDIES

Dr. Desmond Carney and coworkers undertook the task of evaluating the responsiveness of these cells to a variety of lymphocyte mitogens and then to establish permanent cell lines by culturing the cells with these mitogens and/or lymphocyte conditioned media [25–27]. We found that the cells had poor spontaneous proliferation in response to mitogens. We were also disappointed that we failed to obtain permanent cultures from the vast majority of samples. In 1977 and 1978 we had the good fortune of finding that the cultures from two patients continued to proliferate in culture beyond several months (these two cell lines were HUT78 and HUT102, respectively) [26,27]. Our flow cytometric studies confirmed that these were helper T-cells with cell surface antigens which were identical to those in the patients from which they were derived and that their DNA content and karyotypes were also identical. These cell lines, originally cultured by Dr. Carney, were maintained in culture by Ed Russell under the direction of Dr. Adi Gazdar.

HUT78 was derived from peripheral blood of a 53-year-old white male with the Sezary syndrome. The patient had a typical clinical presentation with extensive cutaneous erythroderma and histopathologic involvement of lymph nodes and liver. This patient's circulating neoplastic lymphocytes proliferated in vitro in the presence of ConA 10 μg/ml with tenfold increase in cell number/week and, after surviving two crises began to proliferate without mitogen stimulation after 12 weeks in culture. The cell morphology, shown in Figure 1b,d, was similar to that of the original patients' cells (Fig. 1a,c), with hyperconvoluted nuclei and large nucleoli. After several passages in culture, the cells demonstrated decreased E-rosette formation and failed to respond to mitogen stimulation. The doubling time of the cells after 52 weeks in culture was 26 h. DNA content analysis showed a bimodal distribution of cells which were hypodiploid and subtetraploid. The hyperdiploid populations were believed to arise from the hypodiploid cells by endoreduplication [28,29]. While the fresh CTCL cells from the patient failed to form tumors in nude mice by a variety of routes, the cell line Hut78 induced invasive tumors after intrathecal injection, and these tumors had a subtetraploid karyotype.

In contrast to the classic features of Sezary syndrome described above, there were many unusual features in the history of the patient from whom HUT102 was derived. His cells had an abnormal morphology and T-cell phenotype as well. The patient was atypical in his young age [30], the initial presentation with a rapid onset of skin tumors, the early widespread dissemination to visceral sites including lytic bone lesions at presentation, hypercalcemia, and early relapse in the leptomeninges after aggressive combination chemotherapy (Fig. 2) [30–34]. The

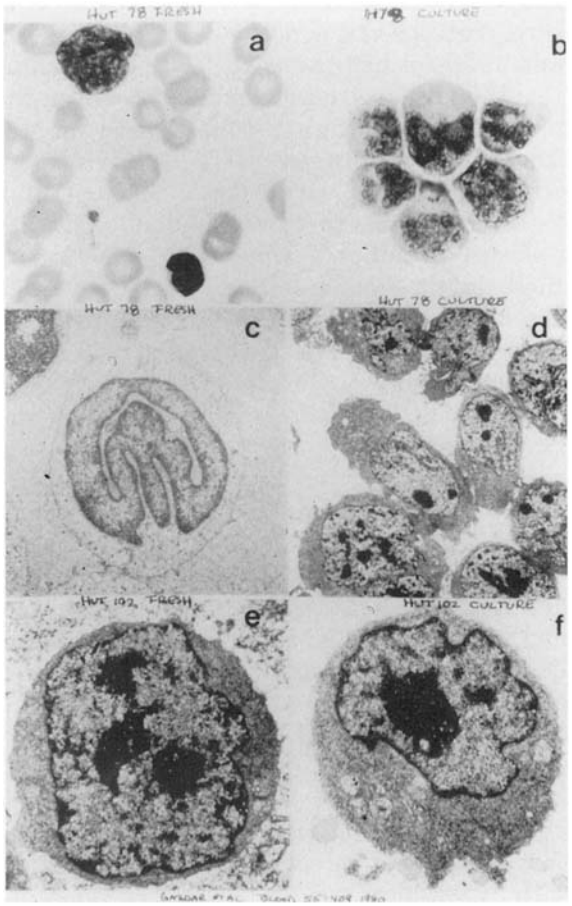

Fig. 1. Morphologic features of the cell lines. Light microscopic (**a, b**) and ultrastructural (**c, d**) features of peripheral blood smear from patient from whom Hut78 cell line was derived (a, c) and the cell line in culture (b, d); ultrastructural features of tumor lesion from patient from whom HUT102 was derived (**e**) and the cell line in culture (**f**). Magnifications, a and b, ×640; c and d, ×1,600; e and f, ×6,300. (Reproduced from Gazdar et al., with permission of the publisher.)

Fig. 2. Cutaneous tumor lesions from a 26-year-old black male from whom HUT102 cell line was established.

cells' nuclear morphology was larger than most MF cells and some nuclei had a cloverleaf contour (Fig. 1e,f) [35]. Nonetheless, typical Pautrier microabscesses were seen in the epidermis and the patient appeared to have the D'emblee tumor variant of mycosis fungoides. The cells were unusual in the high expression of the IL-2 receptor (known as the T-cell growth factor receptor [TCGF] at the time) [36,37].

The HUT102 cell line was originated from lymph node tissue which was disaggregated by passage through a cytosieve. Mononuclear cells were separated by ficoll-hypaque density gradient centrifugation and placed in culture. The fresh tumor cells appeared to have polylobated nuclei and were E-rosette positive and Tdt (−). The cells proliferated in vitro in the presence of T-cell growth factor conditioned media but not with PHA, Con A, PWM, or staph toxin A. After the fifth passage, the cells became mitogen independent with a doubling time of 36 h and maintained the blastic morphologic features of the original cells. Unlike HUT78, the HUT102 cells did not form tumors when injected into nude mice by any route. DNA content studies of HUT102 showed that the cell line was near-diploid with a modal chromosome number of 46 (range 44–46).

DISCOVERY OF HTLV-1 IN HUT 102

Dr. Bernard Poiesz was a clinical fellow who cared for some of our CTCL patients and knew that we had successfully maintained several cell lines in continuous culture. After his clinical year of fellowship, Dr. Poiesz elected to work in the laboratory of Dr. Robert Gallo to study reverse transcriptase and human retroviruses. He also worked with Dr. Frank Ruscetti who was working to purify TCGF in Dr. Gallo's lab. It was postulated that HUT102 might be an excellent source of TCGF since it grew without exogenous growth factor and expressed high levels of

the TCGF receptor [36,37]. The HUT78 and HUT102 cells were given to Drs. Poiesz and Ruscetti to determine whether they produced and secreted TCGF. Since Dr. Poiesz was studying reverse transcriptase, he fortuitously used HUT102 in one of his assays and found that it had extremely high levels of this enzyme [38]. This led to the discovery of the first human retrovirus which was called HTLV-I by Dr. Gallo's lab [39]. HUT78 had no evidence of retroviral infection.

Another NCI clinical fellow who elected to work in Dr. Gallo's lab, Dr. Larry Posner, developed a serum assay for anti-HTLV-1 antibodies [40]. It was shown that the patient from whom HUT102 was derived had high levels of antibody whereas the patient from whom HUT78 was derived had none [41–45]. Analysis of stored serum from a large number of our patients showed that the presence of anti-HTLV-1 antibodies was rare. However, Dr. Gallo's lab analyzed serum samples from around the world and found several endemic areas of seroprevalence including Japan, the Caribbean region, and the Southern United States [41–45].

ADULT T-CELL LEUKEMIA-LYMPHOMA

Around the same time, a group of Japanese investigators described a new form of adult T-cell lymphoma which they called "Adult T-cell Leukemia-Lymphoma" [46]. The patients were reported to have a rapid onset of widespread disease with peripheral blood involvement, frequent skin involvement, universal lymph node involvement, and clustering in the Southern provinces of Japan. Shortly thereafter Dr. Daniel Catovsky, across the globe in London, described a small series of patients with similar clinical features and hypercalcemia as well [47]. These patients had all come to the UK from the Caribbean region. Dr. Gallo's lab analyzed the serum from these patients and they all had high levels of anti-HTLV-I antibodies [41–45].

The clinical features of the disease produced by HTLV-1 were becoming clear and a number of these patients were found among the T-cell lymphoma patients referred to the NCI and the Veterans Administration Medical Center [30–34]. We reported that the patients had high grade clinical features such as rapid onset of symptoms, hypercalcemia and lytic bone lesions, opportunistic infections, universal presence of visceral disease including frequent leptomeningeal metastases, increased expression of the IL-2 receptor on the malignant cells which had cloverleaf nuclei, and poor response to aggressive chemotherapy. Table I provides a summary of the clinical features of ATLL in contrast to the low grade T-cell lymphomas, mycosis fungoides, and the Sezary syndrome. Dr. Whang-Peng reported the cytogenetic abnormalities seen in the NCI series of patients and similar findings were reported by Japanese investigators [48,49]. Nearly all patients had abnormalities and these were usually clonal. Although some cytogenetic changes were frequent, there were no abnormalities that occurred in all patients. The integration site of the HTLV-I virus varied from patient to patient [50,51].

OTHER HTLV-1 RELATED DISEASES

Seroprevalence studies for anti-HTLV-I antibodies around the world showed several endemic areas and the seroprevalence was low in most areas in the United States [41–45]. Nonetheless, several areas had high prevalence and it was shown that the virus could be transmitted through infected blood [52]. This led to mandated routine screening of all blood products in the United States, thus preventing transmission through infected blood products [53].

Other clinical features of HTLV-I infection were subsequently described including chronic low grade leukemic disease and neurologic syndromes often termed spastic paraparesis [54–56]. Most infected persons in endemic areas appear to acquire the infection at the time of

TABLE I. Clinical Features of T-Cell Lymphomas*

Clinical feature	ATLL (HTLV-1) (n = 10)	CTCL (n = 49)
Age	34 (24–62)	53 (22–78)
Duration Sx to Dx	2 months	5 years
Hypercalcemia	90%	2%
Bone lesions	90%	2%
Skin lesions	70%	100%
Circulating tumor cells	80%	25%
Lymph nodes	100%	70%
Viscera	100%	18%
Opportunistic infections	Common	Rare
Response	Prompt CR	LowerCR rate
Survival	Short	Long

*From references [31, 32].

birth. Only a small minority of these patients subsequently develop disease. The reasons why some control the infection indefinitely and others develop severe disease are unknown.

IDENTIFICATION AND ISOLATION OF HIV

The syndrome of acquired immune deficiency syndrome had been recognized in the early 1980s, and epidemiologic data suggested a horizontal transmission by intimate contact or blood products. Gallo and his colleagues proposed that the etiologic agent of this syndrome was a retrovirus of the HTLV family, due to the propensity of the agent to infect helper T-cells and the similarities to feline leukemia virus, a retrovirus causing immunodeficiency in cats [57]. Because initial cocultivation studies of lymphocytes from infected patients with various T-cell targets, including umbilical cord blood, proved to be transient and cytopathic rather than permissive, as was the case for HTLV-I, Gallo's lab began an exhaustive search for a cell line which would be permissive for infection and propagation of the proposed new retrovirus. In a landmark article, Popovic and Gallo and coworkers reported in 1984 that an aneuploid T-cell line from a patient with lymphoid lymphoma, named HT, was permissive for the in-vitro propagation of a new virus, called HTLV-III [57–60]. Subcloning of that cell line led to the H9 clone, which had the highest proliferation rate after infection with the virus. Popovic et al. subsequently published data comparing the viral expression of HTLV-III in a number of hematopoietic cell lines, including HUT78, and showed that H9 was clearly the highest producer, as measured by reverse transcriptase activity and presence of viral proteins p15 and p24 by immunofluorescence [61].

The identity of the parental line from which H9 was subcloned was not elucidated until 1988 when it was demonstrated by DNA fingerprinting that HUT 78 and H9 were identical, proving that H9 was a subclone of HUT78 sent to Dr. Gallo's lab by our group [62,63]. A further study by Chen confirmed by karyotypic analysis that H9 was a subline derived from HUT78 [28]. Gallo's access to the HUT78 cell line and Popovic's success in isolating a subline highly permissive for HTLV-III replication allowed further molecular characterization of the virus, now named HIV, and led to the development of immunological reagents to screen patients and the blood supply for the presence of this virus [59,60].

GROWTH CHARACTERISTICS OF HUT 78 AND HUT102

Both HUT78 and HUT102 cells grow as single cells or as clusters in non-adherent suspension cultures. Serum deprivation studies demonstrate that optimal serum concentration is 10%, although the cells can be maintained in as little as 3% serum, with a slower doubling time (Fig. 2). Growth of HUT78 cells cannot be supported in serum-free media even with the addition of purified growth factors, including IL2, IL4, IL-5, IL-6, IL7, or IL2 + IL4 (Foss et al., unpublished data). Further, growth is not enhanced in 10% serum containing media with the addition of any of the above growth factors. HUT102 cells likewise demonstrate autonomous growth, although addition of IL-2 or TCGF has been shown to increase proliferation in a concentration-dependent manner [37]. Recently, a clone of HUT78, H9, has been successfully adapted to serum free media supplemented with transferrin, insulin, and sodium selenite [64].

EXPRESSION OF CYTOKINES AND CYTOKINE RECEPTORS

The expression and secretion of cytokines by HUT78 has been studied by biological assays and by reverse transcription and polymerase chain amplification (RT-PCR). Low levels of expression of mRNA for IL2, gamma interferon, TNF, and TGF-beta were detected [65]. With activation by PHA (10 μg/ml for 2 h), IL2 and gamma interferon expression increased and IL4 was expressed. IL4 expression was also induced by CD3 stimulation under cross-linking conditions or by soluble CD3 monoclonal antibodies in the presence of PMA [66].

HUT102 has been demonstrated to constitutively produce IL-2, or TCGF [37]. Messenger RNA has been detected by RT-PCR for IL-1a, IL-2, IL-4, IL-6, and IL-7. Like other HTLV-I infected cells, the HUT102 cell line constitutively expressed the ICAM-1 cell adhesion molecule but lacked expression of its receptor, LFA-1 [67]; HUT 78 lacked expression of either.

Immunophenotypic studies using the anti-TAC and anti-TU27 antibodies and the IL-2 phycoerythrin fluorokine (R + D Systems, Minneapolis, MN) show that HUT78 cells do not express the IL2 receptor at baseline or after

exposure to mitogens, such as PHA or ConA, while HUT102 cells constitutively express IL2R [68]. Binding assays using 125I-IL2 and mRNA analysis confirm that HUT 102 but not HUT78 cells express the high affinity ($\alpha\beta\gamma$)IL2R.

The IL-7 receptor, which has been identified on normal and neoplastic T-cells, including fresh Sezary cells, and which has been shown to promote the growth of Sezary cells in culture, is expressed on HUT102 but not HUT78 cells as assayed both immunophenotypically using the IL-7-biotin-FITC fluorokine (R + D Systems) and by mRNA and cross-linking studies [69,70]. We found a low affinity binding of ^{125}I-IL7 to a 70 kDa receptor on HUT78 cells, similar to a putative low affinity receptor reported by Armitage et al. [71].

EXPRESSION OF TYROSINE KINASE PROTO-ONCOGENES

Several of the *src*-related protein tyrosine kinases are overexpressed in HUT78, including c-*src*, *lck*, which has been shown to associate with the CD4 receptor, and *fyn*, which complexes with the intracellular δ-chain of the T-cell antigen receptor complex [72,73]. A related kinase, *lyn*, is overexpressed in HUT102 and other HTLV-1 transformed cell lines but not in normal T-lymphocytes or in HUT78 [74]. Blake et al. recently described a truncated form of the c-*abl* proto-oncogene in HUT78 cells [75]. A rearrangement introduces a stop codon removing 259 amino acids from the carboxyterminus, resulting in a 72 kDa protein lacking the leucine zipper domain of native c-*abl*.

C-*MYC* REARRANGEMENT IN HUT78

A chromosomal t(2;8) translocation was described in HUT78, resulting in a c-*myc* fusion transcript. Finger et al. identified a translocation of the TCL4 gene from chromosome 2q34 to a region of the *myc* locus which is 271 bp downstream of the translation termination codon, creating novel transcripts of 6.8 and 3.8 kb, and a shortened 2.4 kb version of the normal *myc* mRNA [76]. The half-life of the *myc*-TCL4 fusion transcript was prolonged, and transfection of this mutant myc gene into NIH3T3 cells demonstrated that it was tumorigenic, suggesting that the role of deregulation of *myc* in transformation in the HUT78 cell line may be analogous to Burkitt lymphoma [77]. Our studies have failed to demonstrate rearranged *myc* genes in HUT102 or in Sezary cells from other patients (unpublished data).

MUTATIONS IN TUMOR SUPPRESSOR GENES

HUT 78 has been shown to harbor a homozygous point mutation in codon 196 of p53, converting an arginine at the end of exon 3 to a stop codon. Interestingly, the T-cell leukemia line, JURKAT, contains the identical mutation [78]. It has further been demonstrated that HUT78 also lacks expression of the normal pp110 retinoblastoma protein, suggesting that loss of tumor suppressor gene function may have been a critical event in the transformation of this cell line [78]. Our studies of p53 in Sezary cells from 19 patients show that one-third of patients have mutations in exons 5–9 and that the finding of mutated p53 correlates with more advanced clinical disease.

THERAPEUTIC IMPLICATIONS FOR ATLL AND CTCL

IL-2 Receptor

The IL-2 receptor was shown to be overexpressed on nearly all malignant cells from ATLL patients. This led Waldmann and colleagues to test the therapeutic role of the anti-Tac monoclonal antibody which reacts with the IL-2 receptor [79,80]. Unlabeled anti-Tac antibody produced some responses in ATLL patients but long lasting complete responses were not observed. These studies were followed by studies of anti-Tac immunoconjugates. These included toxin conjugates with ricin-A chain and Pseudomonas exotoxin and radioimmunoconjugates [81,82].

Although the cell line HUT78 lacks IL2R expression, immunohistochemical studies demonstrate low levels of IL2R expression on the neoplastic lymphocytes infiltrating the skin in about 50–70% of patients with mycosis fungoides and the Sezary syndrome [83–86]. Murphy and colleagues developed recombinant fusion toxins capable of targeting the high affinity IL2R by replacing the receptor binding domain of native diphtheria toxin with the full length IL-2-gene [87]. The recombinant fusion protein, expressed in *Escherichia coli*, binds to cells bearing high affinity IL2R and is internalized by receptor-mediated endocytosis into endosomal lysozymes, where the active fragment of diphtheria toxin is liberated into the cytosol and kills the cell by inhibiting ADP ribosyl transferase and subsequently protein synthesis [88–90]. The original

protein, $DAB_{486}IL$-2, produced objective responses in 6/29 patients (21%) with CTCL [91–93]. No responses were observed among patients whose cells did not express the IL-2 receptor. The dose limiting toxicity was renal dysfunction. A modified form of the IL2 fusion toxin, DAB389IL2, had a higher binding affinity and produced fewer toxicities in experimental models. In phase I-II trials objective responses were noted in 5/11 CTCL patients (45%) [94]. The IL2 fusion toxins are also active against ATLL cells, including HUT102, in vitro [95] but no human clinical trial data have been reported.

Adenosine Analogs

Clinical studies showed that adenosine deaminase deficiency led to immunodeficiency. This led to studies of nucleotide metabolism in lymphocytes and malignant T-cells. We reported that malignant T-cells have aberrant adenosine metabolism [96]. This led to the study of adenosine analogs in CTCL and ATLL patients. Deoxycoformycin was the first analog studied and responses were reported in 26/63 patients (41%) [97–103]. Fludarabine monophosphate was studied by the Southwest Oncology Group who reported objective responses in 6/31 heavily pretreated patients (19%) [104]. Most recently, 2-chlorodeoxyadenosine was studied and shown to produce an objective response in 41% of 27 CTCL patients [105,106]. Deoxycoformycin was also reported to be active in ATLL patients [107]. More recent studies by Foss and colleagues have evaluated the combination of recombinant interferons with deoxycoformycin and fludarabine [108,109]. Although responses were observed in 41 and 53% of the patients treated with each combination, the response rates were not clearly superior to either agent alone.

Interferons

When recombinant interferons became available in large quantities it was logical to examine their activity in CTCL and ATLL patients because of their anti-proliferative effects on some cell lines and the immunostimulatory properties. We reported that both recombinant alpha and gamma interferons had activity in CTCL [110–113]. Responses were uncommon in patients with any high grade T-cell lymphoma. We also reported that the combination of rIFNa2 and PUVA produced responses in 90% of patients including complete responses in more than half of the patients [114]. These response were higher than those observed with the combination of multi-agent chemotherapy and whole skin electron irradiation [115].

Anti-CD5 Monoclonal Antibodies (T101, T1)

After a report from Stanford University showed objective responses in 4/9 CTCL patients treated with an anti-CD5 antibody [116], we studied 11 patients and reported transient and minor responses but no objective partial or complete responses lasting 30 days or more [117]. We showed that a major problem in vitro and in vivo was rapid antigen modulation of the antibody-receptor due to its internalization. This rendered the cells non-responsive to recognition by the immune system. Other studies were also done with other dose schedules and overall only 5 responses were reported among 46 patients [116–119]. However, the internalization made it logical to evaluate immunoconjugates. We showed that radioimmunoconjugates were highly cytotoxic in vitro [120]. This led to clinical trials of radiolabeled T101 [121–123]. These studies showed that the radiolabeled antibody reached sites of disease and that radio imaging could assist in the staging of the patients. Higher levels of antibody in nodal sites were achieved with subcutaneous or intralymphatic administration compared to intravenous administration. This led to a trial of intravenous ^{131}I-T101 at Northwestern University where objective responses were reported in 3 of 6 patients [124]. Unfortunately, these responses were partial and of short duration. This was attributed to the rapid dehalogenation in vivo. An anti-CD5 toxin conjugate was also studied and shown to produce objective responses in 29% of 16 patients [125]. These immunoconjugates are undergoing further clinical study.

CONCLUSIONS

The story which lies behind the clinical-laboratory collaborations and interactions which led to these discoveries is an example of the synergy that can occur by such collaborations, the importance of translational research, and the importance of the clinical investigator in the study of human diseases.

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