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16. Blood, drawn from six normal subjects, was separated by Hypaque-Ficoll density centrifugation. T cells were identified and isolated by sheep erythrocyte rosette formation and density centrifugation. Data in Table 1 on the reactivity of monoclonal antibodies with T cells were determined by an indirect fluorescent assay. In addition to testing primate cells for T cell–specific reagents, we determined reactivity with antibodies that define nonpolymorphic determinants of the human histocompatibility antigen, A, B, and C molecule (3F10) and an Ia-like molecule (L-243). Cells from all the primates we tested reacted with antibody to human histocompatibility antigens, and a subset of all primate peripheral blood cells was positive for the Ia-like antigen. All primate T cells formed rosettes with sheep erythrocytes (81 ± 2 percent of lymphocytes)
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20. Antibodies L17F12, T101, and 10.2 may bind to the same antigenic determinant on the 65,000-dalton human Lyt 1 analog [R. I. Fox, P. Kung, R. Levy, in *Lymphocyte Differentiation*, N. Warner, Ed. (Academic Press, New York, in press)]. In Table 1, each monoclonal antibody to T cells is reported separately and considered to bind to a distinct determinant. Monoclonal antibody DU-SKW3-1 was raised against the T cell chronic lymphocytic leukemia cell line SKW-3. Analysis by sodium dodecyl sulfate–polyacrylamide gel electrophoresis has not resolved whether the 65,000-dalton molecule detected by DU-SKW3-1 is the same as that recognized by antibodies L17F12, T101, and 10.2 (unpublished data).
21. While 65 percent of human peripheral T cells are positive for OKT4 and 30 percent are positive for OKT8, it was not uncommon to see reversal of this pattern of T cell subset antigens. Thus in gibbons only 19 ± 7 percent of the T cells were positive for OKT4 and 87 ± 11 percent were positive for OKT8. Moreover, in orangutans and chimpanzees, significant proportions of peripheral T cells expressed both the OKT4 and OKT8 antigens (Table 1).
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23. The evolutionary divergence date for New World monkeys is unknown, but plotting the number of absent human T cell antigen determinants yields an apparent divergence time of 40 million years ago for New World monkeys. This time may be arbitrary since the total number of human T cell antigens is not known. Moreover, an assumption made in the interpretation of data in Fig. 1 is that it is valid to consider the T cell antigens as a group in estimating evolutionary divergence.
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Developmental Equations for Postural Tremor

Abstract. *Developmental equations for the electroencephalogram have been reported previously for normal children and brain disorder has been shown to cause substantial deviations from this developmental norm. The present report describes directly parallel phenomena with regard to postural tremor.*

Developmental equations that describe electroencephalographic (EEG) changes in children aged 6 to 16 years have been reported by John *et al* (*1*). These authors noted that the regression coefficients associated with the β, α, θ, and δ frequency bands taken from the parieto-occipital, central, temporal, and frontotemporal regions of the brain change systematically with age. Data based on 306 U.S. children agreed well with data collected on 342 Swedish children. A third group of 91 normal children were reported to be quite similar in their development to the other two groups of normal children (*2*). Substantial deviations from this normal developmental sequence were then reported for 474 children "at neurological risk," 143 learning disabled children, and 163 specific learning disabled children (*2*). Normal development is associated with an increase in the dominant EEG frequency; brain damage or deterioration is associated with a lowering of this dominant frequency (*1*).

The purpose of the study reported here was to identify parallel developmental and pathological changes related to postural tremor. The developmental equations stem from a reanalysis of previously published data on 287 children aged 2 to 16 years (*3*). The data on the effects of brain pathology on postural tremor come from two previously published studies on adults (*4, 5*).

Marshall (*3*) asked 287 normal children, ranging in age from 2 to 16 years, to hold an accelerometer (weighing 65 g and measuring 9.5 cm in length and 3.3 cm in diameter) in the palm of their outstretched hand for a brief but unspecified time. Although the subjects were instructed or coached to hold their arm as steady as possible, small movements, described as physiological tremor, remained. Marshall calculated the dominant or peak frequency for each child and displayed these data in a figure relating tremor frequency to the subject's age. Upon reanalyzing Marshall's data, I discovered an unreported correlation [$r(13) = .9433, P < .001$] between average age and average peak frequency. This result clearly establishes an average developmental sequence that is well described by Eq. 1.

$$Y = .2612X + 4.4417 \quad (1)$$

Table 1 shows the average peak frequency and standard deviation associated with each age group studied by Marshall plus the value predicted for that age group by Eq. 1. The difference between the observed and predicted peak frequency values is also reported. Both the obtained data and the theoretical calculations show that the peak frequency slowly and regularly increases as a function of chronological age. The slope of Eq. 1 reveals that the peak frequency increases by 0.2612 Hz or about 0.25 Hz per year. This developmental sequence continues until the adult frequency of 10 Hz is reached. Equation 1 predicts that the 10-Hz peak frequency is reached

Table 1. A statistical analysis of data reported by Marshall (*3*) on the peak frequency of physiological tremor in 287 normal children (in hertz).

N	Age (years)	Average peak frequency	Standard deviation of peak frequency	Predicted peak frequency	Deviation from prediction
3	2	5.33	5.77	4.96	0.37
4	3	5.75	0.50	5.23	0.52
10	4	5.80	0.79	5.49	0.31
20	5	5.60	1.05	5.75	−0.15
14	6	6.00	1.04	6.01	−0.01
18	7	5.78	1.06	6.27	−0.49
20	8	5.90	1.21	6.53	−0.63
22	9	6.23	1.41	6.79	−0.56
25	10	7.28	1.93	7.05	0.23
34	11	7.06	1.74	7.32	−0.26
30	12	7.60	1.73	7.58	0.02
22	13	7.45	1.68	7.84	−0.39
30	14	8.23	1.61	8.10	0.13
22	15	8.50	1.50	8.36	0.14
13	16	9.38	1.61	8.62	0.76

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when the subject is 21.28 years old, thus marking the end of this developmental epoch.

It should be noted that Eq. 1 predicts the average peak frequency for postural tremor from average age. Although this equation suitably describes the underlying developmental sequence, it is not appropriate for predicting the specific peak frequency for a single person. Hence, a correlation over all 287 subjects was calculated between age and peak postural frequency [r (285) = .5610, $P < .001$]. The corresponding regression equation is given as Eq. 2.

$$Y = .2901X + 4.0593 \quad (2)$$

This equation also specifies a developmental rate of approximately 0.25 Hz per year. Moreover, the Y intercept value is in rather good agreement with that found in Eq. 1. In sum, the regression equation based on all 287 individual subjects agrees rather well with the regression equation based on average age and average peak tremor frequency.

Nashold (*4*) reported that the peak frequency of postural tremor in patients with Parkinson's disease is about half (5 Hz) that of normal persons (10 Hz). Friedlander (*5*) reported the peak frequency of postural tremor in parkinsonian patients to range from 4 to 7 Hz. This same author reported the dominant frequency of postural tremor in alcoholics to be 6 Hz. He also reported that the dominant frequency of patients with unilateral damage of the central nervous system ranges from 3 to 7 Hz.

There are two striking parallels between the previously reported data on developmental equations (*1, 2*) and those reported here concerning postural tremor. First, well-fitting regression equations are available that accurately describe normal development. Second, brain disorder decreases the dominant frequency of both the EEG and postural tremor. Hence, it now appears possible to obtain two separate physiological measures of development that are sensitive to organic impairment. Perhaps more such measures will soon be reported.

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Migration Inhibition of Endothelial Cells by Lymphokine-Containing Supernatants

Abstract. *Many of the reactions of cellular immunity are mediated by soluble lymphocyte-derived factors (lymphokines). One important category of lymphokine action involves effects on cell motility. These effects have been described mainly with respect to inflammatory cells. In this report, we describe the ability of a lymphocyte product to inhibit the migration of endothelial cells in a system in vitro. The responsible factor is distinct from a previously described mediator that inhibits the migration of tumor cells. The ability of lymphocytes to influence the migration properties of endothelial cells is consistent with data of others showing a relation between the immune system and processes involving neovascularization.*

Many of the reactions of cellular immunity are mediated by lymphocyte-derived soluble factors known collectively as lymphokines. These mediators exert profound effects on inflammatory cells such as monocytes, granulocytes, and lymphocytes themselves. Such actions fall into three main categories: effects on cell motility (migration inhibition, chemotaxis, and chemokinesis), effects on cell proliferation or cellular viability, and effects on cellular activation for specific specialized functions [reviewed in (*1*)]. Of these, migration inhibition has been considered the prototype, in part because a migration inhibition factor was the first lymphokine to be described, and in part because such factors could play important roles in vivo by virtue of their capacity to immobilize or retain cells at critical tissue sites.

Migration inhibitory factors for macrophages (MIF) and neutrophils have been studied extensively (*1*). More recently, we have described a lymphokine, TMIF, that inhibits the migration of a variety of tumor cells including P-815 mastocytoma, Ehrlich ascites, hepatoma 129, sarcoma 37, and the Walker carcinosarcoma (*2*). TMIF is distinguishable from both neutrophils and MIF on the basis of molecular weight, monosaccharide inhibition profiles, and enzyme inactivation spectra. In addition, it is possible to dissociate the production of these factors by appropriate experimental conditions (*2, 3*).

The present study was undertaken in part to explore the specificity of TMIF for tumor cells and in part to determine whether lymphokines can influence the migration of cells that participate in reparative processes in a manner similar to their well-known effects on the migration of inflammatory cells. In this report we present evidence that human lymphokine-containing supernatants from a variety of sources have the capacity to inhibit the migration of endothelial cells. This activity is separable from TMIF but not from MIF activity by Diaflo ultrafiltration (Amicon).

For these studies, the human lymphoblastoid line RPMI 8392 was the source of most of the supernatants. Such culture fluids, which we have previously characterized, are known to contain lymphokines that are indistinguishable from those obtained from antigen- or mitogen-stimulated normal human lymphocytes (*4*). In addition, normal human lymphocytes were cultured with concanavalin A, or, when obtained from a suitably sensitized individual, purified protein de-

Table 1. Migration inhibition of endothelial cells by lymphokine-containing supernatants. Confluent cultures of endothelial cells were harvested by incubation with warmed trypsin-EDTA for 10 minutes at 37°C. The reaction was stopped by the addition of cold Hanks buffered salt solution (HBSS) supplemented with 10 percent FCS. The cells were washed three times with HBSS and resuspended in RPMI 1640 medium supplemented with 10 percent FCS and anitbiotics, placed on a rocker (Uni-Mixer, Lab-Line Biomedical Products), and incubated at 37°C for 3 to 4 hours before use in the agarose microdroplet assay (*8*). Migration indices (MI ± standard error of the mean) are calculated as follows: MI = $(A_E/A_C) \times 100$, where A_E is the area in the experimental supernatant and A_C is the area in the control supernatant. MI ≤ 80.0 represents significant migration inhibitory activity. Each MI value is the average of at least six determinations.

Experiment No.	Migration index
RPMI 8392	
1	66.2 ± 2.9
2	61.8 ± 2.2
3	67.0 ± 3.0
4	63.1 ± 2.8
5	72.8 ± 2.7
*Concanavalin A activated lymphocytes**	
6	75.2 ± 1.8
7	76.5 ± 4.3
8	70.0 ± 3.6
PPD activated lymphocytes	
9	71.0 ± 5.0
10	68.3 ± 4.1
Unstimulated lymphocytes†	
11	98.4 ± 3.2
12	102.7 ± 4.6
13	96.5 ± 5.1

*Concanavalin A was removed from experimental and control supernatants by incubation with 0.1*M* α-methyl-D-mannoside for 30 minutes at 37°C prior to assay. †Lymphokine-free control.

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