

CELL DEATH IN THE ~~MURINE~~ IMMUNE SYSTEM

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ABSTRACT

A distinction based on morphological criteria has been made between two forms of mammalian cell death: necrosis, which is mediated by agents external to the cell, and apoptosis, which is believed to be the result of the triggering of an active suicide mechanism in a cell that dies as a result of a physiological, developmentally-regulated process. In the immune system, apoptosis has been implicated as a mechanism of thymic selection and of cytotoxic T lymphocyte (CTL) killing. DNA fragmentation is regarded as a hallmark of apoptosis.

This thesis examines three forms of cell death in the immune system. First, I show that the cell death induced by the removal of the specific growth factor from IL2- and IL3-dependent cell lines falls into the category of apoptosis, as defined morphologically. The DNA is cleaved into nucleosome-sized pieces and survival is enhanced by the nuclease inhibitor aurantricarboxylic acid and by protein synthesis inhibitors. The effect of the protein synthesis inhibitors does not seem to be due to partial cell cycle arrest, as synchronization of the cells does not alter the kinetics of death.

Second, in an attempt to confirm a report that acquisition of resistance to glucocorticoids correlates with acquisition of resistance to CTL killing, I isolated a series of dexamethasone (dex)-resistant mutants from a dex-sensitive clone of the mastocytoma P815 and tested them for susceptibility to killing by CTL. I have used Northern-blot analysis, with a probe to the glucocorticoid receptor, to see if dex resistance is due to a loss of receptor expression or to an increased ability to down-regulate receptor expression.

Third, I have developed an assay to measure the extent of apoptosis in a tissue *in vivo*, using radiolabelled DNA precursors. Apoptosis was shown to be induced in double positive thymocytes *in vivo* by injection of a monoclonal antibody anti-CD3.

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ABBREVIATIONS

ADP	adenosine diphosphate
ATC	aurintricarboxylic acid
ATCC	American tissue culture centre
ATP	adenosine triphosphate
5azaC	5azacytidine
BDH	British drug house
BrdU	bromodeoxyuridine
BSA	bovine serum albumin
[Ca ²⁺] _i	internal concentration of calcium ions
Ci	curie
CTL	cytotoxic T lymphocyte
CO ₂	carbon dioxide
ConA	concavalin A
Cpm	counts per minute
CSF	colony stimulating factor
dex	dexamethasone
DMEM	Iscove's modified Dulbecco's medium
(c)DNA	(complementary) deoxyribonucleic acid
DTT	dithiothreitol
E20	embryonic day 20
EDTA	ethylenediamine tetra-acetic acid
EMS	ethylmethanesulfonate
E:T	effector:target
FCS	foetal calf serum
FDC	follicular dendritic cell
FL	fluorescence
FPLC	fast performance liquid chromatography
FSC	fluorescence side scatter
g	gravity (units of)
GR	glucocorticoid receptor
GRE	glucocorticoid response element
h	hour(s)
HEPES	N-2-hydroxyethylpiperazine-N-2-ethane-sulphonic acid
HCl	hydrochloric acid
HS	horse serum
Hsp	heat shock protein
³ H-MNU	N-methyl- ³ H-N-nitrosourea

HRF	homologous restriction factor
³ HTdR	[⁶³ H]-thymidine
ICRF	Imperial Cancer Research Fund
γIFN	γIFN
(s)Ig	(surface)immunoglobulin
IL2	interleukin 2
IL3	interleukin 3
i.p.	intra-peritoneal
¹²⁵ IUdR	[⁵¹²⁵ I]iodo-2'-deoxyuridine
k b	kilobase
m a b	monoclonal antibody
2-ME	2-mercaptoethanol
MeG	methylguanine
MEM(-H)	Minimum essential medium (buffered with 0.02M HEPES)
MHC	major histocompatibility complex
MLR	mixed lymphocyte reaction
Mls	mouse lymphocyte stimulating
MOPS	morpholinopropanesulfonic acid
MTOC	microtubule organizing centre
MTT	3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium salt
NAD	nicotinamide adenine dinucleotide
NGF	nerve growth factor
NaOAc	sodium acetate
PBS	phosphate buffered saline
PI	propidium iodide
PO	propylene oxide
(m/t)RNA	(messenger/transfer) ribonucleic acid
RPMI	Roswell Park Memorial Institute 1640 medium
SDS	sodium dodecyl sulphate
σ _n	standard deviation of mean
t	time
TCA	trichloroacetic acid
TCDD	2,3,7,8-tetrachlorodibenzo-p-dioxin
TCR	T cell receptor
tk	thymidine kinase
TNF	tumour necrosis factor

CHAPTER ONE:
GENERAL INTRODUCTION

INTRODUCTION

The death of a cell might be brought about by external damage, or might result from the triggering of an active suicide mechanism intrinsic to the cell. The latter possibility assumes that cell death is a physiologically controlled event, for which the cell has a genetically programmed capability, and its control might be considered to be analogous to the control of cell proliferation or cell differentiation. Evidence for programmed cell death in mammalian cells is still largely circumstantial, as the process has not been characterised at a molecular level. The existence of programmed cell death is, however, well established in the nematode, *Caenorhabditis elegans*. I shall, therefore, first review the evidence for programmed cell death in *C. elegans* development, before considering its possible roles in the development and maintenance of tissue homeostasis in vertebrates and, more specifically, its relevance to the murine immune system.

Programmed cell death in *C. elegans*

C. elegans has a small, invariable number of cells, and all lineage relationships between these cells are known (reviewed by Kenyon 1988). During the development of the hermaphrodite, which has 959 somatic cells, 1090 somatic cells are generated of which 131 subsequently die (Sulston and Horvitz, 1977; Sulston et al, 1983; reviewed by Horvitz 1988). The dying cells all undergo the same sequence of morphological changes, which include the initial condensation of the nucleus followed by its disappearance (Sulston et al 1983), and in all cases, death requires the activities of the same genes (Hedgecock et al, 1983; Ellis and Horvitz 1986). Thus, undergoing programmed cell death can be regarded as a genetically-determined

specific cell fate, like any other fate in differentiation. Mutant animals, in which the predicted cells do not die on schedule, have enabled the genes that control both the decision to die (determination) and the expression of that decision (ie. death), to be defined. *C. elegans* is therefore a powerful system in which to study programmed cell death, and it may provide a way into the molecular analysis of mammalian programmed cell death, as there are similarities between both the morphology and the occurrence of death between phyla. As in mammals (Cowan et al, 1984), programmed cell death in *C. elegans* is particularly common in the cells of the nervous system, and about 20% of presumptive neurons die (Sulston et al, 1983; Horvitz et al 1982).

Cell death determination genes have been recognized on the basis of mutations which alter the pattern of death without affecting the machinery of death per se. One mutation (*ces-1*) has been defined which causes some cells that would normally die to survive (Horvitz 1988) and the genes *egl-1* and *lin-39* are defined by mutations which cause cells that would normally become motor neurons to undergo programmed cell death (Trent et al, 1983; Ellis and Horvitz 1986).

Five genes involved in the mechanism of death have been identified by mutations. Two genes, *ced-3* and *ced-4*, are necessary for the onset of programmed cell death (Ellis and Horvitz 1986): in *ced-3* and *ced-4* mutants, cells that would normally die survive and differentiate, and in some cases function (Ellis and Horvitz, 1986; Avery and Horvitz 1987). Surprisingly, animals which are mutants in *ced-3* and *ced-4* do not display any gross behavioural abnormalities, indicating that programmed cell death is not an essential part of *C. elegans* development (Ellis and Horvitz 1986). Two genes, *ced-1* and *ced-2*, are required for engulfment of dying cells by their neighbours, and in mutants of these genes, cells destined to die undergo the initial

morphological changes associated with death, but they are not phagocytosed (Hedgecock et al 1983). The gene *nuc-1* controls a nuclease which degrades the DNA of dying cells and in mutants of this gene the remains of cells that have died can be seen as pycnotic nuclei containing undegraded DNA (Sulston 1976, Albertson et al 1978; Hedgecock et al 1983). Complementation studies, in which animals with multiple mutations were constructed, have indicated the order of gene action to be (*ced-3, ced-4*), (*ced-1, ced-2*), *nuc-1* (Ellis and Horvitz 1986).

The question of whether these genes act cell autonomously or in neighbouring cells to those which die (suicide vs murder) has been addressed using mosaic analysis, and has revealed that both *ced-3* and *ced-4* act cell autonomously (Horvitz 1988). Thus programmed cell death in *C. elegans* can be regarded as suicide. Whether *ced-1, ced-2* and *nuc-1* also act within the dying cells rather than in the cells that engulf them has not yet been determined. When engulfment is blocked by mutations in *ced-1* or *ced-2* alone, only two male-specific cell deaths fail to occur (Hedgecock et al 1983), and so these two deaths apparently result from murder, rather than suicide, a view that is supported by the finding that they can be prevented by ablation of the cells that would engulf them (Sulston and White 1980).

The cDNA for *ced-4* has been cloned and sequenced, and has no homology to previously cloned genes (H.R.Horvitz, personal communication). The other cell death genes are as yet uncloned.

Cell death in vertebrates

Necrosis and apoptosis

A morphological distinction has been made in vertebrates between cell death due to external damage (necrosis) and cell death which is presumed to be the result of suicide (apoptosis) (reviewed by

Wyllie 1981). Necrosis is characterized by plasma membrane damage and eventual lysis due to the cell swelling. In apoptosis the earliest changes are in the cell nucleus, where the chromatin becomes condensed, while the plasma membrane and other cellular organelles remain intact; eventually the cell breaks up into membrane-bound apoptotic bodies, which often contain pieces of condensed nucleus (Kerr 1971, reviewed by Duvall and Wyllie 1986). Apoptotic cells and apoptotic bodies are rapidly phagocytosed *in vivo* (Duvall et al 1985, Wyllie et al 1980, Ijiri and Potten 1983), and it has been shown that there are changes in cell-surface carbohydrate which make them particularly susceptible to phagocytosis by macrophages (Morris et al 1984, Wyllie 1985). In apoptosis DNA is cleaved into nucleosome-sized fragments by an endonuclease(s) (Cohen and Duke 1984) and this is thought to account for the nuclear morphology (Wyllie et al 1984). Apoptosis has been regarded as cellular suicide because it has been shown to be inhibited or delayed by protein synthesis inhibitors (eg Duke and Cohen 1986, Shi et al 1989, Pratt and Greene 1976). It tends to occur when death is a physiologically or developmentally regulated process (Wyllie et al 1980, Wyllie 1987), such as in the disappearance of the tadpole's tail during morphogenesis Kerr et al 1974).

Clearly there are striking functional similarities between programmed cell death in *C. elegans*, which has been shown to be genetically programmed cell suicide, and apoptosis. Both processes involve nuclear condensation due to cleavage of DNA, both seem to be cell autonomous (in *C. elegans* from cell ablation and complementation studies, and in vertebrate apoptosis from inhibitor studies), and both involve changes which lead to rapid phagocytosis of the dying cells. It would seem surprising if these correspondences were the result of convergent evolution, and not due to evolutionary conservation,

particularly given that the cell death occurs during the development of the nervous system in nematodes (Ellis and Horvitz 1986), insects (Goodman and Bate 1981), birds (Pittman and Oppenheim 1979), and mammals (Cowan et al 1984). This adds weight to the contention that apoptosis is cell suicide and also suggests that cloning the cDNAs for the nematode cell death genes may enable one to identify mammalian homologues involved in apoptosis.

Cell death in the development of the vertebrate nervous system

Cell death is a major feature of the development of the nervous system (Collin 1906; Hamburger and Levi-Montalcini, 1949; reviewed by Cowan et al, 1984). In many regions of the nervous system, about 50% of the neurons produced die. This over production seems extremely wasteful, especially given the observation that both in *C. elegans* (Ellis and Horvitz, 1986; Avery and Horvitz 1987) and in rats (Zamenhof 1942) the animal seems phenotypically normal even if the predicted cell death does not occur. What then are the selective pressures that favour neuronal death? Williams and Herrup (1988) have argued that for a small animal such as *C. elegans*, where the nervous system takes up such a large proportion of the body, the primary consideration will be energetic, particularly as neurons have high energy requirements relative to other cell types (Kety and Schmidt 1948, Kreisman et al 1986). *Ced-3* and *ced-4* mutant animals, which have 20% increase in the normal neuron number, have a brood size of 15-30% below normal (Ellis and Horvitz 1986). Thus, as metabolic constraints in a small species seem to limit brain size (Martin, 1981), one would expect every neuron to be necessary. In larger species these constraints seem not to exist, and excess neurons may increase evolutionary plasticity.

In vertebrate development the phase of cell death is usually confined to a well-defined period that is distinctive for each neuronal population, and which seems to be the time at which the majority of axons of that neuronal subpopulation are beginning to establish connections with their targets. Studies in which target fields were removed (eg Hamburger 1958, Cowan and Wenger, 1967; Oppenheim et al 1978), partially ablated (eg Hamburger 1975, Landmesser and Pilar, 1974), or artificially extended (eg Hollyday and Hamburger 1976; Boyston and Sohal, 1979), have shown that the normal target field can support a smaller number of neurons than are initially produced and that cell death provides a means of matching the size of each neuronal population to the magnitude of its target field.

The mechanism of matching seems to be the competition by neurons for limiting amounts of survival (trophic) factors produced by the target cells. The best characterised neurotrophic factor, nerve growth factor (NGF), is required for the survival of sympathetic and some sensory neurons (reviewed by Levi-Montalcini 1987, Davies 1988). Loss of sympathetic and sensory neurons occurs when endogenous NGF is neutralized by administration of anti-serum against NGF (Levi-Montalcini and Brooker 1969), or by making the animal autoimmune to NGF (Johnson et al 1980). Conversely, exogenously applied NGF can increase the survival of these neurons during development (Hendry and Cambell 1976; Hamburger et al 1981) and after injury (Rich et al 1987). NGF is taken up by the axon terminals at their targets and retrogradely transported back to the cell body (Claude et al 1982; Palmatier et al 1984), where it exerts its survival effect. It is assumed that there are other neurotrophic factors which are specific for the survival of other populations of neurons (Johnson and Yip 1985, Oppenheim et al 1988); one candidate is a brain-derived neurotrophic

factor (BDNF), whose cDNA has recently been cloned (Leibrock et al 1989).

How does NGF exert its effect? Intuitively one might expect that a survival factor would allow a cell to survive by providing it with something that it needs, so that in its absence, the cell would gradually decline and die. This does not seem to be the case. In the absence of NGF, rat sympathetic neurons die actively, and their survival can be enhanced by inhibitors of protein synthesis and RNA synthesis (Martin et al 1988; Oppenheim and Prevet 1988). In culture, on NGF deprivation, a minority of dying neurons display the morphology of apoptosis (Martin et al 1988). Apoptosis has been observed *in vivo* in the cerebellar cortex of homozygous staggerer mice (Kerr et al 1987).

All neurons seem to be destined to commit suicide at a fixed point in their development, unless their neurotrophic factor rescues them. Thus, a mechanism that evolved in simpler organisms to limit neuron numbers (ie for efficiency of metabolism) may have been adapted to fine tune the development of more complex nervous systems, and so increase fitness by improving efficiency of information processing. The strategy of neuronal overproduction followed by death ensures that all target cells get approximately innervated and also has the advantage of facilitating evolution: if a mutation alters the size of part of the body, its innervation is automatically adjusted, without the need for a corresponding mutation that changes the number of innervating neurons.

Cell death in the control of cell life-span

Mammalian somatic cells have a finite life-span and proliferative potential in culture (Hayflick 1965), that is partly dependent on the age and type of tissue from which the cells are derived (Martin et al 1970).

This phenomenon of senescence cannot simply be due to accumulation of errors, as has frequently been proposed (Orgel 1973, Holliday, 1984, 1986): sister cells do not always exhibit the same loss of proliferative potential (Smith and Whitney 1988); in fusions between senescent and cycling cells, senescence is often dominant (Norwood et al 1974); Proteins (Drescher-Lincoln and Smith 1984) and polyA⁺ RNA (Lumpkin et al 1986) from senescent cells, when injected into proliferating cells, can cause them to drop out of cycle. Senescence, therefore, seems to be a state of differentiation (Bell et al 1978), which is distinct morphologically (Kerr et al 1987) and biochemically (Bulmer et al 1984) from quiescence of young cells.

Most studies of senescence have concentrated on the loss of proliferative potential of fibroblasts, and not on their actual death, and it has been reported that non-cycling senescent fibroblasts can be maintained for several months in culture (Pereira-Smith et al 1985), whereas senescent T cells have been reported to die rapidly on becoming quiescent (Walford et al 1981). An ultrastructural comparison of fibroblasts from young and senescent cultures, however, showed an increase in the proportion of non-viable cells in senescent cultures, and that the dying cells had the morphology of apoptosis (Brock and Hay 1971). It is therefore tempting to speculate that in addition to the very specific role of matching target-neuron interactions in nervous system development, apoptosis may play a more general part in the determination of life-span of maturing cells (Umansky 1982). Unfortunately, cells from *C. elegans*, have not yet been cultured and so the participation of the *ced* genes in senescence *in vitro* cannot be assessed.

Growth factors appear to influence the onset of senescence in vertebrate cells. Maintaining rodent fibroblasts in low-serum medium

delays senescence (Loo et al 1987). Fibroblasts of patients with Werner's syndrome become senescent more rapidly than normal fibroblasts, and have a diminished response to PDGF (Bauer et al 1986). Transfection of a single oncogene can be sufficient to confer immortality on somatic cells (Spandidos and Wilkie 1984a and b, Wilkie and Spandidos 1984) and many oncogenes are known to encode for growth factors (eg *sis*), growth factor receptors (eg *mas*, *erbB*, *neu*, *frus*), tyrosine protein kinases (eg *src*, *fps*, *abr*), GTP-binding proteins (eg *ras*, *abl*) and nuclear localized proteins that are cell cycle regulated (eg *myc*, *myb*, *fos*, *jun*) (reviewed by Sigal and Gibbs 1989). Transfection of non-growth-factor-encoding oncogenes (eg *ras*) can induce cells to release growth factors and become autonomous for cell proliferation (Spandidos 1985). Thus, many oncogenes encode products involved in growth factor signal transduction, implicating these pathways in the control of cell lifespan. immortalization of diploid cells by oncogenes is associated with reduction in growth factor dependence (Rassoulzadegan et al 1983, Mougneau et al 1982), and it has been suggested that normal cells differ from immortalized cells only in having a higher requirement for growth factors (Brooks and Riddle 1988).

In the case of developing sympathetic neurons, NGF is necessary for survival because it prevents programmed cell death, but since these cells are post-mitotic, the growth factor does not immortalize them in the sense that a fibroblast can become immortal; and as they mature their NGF dependency is diminished (Koike et al 1989). However, if one considers growth factor dependence of proliferating cells, such as IL2-dependent T cell clones, then providing the cells with a constant supply of growth factor might be sufficient to immortalize them. For example, cytotoxic T cell clones that have lost their antigen-dependence, (and so may have already undergone a genetic change), can be maintained for

years in culture by addition of IL2 (Smith and Gillis 1977). On removal of IL2 the cells do not become quiescent, but die by apoptosis (Duke and Cohen 1986). Spontaneous loss of IL2-dependence in rat x mouse IL2-dependent CTL hybrids does not correlate with loss of CTL-derived chromosomes, but is accompanied by acquisition of glucocorticoid-sensitivity, vicia villosa lectin-resistance, loss of cytolytic activity and morphological changes (Samoza et al 1989). IL-2 dependence, therefore, seems to be determined by the state of differentiation of the cell, and the transition to independence seems to involve a stable, pleiotropic change in gene expression.

Thus, it seems that a cell might have three possible fates, which are dependent on its stage of differentiation, growth factor environment, and probably also a stochastic element (Brooks 1985): (1) to progress through the cell cycle; (2) to become quiescent; or (3) to commit suicide. Interestingly, the same sequence of transient nuclear protein expression (ie myc, fos, Hsp70) that was seen when quiescent cells were stimulated with growth factors (Lau et al 1986; Milarski and Morimoto 1986) has also been reported in prostate cells dying by apoptosis (Buttayan et al 1988). Just as genes involved in the regulation of proliferation have been found to be implicated in oncogenesis, one might predict that a mutant gene in the pathway of cell suicide might be potentially oncogenic, though it would presumably be recessive.

Further evidence in favour of the viewpoint that suicide is a physiological option for a cell, controlled by the same kinds of signals as control proliferation and differentiation, comes from studies in which primary cultures of endometrial cells were grown on collagen (Lynch et al 1986). In this system homeostasis in total culture mass is achieved by positive feedback mechanisms in which soluble factors control both the rate of proliferation and the rate of apoptosis.

Evolutionary arguments against genetic control of cell life-span have often rested on the assumption that *in vitro* senescence directly correlates with aging of the organism as a whole. Most organisms die in a natural environment from disease, predation, or starvation, and so an organism will tend to benefit from diverting metabolic resources into efficient reproduction rather than avoidance of aging (Medawar 1952). (This may not always hold, as genes that control the life-span of the whole organism in *C. elegans* do not exert their influence until after reproductive maturity is reached, Johnson and Wood 1982, Johnson 1987). It has been argued that the continuity of the germ-line is best achieved by investment of resources in proof reading and processes that preserve the integrity of macromolecules, and not in indefinite maintenance of the soma (Kirkwood and Holliday, 1979). These arguments might hold for the control of life-span of post-mitotic cells but do not seem relevant to the life-span of proliferating cells of hierarchical tissues, such as the cells of the epithelium and the haemopoietic system, where limits on proliferative capacity and cell life-span presumably reduce the risk of the accumulation of mutations leading to cancer.

Apoptosis in the murine immune system

Apoptosis has been implicated in the development, homeostasis, and as an effector mechanism of the murine immune system. As in the development of the nervous system, there is a vast and seemingly wasteful overproduction of cells during the development of the immune system, followed by their subsequent deaths. This overproduction may facilitate the selection of a repertoire that can distinguish non-self from self (Burnet 1961). In addition, cell death seems to be a means of limiting the numbers of effector cells which expand during an immune

response (Duvall and Wyllie 1986). This thesis examines whether the cell death in T cell development in the thymus (Chapter 5) and in the growth factor-dependent determination of life-span of effector T cells and of haemopoietic progenitor cells (Chapter 3) fall into the category of apoptosis. It also considers the hypothesis that one mechanism by which CTL kill is by triggering the target to commit suicide (Golstein 1987), (see Chapter 4). Since apoptosis in relation to T cells is discussed in detail later, here I shall only review cell death of B cells.

Cell death in B cell development

Precursors of B cells arise early during development in the yolk-sac, although the earliest cell identifiable as B cells by their expression of surface immunoglobulin (sIg) appear later in the fetal liver (Owen et al 1977). Shortly after birth, the bone marrow becomes the sole site of B cell development in the mouse (Verlardi et al 1984). It contains about 3×10^7 pre-B cells which give rise to 2×10^7 virgin B cells each day (Opstelten and Osmond 1983), and as the total number of B cells remains roughly constant, an equivalent number must die each day.

B cells were once thought to have a short half-life of 1-2 weeks (Sprent and Basten 1973), but experiments in which partially irradiated rats were reconstituted with thoracic duct lymphocytes of previously immunized rats, and then were themselves challenged with the same antigen, have demonstrated the existence of a population of short-lived host virgin B cells, and a population of donor derived memory B cells whose response was still apparent 3 weeks later (Gray et al 1986). There are, therefore, thought to be two populations of B cells: the short-lived virgin B cells present in the lymphoid organs, and the recirculating

memory B cells which survive for long periods in a quiescent state between each antigen encounter.

The first identifiable stage of B cell development is the progenitor B cell, which has rearranged its V_H genes by recombination of VDJ segments (Alt et al 1986) but does not express μ chains (McKearn and Rosenberg 1985). The pro B cell develops into a pre-B cell (Raff et al 1976), a large rapidly dividing cell in which μ chains are expressed in the cytoplasm. After several divisions the pre-B cell drops out of cycle, decreases in size, rearranges its V_L genes with resultant expression of sIg, and becomes a virgin B cell.

On the leaving the bone-marrow, the virgin B cell with phenotype $IgM^+IgD^+MEL-14^+$ (homing receptor, Gallitin et al 1983) either moves to the spleen, where it (1) is induced by antigen to differentiate into a plasma cell or memory B cell, and then migrates to the spleen, or (2) dies. In the follicular region of the lymph nodes antigen is presented to virgin B cells, followed by cognate T-B interactions with T_H (Van Ewijk and Van der Kwast 1980). The antigen activated B cell is then thought to enter the germinal centres, which play a key role in memory cell formation (Cioco et al 1983). Follicular dendritic cells (FDC) retain large amounts of antigen in the form of complexes held via Fc and C3B receptors (Heinen et al 1985) and stimulate survival and proliferation, but inhibit differentiation into plasma cells. B cells divide rapidly in the germinal centres, but there is also much cell death, and surviving B cells either enter the light zone of the follicle, where they tend to develop into memory B cells, or leave via the opposite pole into the medullary zone, where they develop into plasma cells, which die after several days.

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Thus, there is extensive cell death at all stages of B cell development. Death may result from (i) failure to rearrange VDJ

segments correctly (reviewed by Foerster et al, 1989a), (ii) arguably as a mechanism of tolerance induction (Nossal 1983) or (iii) during affinity maturation in the germinal centres (reviewed by MacLennan et al 1989). Most of the evidence for this cell death comes from 'balance-sheet' arguments, but BrdU labelling studies have recently demonstrated that most B220^{dull} $\mu^+\delta^-$ cells die *in situ* in the bone marrow (Foerster et al 1989b); in addition cell death has been demonstrated in the spleen and lymph nodes by labelling studies (McPhee et al 1979, see chapter 5), and apoptosis has been observed in the spleen (Schwartzendruber and Congdon 1963). Little is known about what controls the onset of death in these tissues, and the issue of B cell life-span remains controversial, but considerably more attention has been devoted to the question of whether clonal deletion is a mechanism for tolerance induction in B cells, as has been shown to be the case for T cells (Kappler et al 1987), and to the conditions favouring affinity maturation and memory cell survival in the germinal centres.

B cell tolerance induction

Studies of B cell tolerance have suggested three alternatives: (i) B cell tolerance does not exist, but autoantibody production is prevented by the absence of autoantigen-specific T cell help (Rolink et al 1987); (ii) autoreactive B cells are functionally inactivated, but still persist in the animal and can still bind antigen (Ventkataraman et al 1977); (iii) autoreactive B cells are eliminated early in development (Sidman and Unanue 1975; Metcalf and Klinman 1977). The third possibility is attractive because it mirrors what is thought to happen in T cell development, where autoreactive cells are deleted in the thymus, perhaps by signaling them to commit suicide by engaging their T cell receptors (Smith et al 1989, Shi et al 1989). One might envisage that at a

stage in B cell development, ligand binding to sIg might trigger the cell to die.

Systems using immunoglobulin transgenic mice which express light and heavy chains specific for model autoantigens have provided an approach to distinguish between these possibilities (Goodnow et al 1988; Nemazee and Buerki 1989a). In Nemazee's mice, which expressed an IgM which binds H-2K molecules of all haplotypes but d and f, the presence of the antigen led to deletion of all idiotype positive B cells (Nemazee and Buerki 1989a) and in bone-marrow chimeras, where the recipient expressed the antigen, all donor autoreactive B cells were deleted in the bone marrow (Nemazee and Buerki 1989b). This work indicates that autoreactive cells are deleted if they see autoantigen in the bone marrow, and that the B cells need not express the antigen themselves in order to be deleted.

Goodnow's experiments, however, provided evidence in favour of clonal silencing, not deletion (Goodnow et al 1988). Here mice that were transgenic for hen egg lysozyme, were crossed with mice, transgenic for rearranged light and heavy chains of a high affinity anti-lysozyme antibody. The double transgenic mice had mature peripheral B cells in a silenced state, which correlated with down-regulation of membrane IgM with no change in IgD (Basten et al 1989).

One explanation for this discrepancy might lie in the stage at which the B cells first see the autoantigen, so that deletion only occurs if the self-antigen is present in the bone marrow (Nemazee and Buerki 1989c). The tolerance sensitive stage of B cell development is believed to be that of a virgin B cell (Lawton and Cooper, 1974; Nossal 1983), whereas in the double transgenic model the B cells see the autoantigen in the periphery. An alternative explanation ascribes the discrepancy to the nature of the antigen (Basten et al 1989). It is argued that in the

H-2k model the antigen is a highly expressed integral membrane protein, whereas lysozyme is a monomeric soluble molecule, and that there may be physiological reasons for deleting high avidity self-reactive cells, but allowing lower avidity cells to persist in an anergic state. It seems, then, that both clonal deletion and clonal anergy play a part in the induction of B cell tolerance. Both mechanisms may also operate in the case of T cells, as though clonal deletion is well established to occur in the thymus, auto-reactive anergic T cells have been recently demonstrated to persist in the periphery (Rammensee et al 1989). The hypothesis that apoptosis induced by binding sIg is the mechanism of clonal deletion of auto-reactive B cells in the bone marrow remains untested, but has a precedent in the deletion of self-reactive T cells (see Chapter 5).

Apoptosis in germinal centres

Apoptosis of B cells has been demonstrated in germinal centres (MacLennan et al 1989) and this is believed to be the result of the production and selection of memory B cells in the follicles.

Memory B cell clones appear to be able to survive throughout the life of mice, rats and humans (Askonas et al 1970; Gray et al 1986; Jerne 1966). They can be transferred to syngeneic or congenic hosts, and will initiate an antibody response if antigen is administered (Askonas and Williamson 1972; Siekevitz et al 1987), but in the absence of antigen the transferred B cell memory can only last for about one month. It seems, then, that antigen is required for the survival of memory clones, and that as memory can last a lifetime, but the life-span of quiescent B cells is unlikely to be more than a month (Strober 1975, Lui et al 1988), there must be a proliferating pool of potential memory B cells.

MacLennan et al (1989) have suggested that B cell follicles are the most likely site for this B cell proliferation necessary to sustain memory B cell clones. They postulate that the high death rate in the germinal centres is associated with selection of sIg-expressing B cells on the basis of their affinity for antigen localised on the FDC. *In vitro* apoptosis of germinal centre B cells isolated from human tonsils can be prevented by cross-linking their sIg with antibodies (Lui et al 1990). These cells seem to conform to the NGF paradigm: at a particular stage in their development the withdrawal of a signal (antigen in this case) induces them to commit suicide.

Affinity maturation of the antibody response by hypermutation (Koch and Rajewsky 1988) is believed to occur in the germinal centres (MacLennan and Gray 1989), and so antigen-dependence at this stage may be a means of selection of cells expressing high-affinity antibodies. There seems, however, to be a problem with this theory, analogous to the problem posed by the need for both positive and negative selection of the T cell repertoire in the thymus. During affinity maturation autoreactive clones can be generated (Siekevitz et al 1987), and if the self-antigen is present in the follicles, these clones would presumably be positively selected. In fact, B cells of the germinal centres seem to be particularly sensitive to tolerance induction (Linton and Klinman 1989). Perhaps the two mechanisms of B cell tolerance induction demonstrated by the experiments with transgenic mice partly explain this conflict. Clonal anergy may play a more important role in B cell tolerance induction than in T cell tolerance induction because of the absence of somatic mutation in the generation of the T cell repertoire.

**CHAPTER TWO:
MATERIALS AND METHODS**

MATERIALS AND METHODS

Materials

Chemical reagents were purchased from Fisons laboratories or from British Drug House, unless otherwise stated. Restriction enzymes were purchased from Bethesda Research laboratories. Radioactive isotopes were obtained from Amersham.

Mice

The following strains were bred and supplied by the Imperial Cancer Research Fund (ICRF) Central Animal Breeding Facility at Clare Hall, South Mimms : BALB/c, CBA, AKR, and B10.BR mice and AO rats.

Media

Eagle's minimum essential medium buffered with 0.02 M HEPES (MEM-H) and Roswell Park Memorial Institute 1640 medium (RPMI) were supplied by ICRF, Lincoln's Inn Fields, London. Iscove's modified Dulbecco's medium (DMEM) (Gibco) supplemented with 0.03% sodium bicarbonate, 5×10^{-5} M 2-mercaptoethanol (2-ME), 100 U/ml penicillin-streptomycin (Gibco), 5ng/ml human transferrin, and 10% heat inactivated Foetal Calf Serum (FCS) was used for culture of thymocytes and cytotoxic T cell clones. All other tissue culture was carried out in RPMI. For growth of FDCP-2, A4 and Wehi-3b 5% Horse serum (HS) was added; for all other cell lines 10% FCS was added. Tissue culture was carried out in a 5% CO₂ incubator at 37°C.

Monoclonal antibodies (Mabs), tumours and cell lines

MAR-18, GK1.5, YTA 156, 2.43, Wehi-3b, MLA-144, CTLL and 2C11 were supplied by ATCC. FDCP-2 and A4 were a gift from Michael Dexter. P815

and CTL-P35.10 were a gift from Jacqueline Marvel. Directly conjugated Mabs against CD4, CD8 and Bromodeoxyuridine (Brd-U) were obtained from Becton Dickinson.

Protein A purification of antibodies (Mishell and Shiigi 1980)

1.5g Protein^A sepharose CL 4B (Pharmacia) was swollen in Tris-buffered saline, pH8.6, and the resin was packed into a column of bed volume of 5 ml. The culture supernatant of the hybridoma producing the antibody to be purified was harvested, by centrifugation, filtered, and adjusted to pH8.6 by addition of dilute NaOH. The culture supernatant was applied to the protein A column and the column washed with Tris-buffered saline, pH8.6. The hybrid cell antibody was eluted by step elution with buffered saline at pH7.0, 5.5, 4.3 and 2.3, avoiding low pH buffers where possible. Antibody elution was detected with a UV monitor. The fractions containing antibody were pooled and dialyzed using Tris-buffered saline, pH8.1. The column was regenerated by washing with the glycine-HCl-buffered saline, pH8.6 (0.02%azide) and stored at 4°C.

Buffers	pH8.6	0.05M Tris 0.15 M NaCl 0.02 % azide (to pH8.6 with 10 M HCl)
	pH7.0	0.05 M phosphate 0.15 M NaCl
	For 1 litre	4.34 g Na ₂ HPO ₄ 2.7 g NaH ₂ PO ₄ monohydrate 8.76 g NaCl
	pH5.5	0.05 M citrate 0.15 M NaCl
	For 1 litre	2.68 g citrate acid monohydrate 10.96 g trisodium citrate dihydrate 8.76 g NaCl
	pH4.3	0.05 M acetate 0.15 M NaCl (to pH 4.3 with acetic acid)

pH2.3 0.05 M glycine-hydrochloride
 0.15 M NaCl
For 1 litre 5.6 g glycine-HCl
 8.76 g NaCl
 (to pH2.3 with 10 M HCl)

Cell Culture

Unless otherwise stated methods were taken from "Selected Methods in Cellular Immunology" edited by Mishell and Shiigi (1980)

Storage of cell lines

Frozen stocks of cell lines were stored under liquid nitrogen in DMEM + 10% FCS + 10% dimethylsulphoxide at a density of 10^6 /ml in round bottomed cryotubes.

Cell suspensions, preparation and counting

Spleens, thymuses and lymph nodes were removed from animals which had been killed by cervical dislocation and cell suspensions were prepared by pulverising the organs through a tea sieve with a syringe barrel in MEM-H. Cells were then washed twice in MEM-H. Gey's treatment of cell suspensions to lyse erythrocytes (Gey and Gey 1936) was carried out by resuspending the cells at 10^8 per ml in MEM-H, with 3 ml Geys for every ml of MEM-H. After 5 min on ice, the cells were washed twice in MEM-H, and viability assessed by trypan blue exclusion.

Growth of CTL:P35:10

CTL:P35:10 was grown in DMEM, supplemented with 10% FCS, 1% glutamine, 1% penicillin/streptomycin, 1% sodium pyruvate, 1% non-essential amino acids, 5×10^{-5} M 2-ME and 30 % T cell growth factor. Cells were restimulated every 3-4 days. 10^5 ml⁻¹ CTL:P35:10 were cultured 5×10^6 ml⁻¹ syngeneic irradiated spleen feeders and 10^5 ml⁻¹ irradiated P815 cells. Spleen cells were irradiated with 2000 rads and P815 cells

were irradiated with 5000 rads. After irradiation cells were washed 2x with MEM-H.

Mixed Lymphocyte Reaction (MLR) for generation of CTL

BALB/c spleen cells were irradiated with 2000 rads and washed 2X with MEM-H. They were placed in 10 ml cultures with CBA spleen cells at a concentration of 10^6 of each cell type per ml for 5 days. The medium was RPMI supplemented with 50 μ M 2-ME, 2mM L-glutamine, 10mM HEPES and 5%FCS (tested previously for its ability to generate CTL).

Chromium release assay for cytotoxicity

Targets were labelled with ^{51}Cr (sodium chromate, Amersham) by incubating $2-10 \times 10^6$ cells with 100-200 μCi ^{51}Cr for 1 h at 37 $^{\circ}\text{C}$ in a total volume of 0.2-0.5 ml MEM-H + 5% FCS . Excess isotope was removed by washing 3x with MEM-H and the labelled targets were adjusted to a final concentration of $1-2 \times 10^5/\text{ml}$ in RPMI + 5% FCS. Graded numbers of effector cells in a total volume of 0.1 ml were mixed in round-bottomed microplates with a fixed number of ^{51}Cr labelled targets (5×10^3 or 10^4) to make a total volume of 0.2 ml. Plates were centrifuged at 500 rpm for 2 min and then incubated for 4 h at 37 $^{\circ}\text{C}$. After incubation 0.1 ml supernatants were removed and counted in a gamma counter (Wallace LKB 80000 gamma sample counter). Each target was assayed at a series of Effector:Target (E:T) ratios and each ratio was carried out in triplicate. Results are expressed as mean per cent specific ^{51}Cr release calculated to the following formula :

$$\% \text{ specific } ^{51}\text{Cr} \text{ release} = \frac{\text{Experimental release} - \text{spontaneous release}}{\text{Maximal release} - \text{spontaneous release}}$$

Spontaneous and maximal ^{51}Cr release were determined by incubating target cells alone or with detergent respectively. Standard errors of the mean of replicate samples were < 5% and spontaneous ^{51}Cr release was < 25%.

Metabolic labelling of cellular proteins

10^6 cells were washed twice with DMEM and resuspended in 1 ml methionine-free DMEM containing 25 μCi ^{35}S -methionine (Amersham).

Proliferation Assay (^3H -thymidine (^3H -TdR) incorporation)

5×10^3 - 5×10^5 cells in 0.2ml volumes in 96-well flat bottom plates were pulsed with 10 μl methyl ^3H thymidine (100 $\mu\text{Ci}/\text{ml}$) and incubated for 6 h at 37 $^{\circ}\text{C}$. The plates were harvested on a Dynatech Microtiter Automash cell harvester. The filter paper was dried and each piece emersed in 3 ml OptiScint scintillation fluid (LKB) and counted on a liquid scintillation counter (LKB Rackbeta 1214). Each assay point was carried out 10 times and the mean cpm calculated.

Fluorescent staining for flow cytometry

To 10^6 cells in 50 μl MEM-H +5% HS +0.1% sodium azide in round-bottomed 96-well plates was added 50 μl antibody, diluted in MEM-H +5% HS +0.1% azide, to achieve a final concentration of approximately 2 $\mu\text{g}/\text{well}$ (individual antibodies or culture supernatants were generally titrated before use). This was incubated for 45 min at 4 $^{\circ}\text{C}$ and washed 3x in MEM-H +5% HS +0.1% azide, by centrifugation of the plate (500g, 5 min) and flipping off the supernatant. In the case of directly conjugated antibodies, cells were resuspended in filtered PBS and analyzed on a flow cytometer (FACScan, Becton and Dickinson). Where a second antibody was required, this was added to the pellet of cells as

before, and the cells were again incubated at 4°C for 45 min, prior to washing and analyzing.

Cell cycle enrichment

In order to enrich for a population of cells at a particular point in the cell cycle, cells were separated according to size on a discontinuous percoll gradient. Osmolarity adjusted percoll was prepared by the addition of nine parts to one part (v/v) 1.5M NaCl. Percoll of densities ranging from 1.04g/ml to 1.08g/ml were prepared by mixture of this osmolarity adjusted percoll with 0.15 M saline in the following ratios:

Density	% osmolarity adjusted percoll
1.04	29
1.05	38
1.06	47
1.07	55
1.08	64

A discontinuous gradient was prepared by layering 2 ml of the different densities of percoll on top of each other in 15 ml Falcon tubes. The cells to be separated were layered on top in 1 ml MEM-H. The tube was centrifuged at 10000g for 20 min without brake. Bands of cells were sucked off with a glass pipette and washed 3x in MEM-H before analysis to assess their cell cycle status.

Cell cycle analysis

Assessment of cell cycle status was carried out by staining cells with Propidium Iodide (PI) and with an antibody to Brd-U, after pulsing with Brd-U. Brd-U is an analogue of thymidine and can be incorporated specifically into the DNA. Hence the antibody identifies those cells in S phase at the time of pulsing. PI is a stain which binds to DNA, and the intensity of staining can be used to distinguish between cells in G₁/G₀ and in G₂/M .

10^7 cells were suspended in appropriate tissue culture medium at 10^6 per ml and Brd-U was added to achieve a final concentration of 10mM. The cells were incubated for 20 min at 37°C, washed 2x in PBS and resuspended in 100 μ l of normal saline. This suspension was chilled on ice and to it was added 2 ml of cold 70% ethanol with vigorous mixing, and it was fixed at 0°C for 30 min. In order to denature the DNA, 2 ml 4N HCl was added and the cells were incubated at room temperature for 30 min. The cells were centrifuged at 500g for 5 min and resuspended in 1 ml 0.1M sodium borate, pH8.5, to neutralize the acid. Cells were aliquoted onto 96 well plates at 10^6 per well, centrifuged again (500g, 5 min) and the pellet resuspended in 50 μ l 0.5% Tween 20 in PBS. 5 μ l directly conjugated antiBrd-U-FITC were added and the suspension was underlayered with 50 μ l 10% (w/v) BSA in PBS and incubated for 45 min at 4°C. The cells were washed 2x in PBS +10% BSA and finally resuspended in 1 ml PBS containing 20 μ g PI, for Facs analysis.

DNA fragmentation Assay (Duke et al 1983)

Target cells (2×10^6) were labeled in 10 ml of medium in a 25cm² flask containing 200 μ Ci ³H-thymidine (or 25 μ Ci ¹²⁵I-uridine) for 24 h. The labelled target cells were washed once, incubated for 2 h at 37°C to chase out unincorporated nucleotides, and then washed twice more before use in the assay. Cells were then used either as targets in a CTL-killing assay, as described previously, or in measurement of the kinetics of death of growth factor dependent cell lines. After appropriate incubation, plates were spun gently (150 x g, 3min), and radiolabel was counted in the culture supernatant. To the residual pellet was added PBS containing 0.2% triton-X 100, this was transferred to eppendorf tubes, the volume made up to 1 ml with PBS + 0.2% triton-X 100, and centrifuged for 10 min at 1500g in the cold. This supernatant was then

counted. Total uptakes were determined by adding 1 ml PBS containing 0.2% triton-X 100 and 3 µg/ml of bovine pancreatic DNase 1 and incubating at 37° C for 1 h before processing as before. The percent ³H-TdR (or ¹²⁵I-UdR) release was calculated in the same way as percent ⁵¹Cr release.

Assessment of cell viability

Trypan blue exclusion

A 20 µl aliquot of cells was mixed with an equal volume of 0.2% (w/v) trypan blue in PBS and counted in a haemocytometer. Cells which failed to exclude trypan blue were scored as dead. In kinetic studies, where time allowed, 3-5 samples were taken at a given time-point and cell death was expressed as a mean percentage. Any time-points for which the standard deviation of the percentage of cells that were dead exceeded 10% of the mean percentage of dead cells were excluded from the study. Trypan blue was dissolved in PBS, filtered through a 0.4 µ filter and stored at room temperature with 0.1% sodium azide.

Propidium Iodide (PI) exclusion

The ability of cells to exclude the fluorescent DNA binding dye PI was used to score percentages of dead cells on the Facs. 5x10⁵ cells were pelleted and resuspended in 1ml PBS containing 20 µg PI and analysed on the Facs. Stock PI was made up in PBS at 2 mg/ml and stored in the dark at -20°C.

MTT assay

This is a colourimetric assay which is dependent on the ability of mitochondria to utilize a tetrazolium salt (Tada et al 1986). Only live cells are capable of taking up the MTT (3-(4,5-dimethylthiazol-2-yl)-

growth medium in Terasaki plates at concentrations ranging from less than 1 to >100 cells per well. One plate (60 wells) was set up at each concentration and left for 5 days before scoring for the number of wells containing at least one viable colony per well. Clonogenic potential was calculated by assuming it conforms to a Poisson distribution. The proportion of cells estimated to be capable of proliferating is estimated by plotting the negative natural log of the proportion of negative wells out of total wells plated, against cells plated per well. If the only limiting factor is the number of cells plated per well, then this plot will give a straight line. The clonogenic potential is estimated from the line, by finding the proportion of cells that would be plated when the $\ln(\text{negative}/\text{total}) = -1$ (Langhorne and Lindahl 1981).

Transmission Electron Microscopy

Fixation and Embedding

Cells were fixed in 2.5% glutaraldehyde, 0.12M cacodylate buffer, pH7.4, for 1 hour on ice, pelleted by centrifugation and the pellet embedded in low melting point agarose. This agar-embedded pellet was then fixed in 1% OsO₄, 0.12M cacodylate buffer for 90 min on ice, washed 5 times in distilled water and incubated overnight in 0.5% aqueous uranyl acetate at 4°C in the dark. Dehydration through an alcohol (EM grade ethanol 99.97% BDH chemicals Ltd) series (25%, 50%, 75%, 90%, 100%(w/v)) proceeded 10 min incubation in propylene oxide (PO), and 2 hour incubation in PO:resin, 1:1, while being mixed on a rotary mixer. The pellet was then placed in 100% resin on the rotary mixer overnight, and the resin was changed and mixed for a further 2 hours prior to pouring out into a plastic flat embedding tray and baking at 60 °C for 2 days.

Resin was Polarbed 812 low viscosity embedding media
(Polaron Equipment Ltd).

For blocks of medium hardness Polarbed 812 (resin) 21 ml
DoDecenyl succinic anhydride 11 ml
Nadic methyl anhydride 13 ml

These components were mixed and aliquoted into 6.4 ml portions which were stored at -20 °C and to which 0.1 ml of the reaction accelerator. Tri[dimethylaminomethyl]phenol was added directly before use.

Sectioning and staining

Resin blocks were allowed to age for a minimum of one week before being sectioned with a diamond knife (Du Pont [UK] Ltd) on an LKB ultra-microtome (LKB Ultratome III). Gold/silver sections (70-110nm) were collected on copper grids (3.05mm diameter, 300 mesh). Grids were stained for 35 min in saturated uranyl acetate (8%w/v in 50% v/v ethanol) and for 5 min in lead citrate stain (Reynolds 1963). Staining was achieved by floating grids, sections face down, on a small volume of the stain on a hydrophobic surface. The grids were washed for 5 min in 50% ethanol and for 5 min in distilled water between stains, and for 5 min in distilled water after lead citrate staining.

Lead citrate stain	lead nitrate 1.33g
	sodium citrate 1.76g
	dH ₂ O 30 ml
	1M NaOH 8 ml

The lead nitrate, sodium citrate, and water were shaken vigorously for 1 min and then allowed to stand for 30 min with intermittent shaking, to ensure complete conversion from lead nitrate to lead citrate. The NaOH was added and the suspension diluted with distilled

water to a final volume of 50 ml. The solution was mixed by inversion and stored at room temperature for up to 6 months; old solutions were centrifuged before use.

Viewing

Sections were viewed with a Jeol JEM-100CX II electron microscope.

Biochemistry

O⁶-methylguanine-DNA methyltransferase assay (Bogden 1981)

This assay measures the removal of a radioactive methyl group from O⁶-MeG by the enzyme in cellular extracts.

substrate: heated ³H-MNU treated M.luteus DNA
(Amersham)

Assay mix: 70mM Hepes KOH, pH7.8
10mM DTT
1mM EDTA
+ substrate to give counts between 1-2 x 10³
cpm/100μl

Extraction Buffer:
50mM Tris HCl, pH7.5
1mM EDTA
10mM DTT
0.2 % Triton X-100

Cell extracts (eg. 0, 5, 10, 20 μl up to about 150 μl protein) were added to 100 μl assay mix and incubated at 37^o C for 20 min. 10 μl heat denatured carrier DNA at 2 mg/ml and 120 μl 0.8M ice cold TCA were added and the solution was mixed and incubated for 5 min on ice. Samples were centrifuged for 10 min at 500 g. Supernatants were removed and counted on a β-counter. To each pellet was added 100 μl 0.1 M HCl and this was incubated at 70^o C for 30 min and on ice for 5 min. Samples were spun at 500 g for 10 min and 80 μl of the supernatant was counted. Activity of the enzyme was expressed as cpm removed by the enzyme, which was determined by subtraction of cpm in the presence of cell

extract from cpm with no extract present. This was plotted against μg protein in the extract. The protein concentration of each cell extract was determined in a Bradford protein assay. In each experiment extracts from cells known to have high activity of the enzyme, or no activity, were run as controls. A Raji tk⁺ cell line was used as positive control and a mutant of this cell line which has lost activity of O⁶ MeG DNA methyltransferase and has lost thymidine kinase expression (P. Karran, personal communication) was used as negative control, and is designated Raji tk⁻.

Bradford Protein Assay

Preparation of protein reagent: 100 mg of Coomassie Brilliant Blue G-250 (Eastman) was dissolved in 95% ethanol, to which was added 100 ml 85% (w/v) Orthophosphoric acid. The solution was made up to 1 litre with distilled water and was stored at 4°C in the dark. To 10 μl of cell extract was added 90 μl distilled water and 1 ml of protein reagent. This was vortexed and the absorbance was read at 595 nm on tungsten between 2 min and 1 h after addition of the protein reagent. A standard curve for the reagent to calibrate the assay was made on each day of use by reading absorbances when the assay was carried out with 0, 1, 2, 4, 8 and 10 μg BSA. The assay is only linear up to 10 μg protein.

Molecular Biology

Methods in this section were taken from Maniatis et al (1982) unless otherwise referenced.

Phenol extraction

UNC phenol	500g phenol ("Analar" grade)
	111ml 2M tris pH7.5
	114 ml dH ₂ O
	28 ml m-cresol
	1.1 ml 2-ME

The phenol was heated to 65 °C until melted and the other ingredients added. Phenol was then stored in a darkened bottle at room temperature. Solutions were phenol extracted by addition of an equal volume of UNC phenol, shaking in a poly-propylene tube, and centrifugation at 10000g, 20 °C, 10 min. The upper phase was taken and extracted with an equal volume of chloroform/isoamylalcohol [IAA] (24:1), centrifuged as before, and the upper phase taken.

Ethanol precipitation of nucleic acid

0.1 volumes of 3M NaOAc and 2 volumes of 99% ethanol were added to the sample, which was incubated on dry-ice for 20 min and centrifuged at 10000g, 4°C, 15 min. The pellet was washed once with 70% ethanol and allowed to air dry, and the nucleic acid was taken up into the appropriate buffer. Where small quantities of DNA/RNA were present 5 µg tRNA was added prior to the addition of the ethanol, to act as a carrier.

Plasmid preparation

Solution 1 100 mM tris pH7.0
 10 mM EDTA
 15% sucrose

Solution 2 0.1M NaOH
 1% SDS

Solution 3 3M sodium acetate
 2M acetic acid

TE-8 10mM tris (pH8)
 1mM EDTA

3ml bacteria cultures were grown overnight, 1.5 ml taken and the cells pelleted in eppendorf tubes. The cells were resuspended in 100 µl solution 1 and incubated at room temperature for 5 min. 200 µl

solution 2 was added, the tubes incubated on ice for 5 min, followed by addition of 150 μ l solution 3 and incubation on ice for a further 10 min. The solution was centrifuged for 10 min at 10000g, 4 °C, the supernatant taken and extracted once with phenol/chloroform and once with chloroform. The nucleic acid was ethanol precipitated and the pellet resuspended in TE-8 and stored at -20 °C.

Restriction digest of plasmid DNA

Restriction enzymes were used according to supplier's recommendations.

10X DNA digestion buffer	100mM Tris-HCl pH7.5 100mM MgCl ₂ 100 mM EDTA 10mM DTT
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NaCl was added to this basic digestion buffer to produce a range of buffers which contained 0mM, 50mM, 100mM, and 150mM NaCl at 1x dilution.

Preparation of RNA

Glassware was chromic acid washed and autoclaved before use.

Plastics were untouched by human hands and autoclaved.

Solution A	4M Guanidine thiocyanate 0.5%(w/v) N-lauroylsarcosine (Na salt) 25mM sodium citrate 100mM 2-ME Adjusted to pH7, filtered through 0.45 μ filter
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Solution B	5.7M Caesium chloride 25mM sodium acetate, pH5 0,2% diethyl pyrocarbonate Autoclaved and filtered through 0.45 μ filter
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3×10^7 cells were pelleted in Falcon tubes and frozen by pouring liquid nitrogen on to the pellet. 8ml Solution A was added to the frozen pellet which was homogenized immediately using a Polytron

probe. The solution was centrifuged for 10 min at 2500g to reduce foaming and loaded onto a cushion of 4 ml Solution B and centrifuged for 18 h at 32000g at 20 °C in a Europa 65 ultra-centrifuge. The supernatant was aspirated and the RNA pellet was air-dried before resuspension in DCP-treated water and ethanol precipitation. Final concentrations of RNA were estimated by reading optical densities at 260 and 280. RNA in aqueous solution was stored at -70 °C.

Poly(A) Selection of RNA (Chromatography on Oligo(dT)-cellulose)

TS buffer	10mM Tris-HCL, pH7.4 0.1% (w/v) SDS
NTS buffer	0.5M NaCl 10mM Tris-HCl, pH7.4 0.1% SDS

The column was prepared by plugging a disposable plastic syringe with siliconized glass wool and filling it with oligo(dT)-cellulose in TS buffer. TS buffer was washed through several times and then 0.1M NaOH was run through the matrix. The column was left to stand at room temperature for 30 min and the NaOH was washed away with NTS buffer. The column, now ready for use, was stored at 4 °C. For fractionation, total RNA was suspended in 5 ml NTS buffer and this solution was applied to the column and the flow-through buffer collected and reapplied to the column twice more. The bound RNA (PolyA⁺) was eluted with 5 ml TS buffer and was ethanol precipitated as described previously.

Electrophoresis of Nucleic acids

Running buffer	10x TAE	400mM tris 200mM NaOAC 100mM EDTA pH adjusted to 8.3
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Loading buffer	(10x)	0.1% solid orange G 20% ficoll 10mM EDTA 9.5x TAE
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DNA was electrophoresed through 1% agarose gels in horizontal submarine gel systems supplied by Pharmacia. Agarose was melted in 1X TAE. Gels were stained with ethidium bromide (5 µg/ml in 1X TAE) for 5 min and the nucleic acid visualized on a u.v. transilluminator (u.v. Products Ltd).

RNA gels (For Northern Blotting)

Running buffer	10X MOPS	0.2 M morpholinopropane-sulfonic acid 50mM sodium acetate 5mM EDTA pH adjusted to 7.5
	Sample buffer	50% formamide (de-ionized) 18% formaldehyde (12.3M) 10% 10x MOPS 22% H ₂ O
	Loading buffer	50% glycerol 1mM EDTA 0.4% bromophenol blue 0.4% xylene cyanol
Gel preparation (per 100 ml)		1g agarose 10 ml 10X MOPS 72 ml dH ₂ O 18 ml formaldehyde (2.2M)

RNA gels were electrophoresed through 1% agarose gels in horizontal submarine gel systems. Agarose was melted in water and 10x MOPS and this was cooled to 50 °C before addition of formaldehyde and pouring of the gel. Aqueous RNA solutions were incubated at 65 °C in 5x volume of sample buffer for 3 min prior to loading in 1x loading buffer. Gels were run at 21mV and running buffer (1x MOPS) was recirculated with a peristaltic pump.

Transfer of RNA

Gels were blotted on to Nylon membranes (Genescreen-Plus). The membrane was soaked in 10x SSC for 30 min and then placed on the gel and any air bubbles trapped between the gel and the membrane were removed. A stack of Whatman 3MM paper soaked in 10x SSC was placed above the gel and a stack of dry 3MM paper was placed below the gel. This was sandwiched between two glass plates, wrapped in cling-film and left for 12 h with a weight on top of it. After transfer the membrane was baked for 2 hours at 80 °C.

20x SSC	per litre	175.3g NaCl
		88.2g sodium citrate
		Adjusted to pH7 with Na OH

Hybridization of Northern blot

Hybridization buffer	50% deionized formamide
	5% 100x Denhardt's
	30% 20x SSC
	1mM EDTA
	1% SDS
	0.01% salmon sperm DNA
	2% H ₂ O
	10% Dextran sulphate

100x Denhardt's	2% (w/v) ficoll
	2% (w/v)
	polyvinylpyrrolidone
	2% (w/v) BSA

Blots were pre-hybridized in a plastic bag at 45 °C for 2 h before addition of the radio-labelled probe. Hybridization was carried out at 45 °C for 12 h in a shaking water bath. The blot was washed at an appropriate stringency (ie. salt concentration and temperature) and exposed to pre-flashed X-OMAT AR diagnostic film (Kodak) at -70 °C.

Preparation of probes

Plasmid DNA was digested with appropriate restriction enzymes and the desired fragment was gel isolated and the DNA extracted from the

labelled with an oligo-labelling kit supplied by Pharmacia, using [α^{32} -P]dCTP (Amersham). Unincorporated nucleotides were separated on a Sephadex G-50 NICK column supplied by Pharmacia. Probes were boiled for 5 min and held on ice for 5 min before addition to separate the strands of DNA.

Bacteriological Methods (Hanahan 1985)

Bacteriological Strains

For general cloning and sub-cloning of recombinant plasmids E. coli strains LE392 and DH5 were used.

Growth Media and Agar Plates

All specialized media components were obtained from Difco Laboratories Ltd, Michigan.

LB medium per litre:	10g bacto-tryptone 5g yeast extract 10g NaCl
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2X agar per litre:	30g bacto-agar
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2x LB per litre:	20g bacto-tryptone 10g yeast extract 20g NaCl
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These solutions were sterilized by autoclaving and stored at room temperature.

1000x ampicillin	40 mg/ml ampicillin
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This solution was sterilized by filtration through a 0.22 μ filter (Millipore Corp.) and stored in aliquots at -20 °C. All strains of E. coli used were grown in LB medium at 37 °C with constant shaking of the culture. Where appropriate the medium was supplemented with ampicillin at a concentration of 40 μ g/ml. Agar plates were prepared

by combining equal volumes of 2x LB solution with 2x agar solution, while heating until the agar had melted. The solution was autoclaved and under sterile conditions was poured onto 10cm diameter petri dishes (Falcon) and allowed to cool until solid. When plates were supplemented with 40 µg/ml ampicillin, the LB/agar solution was cooled to below 55 °C before the ampicillin was added. Plates were stored at 4 °C and were air dried at 37 °C for 1 h prior to use, to remove surface liquid.

Preparation of Competent Bacteria

Tfb I 30mM potassium acetate
 100mM rubidium chloride
 10mM calcium chloride
 50 mM manganese chloride
 15% glycerol (v/v)
Adjusted to pH5.8 with 0.2M acetic acid

Tfb II 10mM MOPS
 75mM calcium chloride
 10mM rubidium chloride
 15% glycerol (v/v)
Adjusted to pH6.5 with KOH

Both solutions were filter sterilized and stored at -20 °C. 200ml of LB medium was inoculated with 50 µl of an overnight culture of DH5 cells and the culture was shaken at 37°C until the O.D._{550nm} was between 0.2-0.4. The cells were chilled on ice for 5 min and pelleted at 6000 rpm at 4 °C for 5 min. The bacteria were resuspended in 40 ml of ice-cold Tfb I by gentle vortexing and placed on ice for 5 min. The bacteria were then repelleted, resuspended in 5 ml Tfb II and placed on ice for 15 min. Aliquots (200 µl) were placed into round bottom screw-cap cryotubes (NUNC) on ice and then snap-frozen in liquid nitrogen and stored at -70 °C.

Transformation of Bacteria with Plasmid DNA

DNA was added to competent cells at less than 100ng DNA per 100 μ l cell suspension and incubated on ice for 10 min, followed by a 5 min heat-shock at 37 °C. The cells were transferred to 3 ml LB (no antibiotics), incubated at 37 °C for 15 min, pelleted and resuspended in 100 μ l LB. This was then spread onto LB-agar plates (supplemented with antibiotics if appropriate) and incubated at 37 °C overnight. Colonies were picked into 3 ml liquid cultures with sterile gilson tips.

Long-term Storage of Recombinant Bacteria

Long-term stocks of bacterial strains and bacteria hosting recombinant plasmids were produced by adding 15% glycerol to overnight bacterial cultures and storing these at -20°C. Bacteria were recovered by inoculating 3 ml cultures with 10 μ l of glycerol stock and growing the culture overnight at 37°C with constant agitation.

**CHAPTER THREE:
DEATH OF GROWTH FACTOR-DEPENDENT CELL LINES**

INTRODUCTION

The aim of this work was to establish an *in vitro* model system in which cell death was readily inducible in order to study the mechanism of apoptosis. Previous studies had frequently used glucocorticoid-mediated lysis of thymocytes or thymomas (Wyllie 1980, Wyllie et al 1984, Cohen and Duke 1984), but these systems seem inappropriate to assess the question of whether or not apoptosis requires protein synthesis, as glucocorticoids act by turning on new gene expression (Yamamoto 1985). IL2- and IL3-dependent cell lines are used in bioassays to measure lymphokine production because they rapidly cease to proliferate and die in the absence of their growth factor (Gillis et al 1978). I have used these cells to try to answer the following questions: (1) Do these cells die by apoptosis (as defined morphologically) on withdrawal of their growth factors? (2) Is cell death an active process? (3) What is the mechanism of death?

The cell lines used in this study were the IL2-dependent T cell line CTLL (Gillis and Smith 1977) and the IL3-dependent cell lines FDCP-2 and A4 (Dexter et al 1980). CTLL is a murine CD8⁺ T cell line which dies rapidly when deprived of IL2. FDCP-2 and A4 are murine cell lines, derived from long term bone-marrow cultures. Early isolates of the latter cell lines had many properties of haemopoietic progenitor cells, and were able to form spleen colonies in irradiated mice. Although these properties were lost in long-term culture, these cell lines have retained their ability to differentiate in response to haemopoietic growth factors and to self-renew in the presence of IL3 (Sponcer et al 1986). Thus these cells provide a model for the study of the mechanism of action of IL3, and the control of self-renewal. It has been shown that FDCP-2 cells die rapidly on removal of IL3 and that their death can be

delayed by addition of ATP to the tissue culture medium (Whetton and Dexter 1983). Here, I show that this cell death falls into the category of apoptosis and seems to be an active process that depends on DNA fragmentation.

RESULTS

All experiments were carried out on the three growth factor dependent cell lines. Except for discrepancies in the results between the different cell lines, however, I shall show data for FDCP-2 cells only.

Kinetics of Death

All three growth factor dependent cell lines examined died rapidly and asynchronously on removal of their respective growth factors. All FDCP-2 cells died within 35 h of IL3 removal, all CTLL cells died within 35 h after IL2 removal, and A4 cells died more rapidly, within 24 h of IL3 deprivation. The disintegration of the plasma membrane is a late event in death by apoptosis (Duvall and Wyllie 1986) and in some instances even apoptotic bodies have been shown to exclude dye (Sheridan et al 1981, Wyllie 1981). For this reason, I measured the ability of IL-3 dependent cells to form clones on re-exposure to IL3. In the case of FDCP-2 cells loss of clonogenic potential on re-exposure to IL3, as assessed by limiting dilution cloning, preceded loss of ability to exclude dye (Fig. 1a). For CTLL cells the kinetics of loss of ability to exclude dye and of clonogenic potential did not differ appreciably (Fig. 1b).

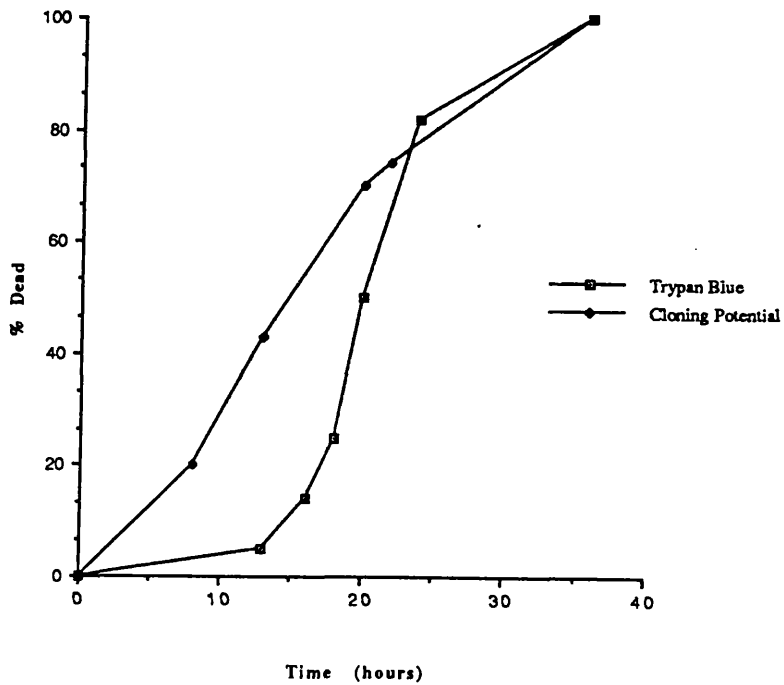


Fig. 1a

Time course of death of FDCP-2 cells on IL3 removal, measured by trypan blue exclusion and clonogenic potential. Clonogenic potential was determined by limiting dilution cloning in Terasaki plates, on readdition of IL3, and was estimated from a best fit line of a plot of cells per well against $\ln(\text{negative}/\text{total wells plated})$. Each point of trypan blue exclusion curve is a mean of 5, with $\sigma_n < 10\%$ of mean.

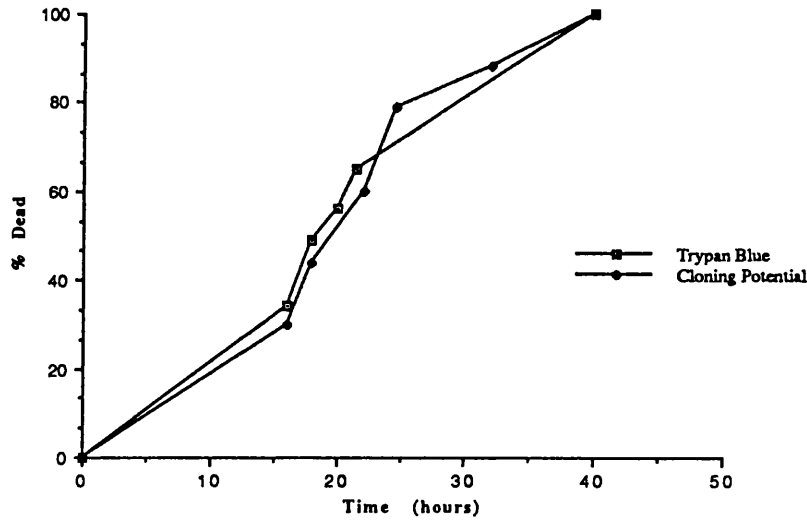


Fig. 1b

Time course of death of CTLL cells on IL2 removal, measured by trypan blue exclusion and clonogenic potential. Clonogenic potential was determined by limiting dilution cloning in Terasaki plates, on readdition of IL3, and was estimated from a best fit line of a plot of cells per well against $\ln(\text{negative}/\text{total wells plated})$. Each point of trypan blue exclusion curve is a mean of 5, with $\sigma_n < 10\%$ of mean.

Electron Microscopy





Only electron micrographs of experiments performed with FDCP-2 cells are shown.

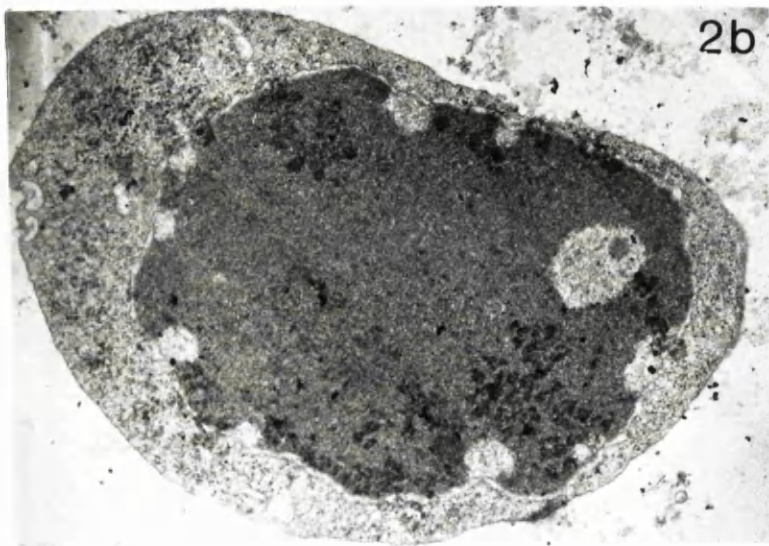
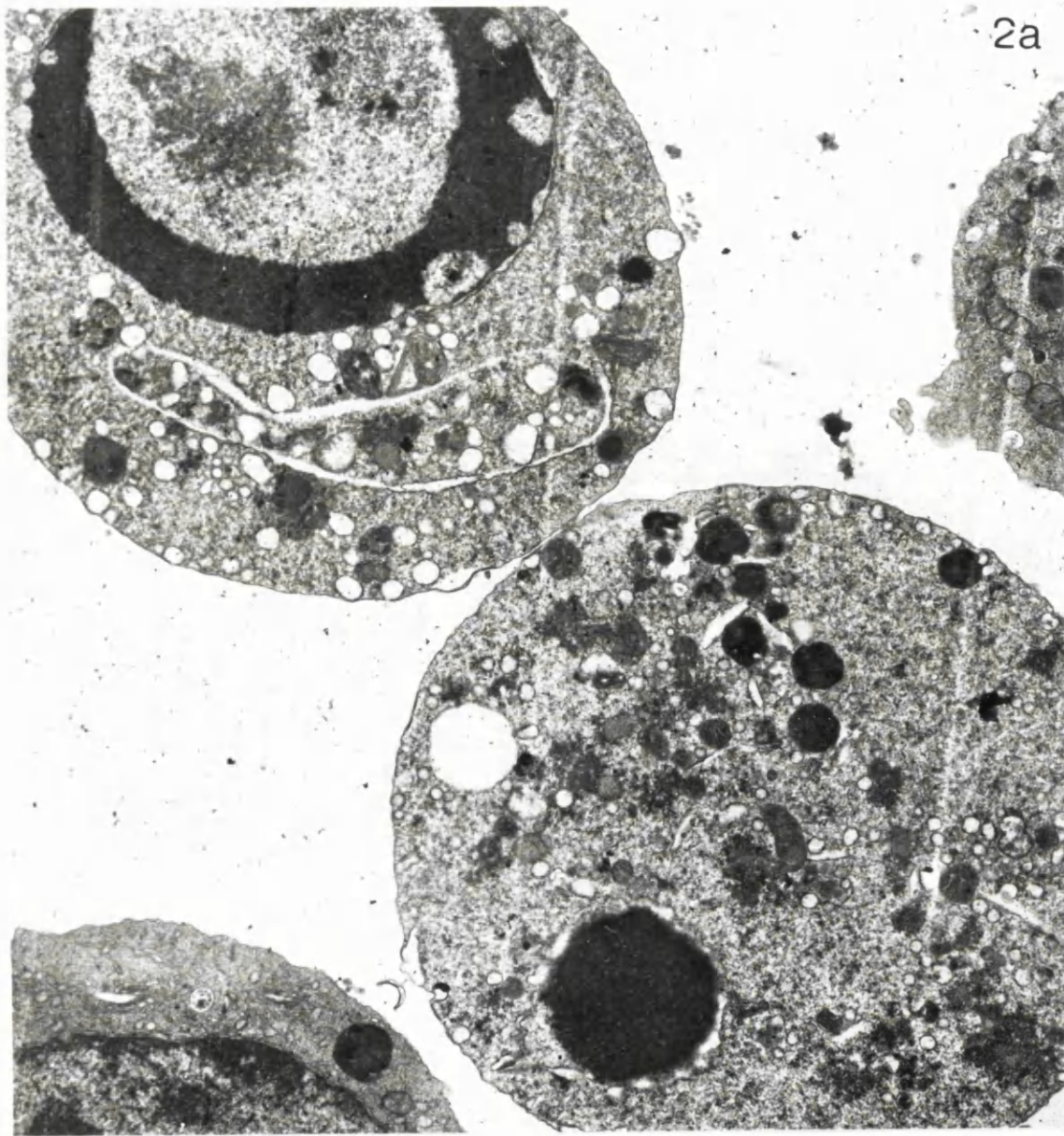
Electron micrographs of FDCP-2 cells 20 h after removal of IL3 indicate that the cells died by apoptosis. The morphology of apoptosis (reviewed by Wyllie et al 1986) is characterized by nuclear condensation and margination of the chromatin to form dense masses that abut on the nuclear membrane, such as is seen in Fig. 2a, in which the chromatin of one FDCP-2 cell has formed a crescent shaped aggregate lining the nuclear membrane. The integrity of organelles is initially maintained. A later event is the break up of the cell into membrane-bound "apoptotic bodies", often containing nuclear fragments, as can be seen in Fig. 2b. In some planes of sections the nucleus may appear uniformly dense (Kerr et al 1987), as in Fig. 2c. In Fig. 2d blebbing can be seen in the nuclear membrane. Only a proportion of cells at a given time-point after IL3 withdrawal displayed apoptotic morphology, but this is explicable by the fact that the cells died asynchronously (Fig 1a). That the nuclear condensation was not an artifact of fixation is shown in Fig. 2e, which shows an FDCP-2 cell which had been maintained in IL3, and in Fig. 2f, which shows an FDCP-2 cell which had been incubated with complement and an antibody to CD45 (Dennert et al 1980), and hence is dying by necrosis. The nucleus of this cell was unchanged but the plasma membrane was disintegrating.

Fig.2

Fig. 2a-d Electron micrographs of FDCP-2 cells 20 h after removal of IL3.

Scale

Fig. 2a:		1μ
Fig. 2b		1μ
Fig. 2c		1μ
Fig. 2d		1μ



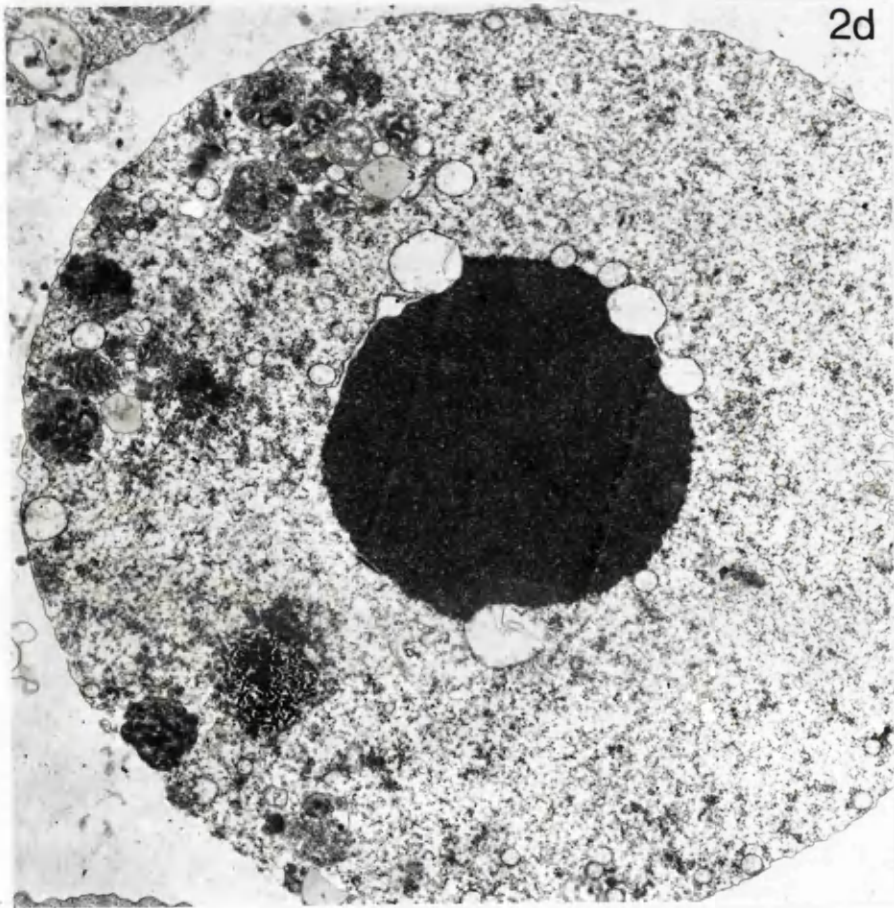
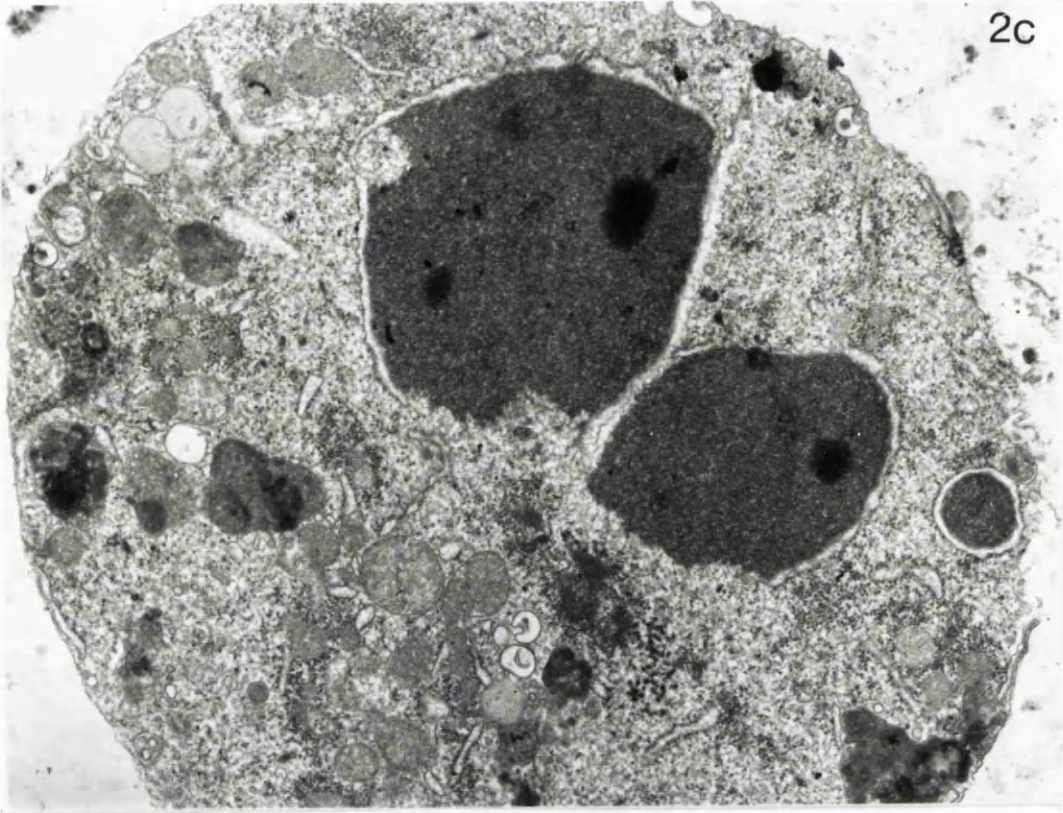


Fig.2

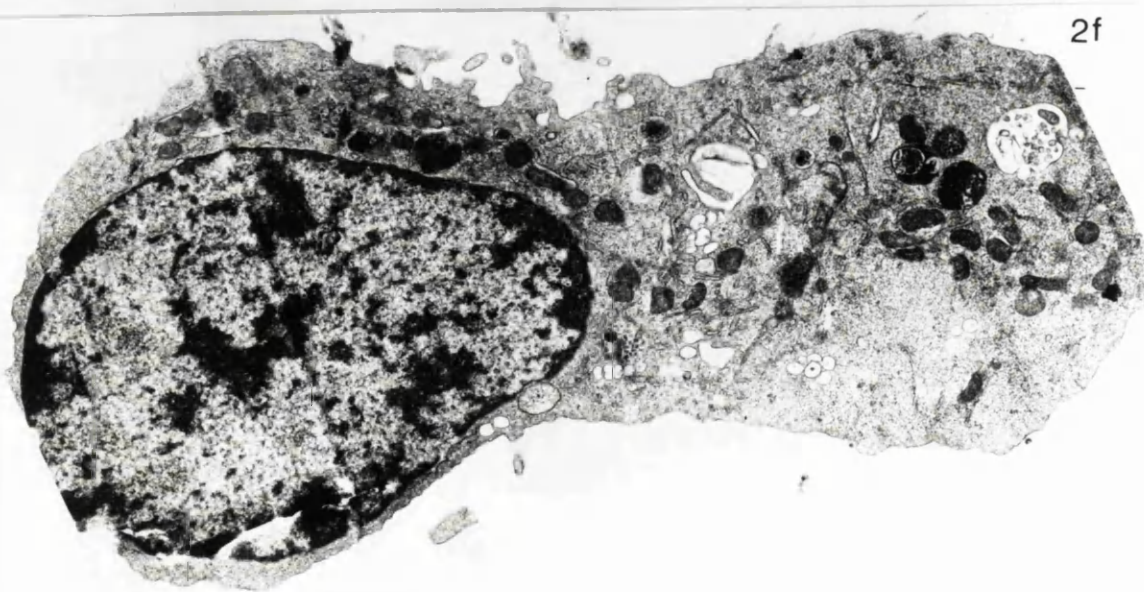
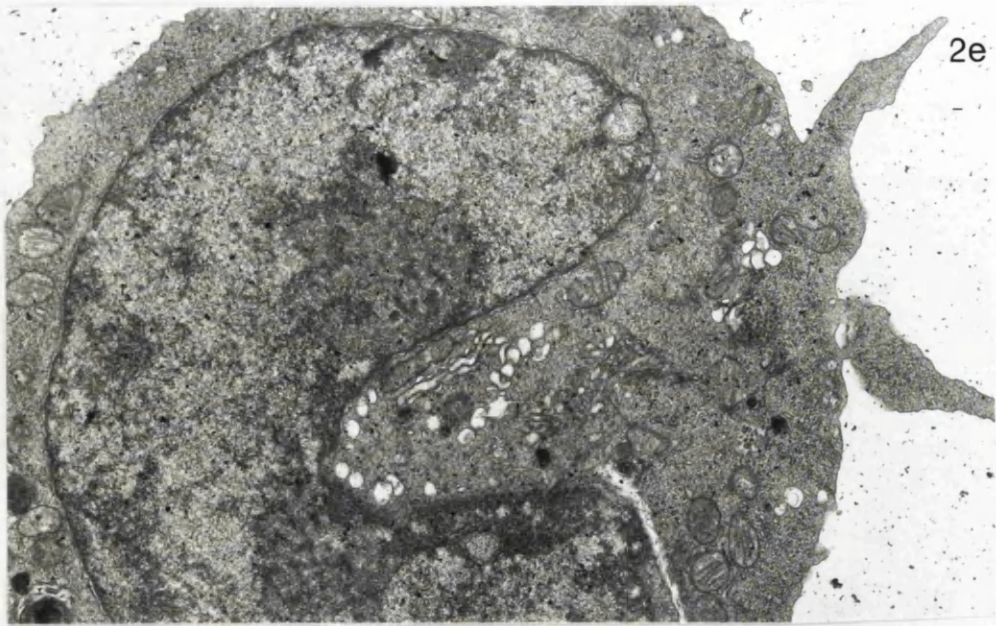
Fig. 2e Electron micrographs of a viable FDCP-2 cell cultured in the presence of IL3.

Fig. 2f Electron micrograph of an FDCP-2 cell that is dying by necrosis due to antibody and complement treatment. The cell was incubated on ice with mab M1-89 (anti-CD45) for 1 h, followed by 20 min at 37°C with complement, prior to fixation.

Scale

Fig. 2e:  1μ

Fig. 2f  1μ



DNA Fragmentation

After incubation of FDCP-2 cells for 18 h without IL3, the DNA had fragmented, so that a typical "ladder" was seen when the DNA was run on an agarose gel (Fig. 3a, tracks c and d). The DNA was cleaved into fragments of multiples of about 200 base pairs, presumably as a result of preferential digestion of internucleosomal DNA by an endonuclease. DNA prepared from cells maintained in IL3 was not fragmented (Fig. 3b, tracks a and b). A ladder was also observed when DNA was prepared from CTLL cells deprived of IL2 for 18 h, and A4 cells deprived of IL3 for 18 h.

When isolated nuclei were prepared from FDCP-2 cells maintained in IL3 and exposed to high concentrations of Ca^{2+} and Mg^{2+} for 2 h internucleosomal DNA cleavage was activated (Fig. 3b, tracks c and d). The DNA of isolated nuclei incubated for 2 h in 2 mM EGTA (to chelate Mg^{2+} and Ca^{2+}) was not fragmented (Fig. 3b, tracks a and b).

The kinetics of DNA fragmentation, as quantified by release of ^3H -thymidine from pre-labelled cells, adapted from the method of Duke et al (1983) (see Materials and Methods), corresponded closely to the kinetics of death. This is shown for A4 cells in Fig. 3c. The shape of the curves suggests that both the loss of ability to exclude dye and the release of radiolabel were normally distributed, and this suggests that in the case of an individual cell DNA cleavage is a fairly fast event after initiation of death. The background ^3H -thymidine release when A4 cells are kept in IL3 is quite low, but nevertheless prohibits the inference that DNA cleavage is occurring before loss of plasma membrane integrity.

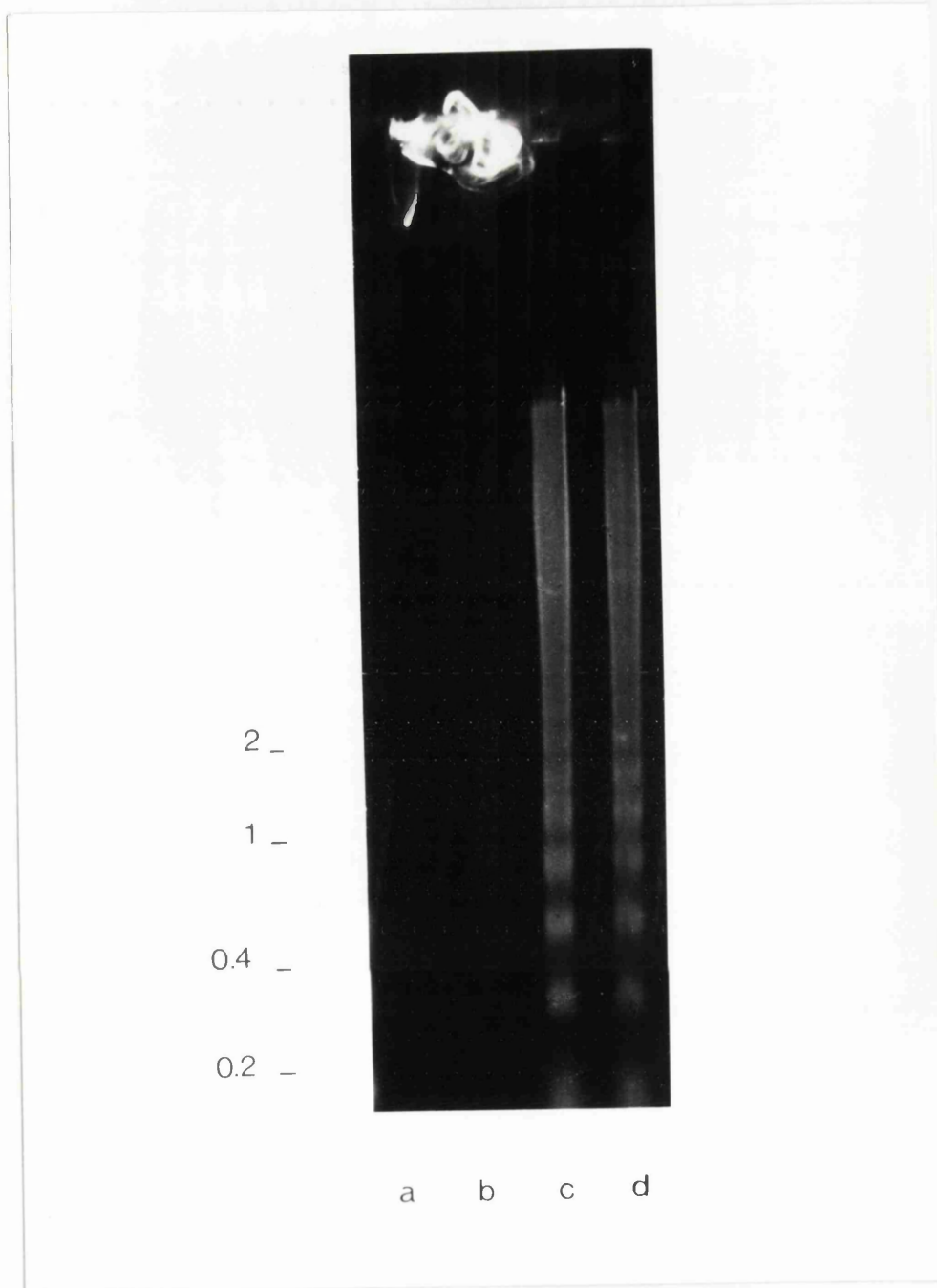


Fig. 3

Fig. 3a Ethidium bromide stained 1% agarose gel showing DNA prepared from FDCP-2 cells grown with IL3 (tracks a and b) and from FDCP-2 deprived of IL3 for 18 h (tracks c and d). Size is given in kilobases.

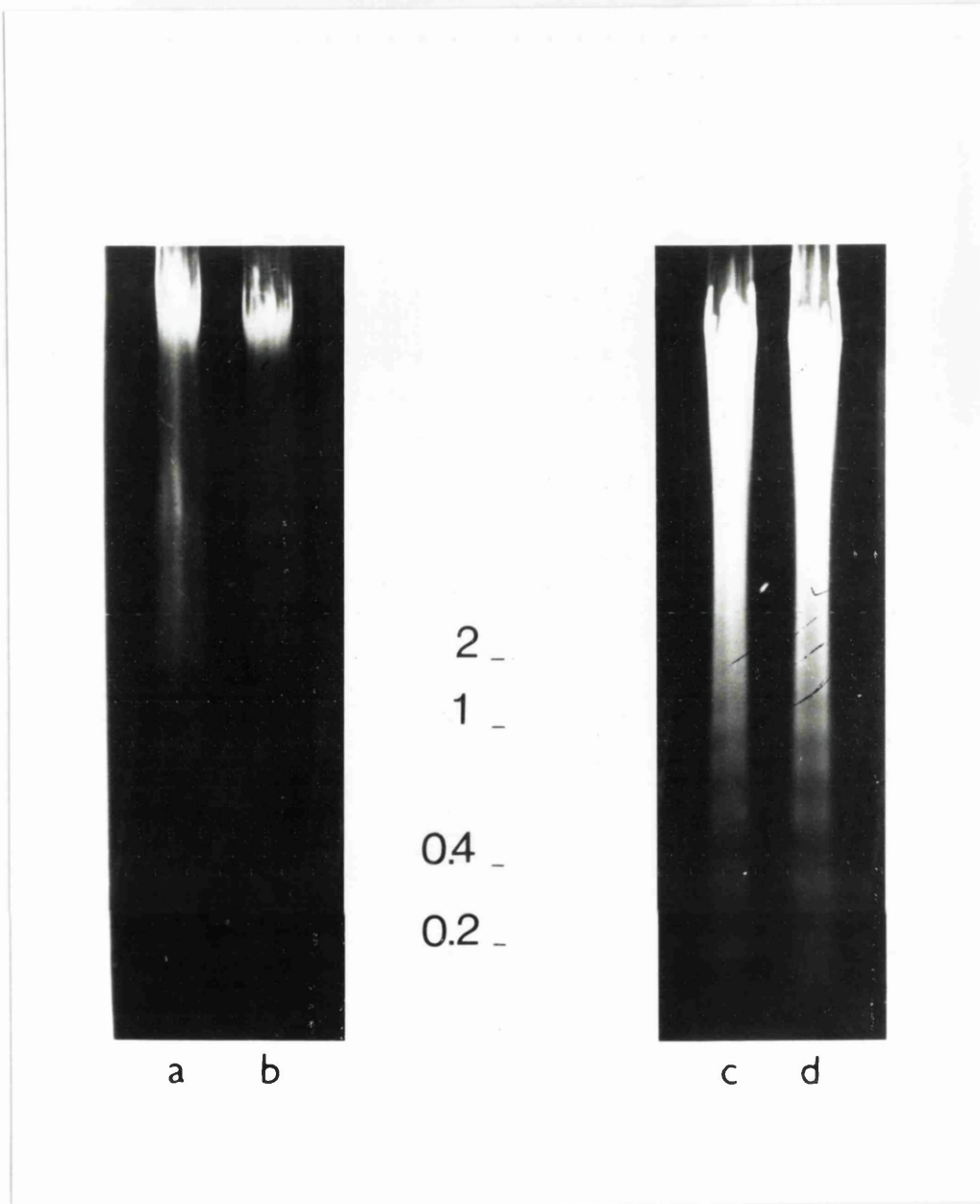


Fig. 3

Fig. 3b Ethidium bromide stained 1% agarose gel showing DNA prepared from isolated nuclei of FDCP-2 cells which were incubated in 1 mM Ca^{2+} and 1 mM Mg^{2+} for 2 h (tracks c and d), and isolated nuclei of FDCP-2 cells incubated in 2 mM EGTA for 2 h (tracks a and b). Size is given in kilobases.

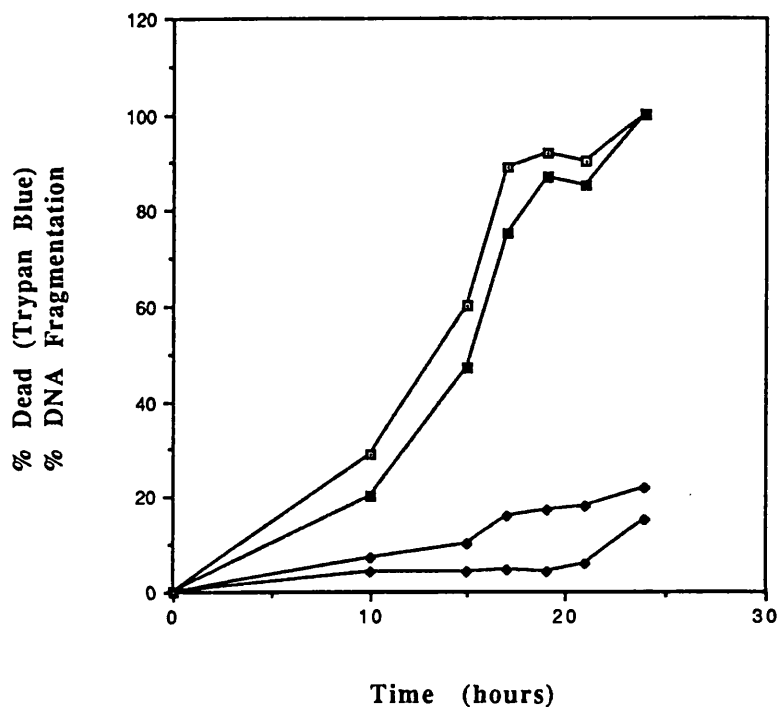


Fig. 3c

Fig. 3

Fig. 3c shows the kinetics of DNA fragmentation and cell death of A4 cells, on IL3 removal. DNA fragmentation was determined by measuring the release of ^3H -thymidine from pre-labelled cells, and is expressed as a percentage of total radiolabel present. Each point is a mean of 6, with $\sigma_n < 10\%$ of the mean. Death was measured by loss of ability to exclude trypan blue. Each point is a mean of 5, with $\sigma_n < 7\%$ of mean.

- % DNA fragmentation - IL3
- % DNA fragmentation + IL3
- % Dead (trypan blue) - IL3
- ◆— % Dead (trypan blue) + IL3

Effect of aurintricarboxylic acid

In order to ask if DNA fragmentation is causal in the death of FDCP-2 cells deprived of IL3, I tested the ability of the nuclease inhibitor aurintricarboxylic acid (ATC) (Hallick et al 1977) to increase viability. As loss of clonogenic potential of FDCP-2 cells preceded loss of ability to exclude dye (Fig. 1a), and loss of plasma membrane integrity is generally a late event in apoptosis (Duvall and Wyllie 1986), alternative measures of viability to dye exclusion were employed. ATC caused a clear dose-dependent increase in viability, as measured by MTT uptake and breakdown (see Materials and Methods) (Fig. 4a-c). In addition, as an alternative assay, I measured the ability of IL3-dependent cells to be stimulated to incorporate ^3H -thymidine on re-exposure to IL3. ATC greatly increased cell survival when this ^3H -thymidine assay was used (Fig. 5). Fig. 4d shows that ATC did not inhibit protein synthesis, as assessed by ^{35}S -methionine incorporation.

Effect of cycloheximide

Apoptosis has been shown in several instances to depend on protein synthesis (Duke and Cohen 1986, Shi et al 1989, Pratt and Greene 1976). As shown in Fig. 6a, cycloheximide prolonged survival of FDCP-2 cells on removal of IL3 over a 32 h period, when cell viability was determined by dye exclusion. That cycloheximide at these concentrations was inhibiting protein synthesis was shown by its inhibition of ^{35}S -methionine incorporation (Fig. 6b). As an alternative measure of viability, the ^3H -thymidine incorporation assay was used. As shown in Fig. 7, cycloheximide increased the proportion of cells able to incorporate ^3H -thymidine on being returned to IL3 after 24 h in its absence. When added at the start of the experiment, cycloheximide (at 0.5 $\mu\text{g}/\text{ml}$ and 0.25 $\mu\text{g}/\text{ml}$) enhanced the response (Fig. 7a), although the

response was much less than that of cells which were exposed to IL3 throughout the experiment (Fig. 7b). Another protein synthesis inhibitor, emitine, had the same effect, and enhanced survival of a small proportion of cells. Both cycloheximide and emitine also increased survival of CTLL and A4 on growth factor deprivation.

Cell Cycle Analysis

To ask if the time it takes a cell to die depends on which point it was at in the cell cycle when its growth factor was removed, cells were synchronized and the kinetics of death in synchronized vs unsynchronized populations of cells was compared. As DNA degradation may be causal in cell death, it seemed inappropriate to use agents that inhibit DNA handling enzymes, such as hydroxyurea (Sinclair 1967), to synchronize cells, and so cells were synchronized by separating the cells by size, and culturing cells of uniform size. That size is an appropriate parameter by which to synchronize FDCP-2 cells is shown in Fig. 8. FDCP-2 cells were incubated with BrdU and then permeabilized and stained with α BrdU (Fluorescence (FL) 1) and with PI (FL 2). Using "paint a gate" soft-ware (Becton Dickinson), cells which stain brightly with PI, and so have more DNA and are in G_2 , can be seen to be larger (painted blue) and comprise 36% of total (Fig. 8a). ^{See arrow} When this staining was carried out after 4 h incubation with 1.25 mM hydroxyurea, a drug which blocks progression from G_1 to G_2 by preventing DNA synthesis through inhibition of ribonucleotide reductase, the volume profile, as assessed by fluorescence side scatter (FSC) becomes clearly bimodal, ^(see arrow) with only 17.6% of cells in G_2 (Fig. 8b).

FDCP-2 cells were separated according to density (volume) on a discontinuous percoll gradient, and FSC, as an estimate of size, was measured by flow cytometry (Fig. 9a). The proportion of cells in each

fraction in G₁ or G₂ was determined by PI staining (Fig. 9b). Each fraction was washed to remove IL3, cultured in the absence of IL3 and cell death was measured by PI exclusion after various times. Fig. 9c shows that there was no difference in the kinetics of death between the different fractions. This experiment was carried out in 5% HS, but as serum contains many factors and hormones, the experiment was repeated in serum-free medium (Iscoe and Melchers 1985) and again no difference in kinetics was observed, except that all cells died slightly more rapidly and after 24 h viability was reduced by approximately 10 % in the controls that were kept with IL3.

It therefore seems unlikely that death is initiated at the putative "restriction point" (R) in G₁ (Pardee 1974). However, it has been suggested that some cells, such as activated B cells, have more than one restriction point (Melchers et al 1985). If FDCP-2 cells had more than one restriction point that required IL3 (or another factor contained in Wehi-3b supernatant) to pass through, then death might be initiated at two restriction points, and hence be cell cycle-dependent, without these experiments being able to detect it. Agents which arrest cells in cycle would theoretically increase the proportion of cells able to recover on re-exposure to growth factor by preventing a proportion of cells from reaching the restriction point(s). Neither hydroxyurea (Fig. 10a) nor aphidicolin, a competitive inhibitor of DNA-polymerase- α (Spadari et al 1982), (Fig. 10c) increased the ability of FDCP-2 cells to be stimulated by re-exposure to IL3. That hydroxyurea and aphidicolin were non-toxic at the concentrations employed is shown in Fig. 10b and Fig. 10d respectively. That hydroxyurea was an effective cell-cycle block for FDCP-2 cells is seen in Fig. 8b. That aphidicolin arrested FDCP-2 cells at 0.015 mM is shown in Fig. 10e.

A final objection to the conclusion that apoptosis is not initiated at the cell cycle restriction point is that commitment to death might take place at R, but that thereafter the cells might take a varying amount of time to die, as defined by dye exclusion. To exclude this objection one would need to perform limiting dilution cloning of synchronized and unsynchronized populations over a time-course after IL3 removal. This experiment seemed impracticable, but as the kinetics of ^3H -thymidine release from pre-labelled cells suggested that the release approximates to a binomial distribution for individual cells (Fig. 3c) and as DNA fragmentation seemed to cause death (Fig. 6), the kinetics of ^3H -thymidine release from pre-labelled synchronized cells was compared. A4 cells were used in this experiment because they died more quickly and so background release was reduced. Fig. 11 shows that there was no difference in the kinetics of DNA fragmentation between the synchronized populations. The possibility that cells take the same interval of time to die once the mechanism of death is initiated but that there is an interval between commitment to death at R and initiation of the mechanism of death, dependent on a stochastic event, is not excluded. A precedent for this suggestion is the control of proliferation, in which after commitment at R there is variability in the time before DNA synthesis is initiated (Zetterberg and Larsson 1985), consistent with a transition probability event (Brooks 1985).

DNA Repair

The activity of the DNA repair enzyme, O^6 methylguanine-DNA methyltransferase was measured in cells deprived of growth factor, using a specific assay for this enzyme (Bodgen et al 1981). Fig. 12 shows that there was no increase in the activity of this enzyme relative to total

cellular protein content in FDCP-2 cells and in CTLL cells on interleukin withdrawal.

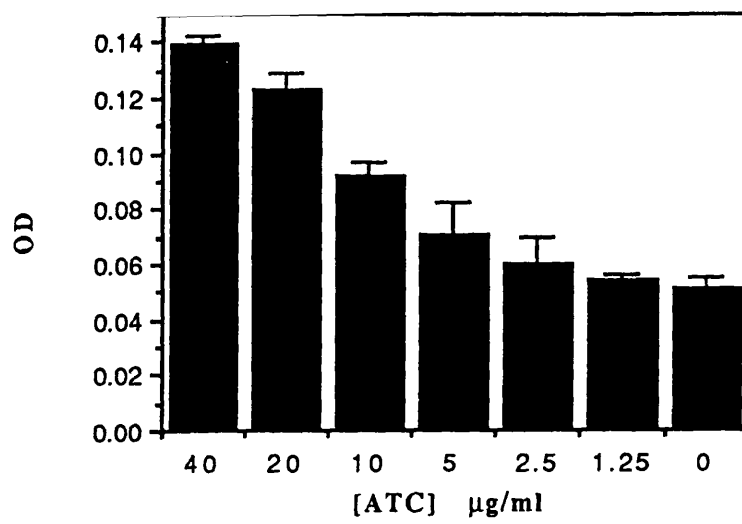


Fig. 4a

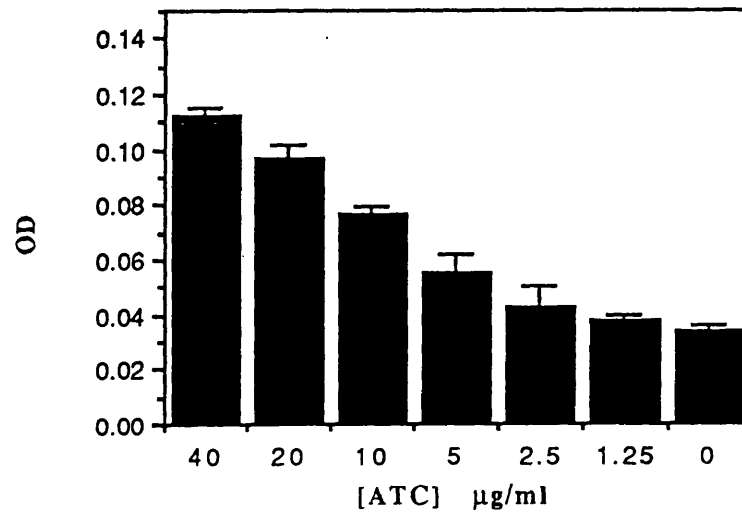


Fig. 4b

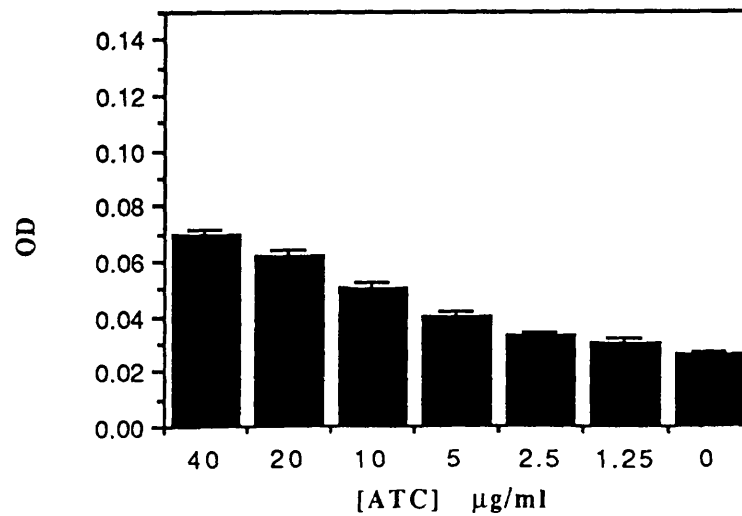


Fig. 4c

Fig. 4

Viability of FDCP-2 cells, measured by their ability to breakdown MTT, when incubated with ATC, after 16(Fig. 4a), 22(Fig. 4b) and 41(Fig. 4c) h of IL3 deprivation. In this and all further figures, bars represent standard deviations. [O.D. of FDCP-2 + IL3 = 0.17]

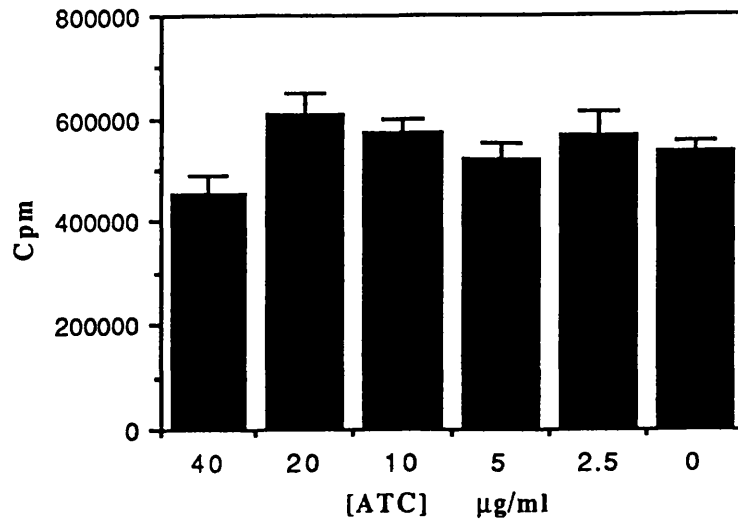


Fig. 4d

Fig. 4d
Incorporation of ^{35}S -methionine by FDCP-2 cells in presence of ATC.

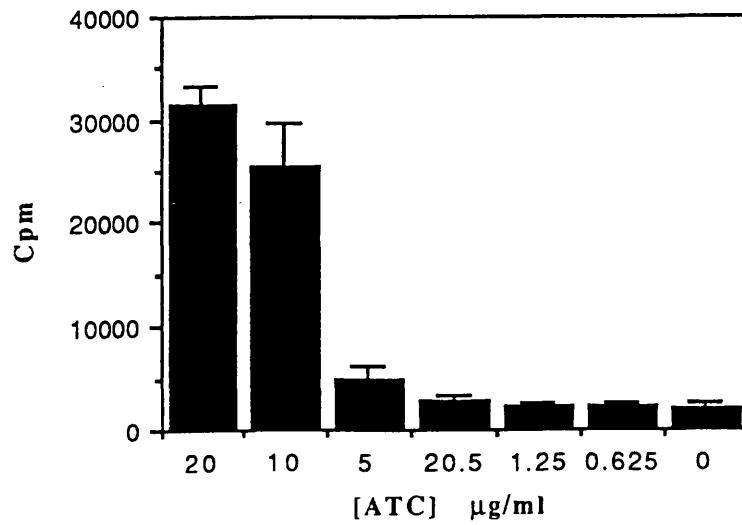


Fig. 5

Fig. 5
Incorporation of ^3H -thymidine by FDCP-2 cells on re-exposure to IL3, after 24 h deprivation of IL3, in the presence or absence of ATC.

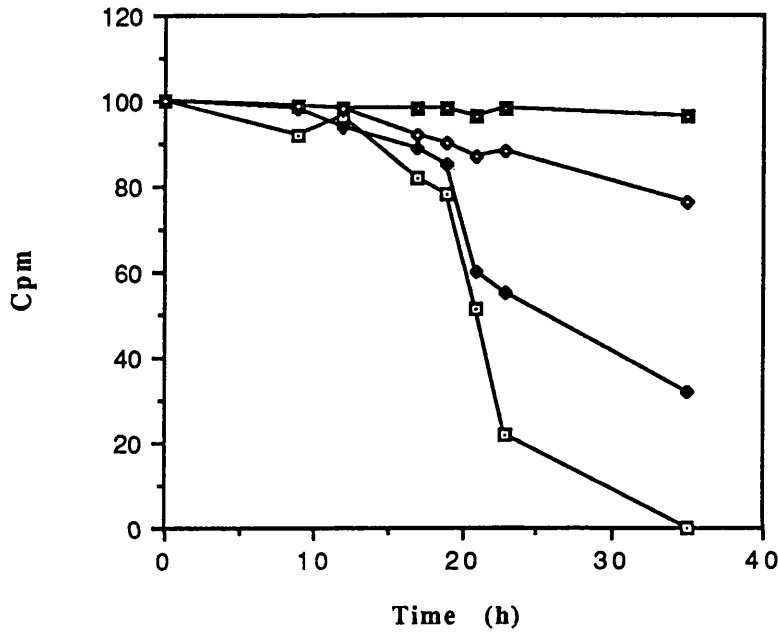


Fig. 6a

Fig. 6a

The kinetics of FDCP-2 cell death, measured by PI exclusion, on IL3 removal in the presence of 0.5 μ g/ml cycloheximide. Each point is a mean of 5, with $\sigma_n < 3\%$ of the mean. Differences are statistically significant from $t = 16$.

- + IL3
- + IL3 + cycloheximide
- - IL3
- ◆— - IL3 + cycloheximide

Fig. 6b

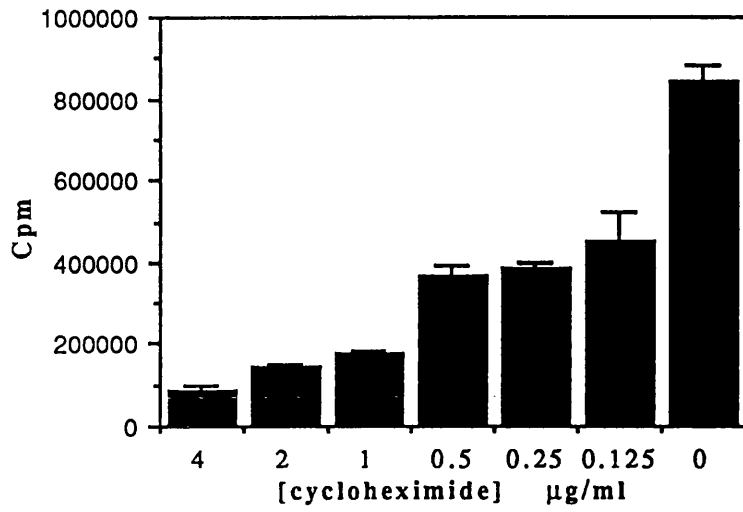


Fig. 6b

Incorporation of ^{35}S -methionine by FDCP-2 cells in presence of cycloheximide.

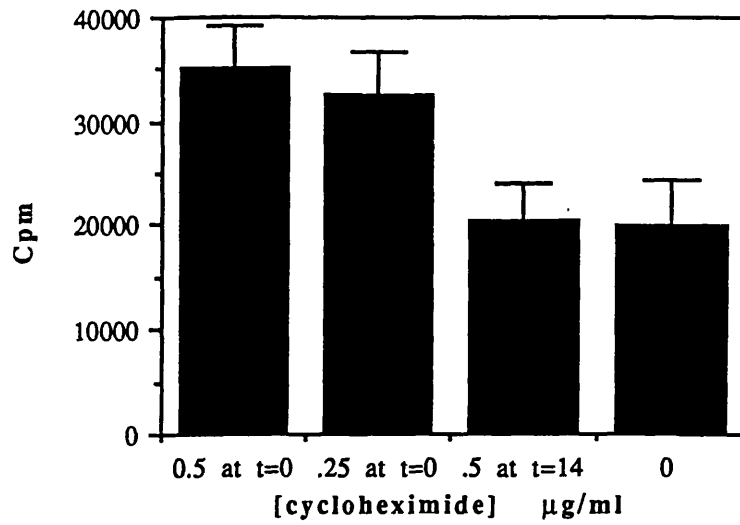


Fig. 7a

Fig. 7a
 ^3H -thymidine incorporation by FDCP-2 cells on re-exposure to IL3, after 24 h incubation in absence of IL3, but presence of cycloheximide.

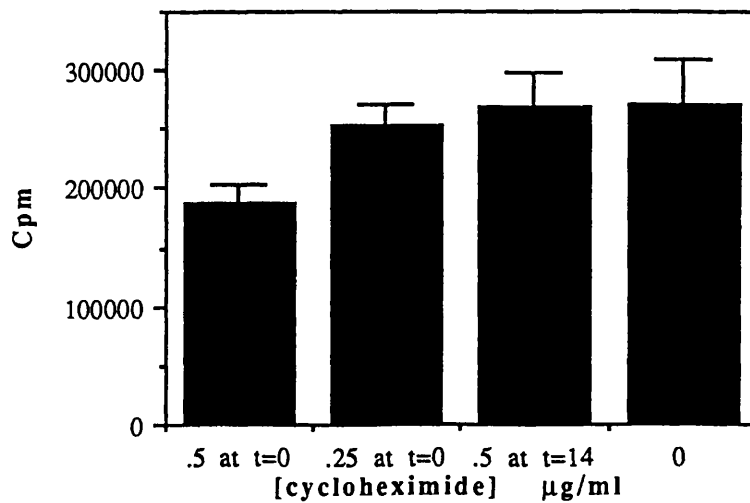


Fig. 7b

Fig. 7b
 ^3H -thymidine incorporation by FDCP-2 cells after 24 h exposure to cycloheximide.

Fig. 8a

Flow cytometry of FDCP-2 cells stained with anti-BrdU (FL1) and PI (FL2), analysed using "paint a gate" soft-ware. Cells painted blue are in G₁/M.

Fig. 8b

As above, but prior to staining cells were incubated with 1.25 mM hydroxyurea for 4 h.

Key

FSC volume

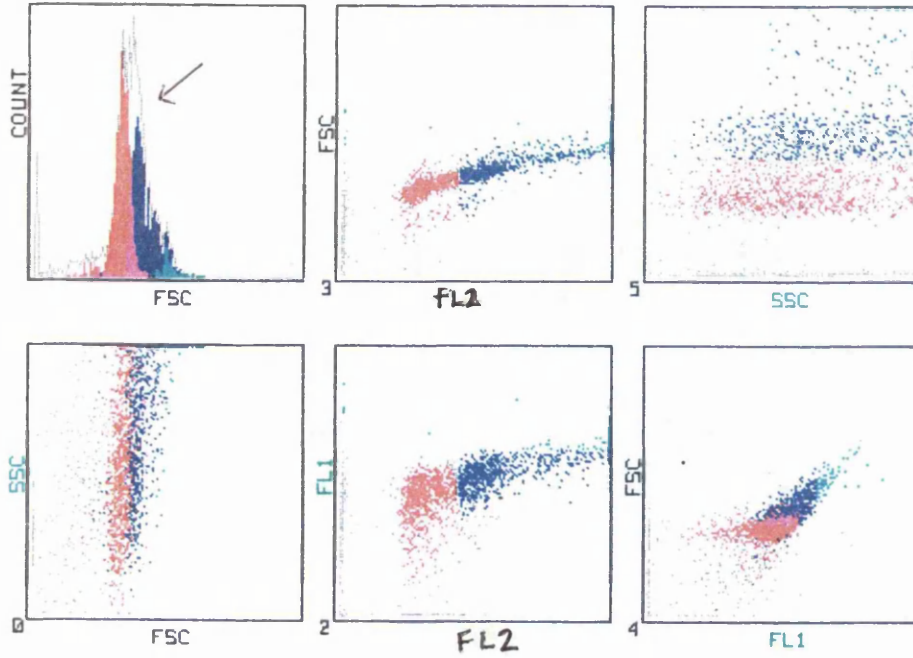
FL1 fluorescence 1

FL2 fluorescence 2

SSC side scatter

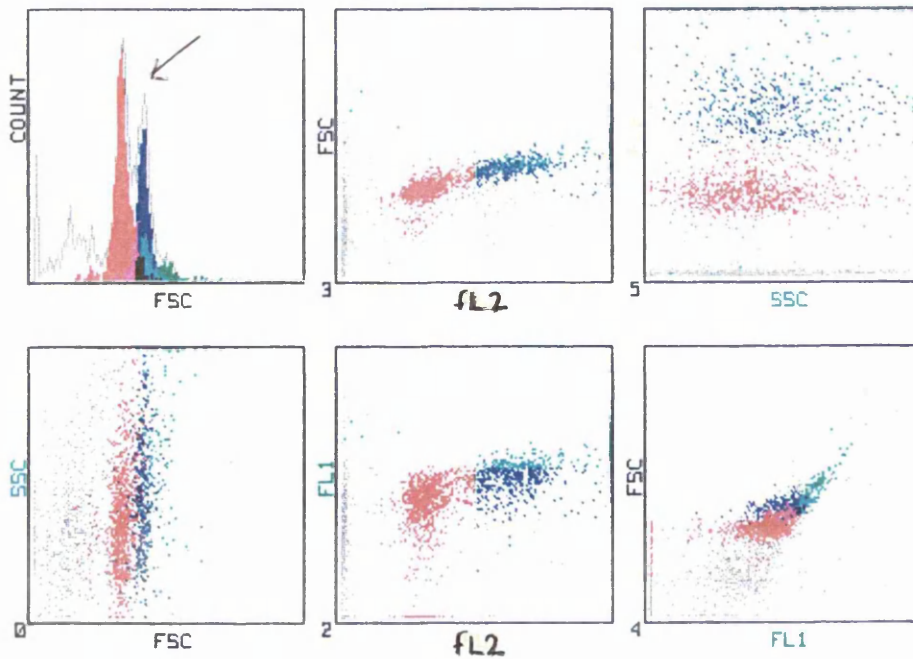
% = 43.0 1.1 36.1 0.0 3.6 0.0
RGB0 gate; +- mode; <> size
0-5 plot; FZH\$s

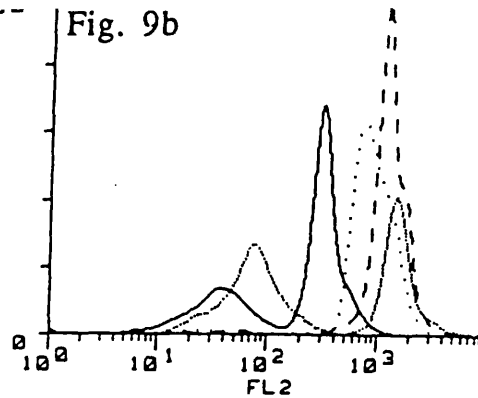
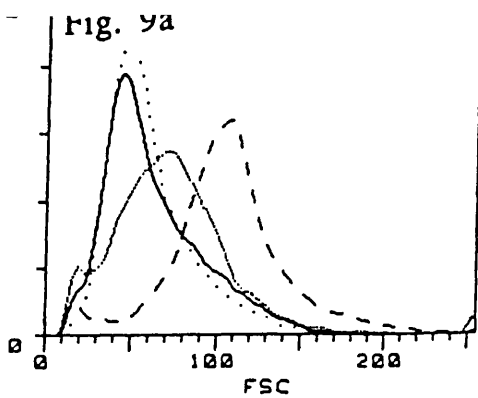
Fig. 8a



% = 43.2 3.3 17.6 0.0 6.8 0.0
RGB0 gate; +- mode; <> size
0-5 plot; FZH\$s

Fig. 8b





1.) DATA002 A

2.) DATA004

3.) DATA005 FDCP-2

4.) DATA006 B

Fraction	% G ₀ /G ₁	% G ₂ /M
FDCP-2	54	46
A	78	22
B	13	87

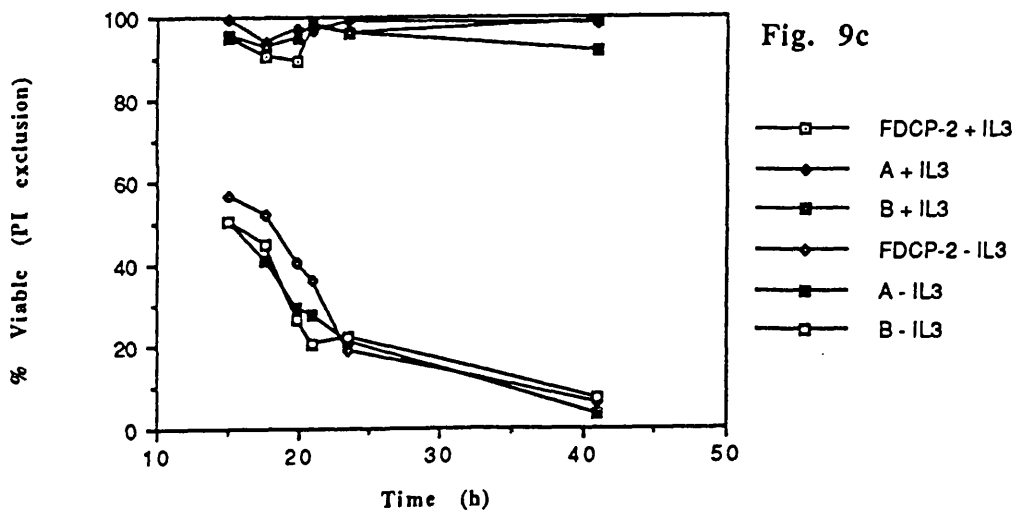


Fig. 9

Fig. 9a Volume (FSC) profiles for the populations of FDCP-2 cells separated on a discontinuous percoll gradient and for unfractionated FDCP-2 cells. Volumes may be slightly distorted because cells have been fixed with 70% ethanol. 'A' is enriched for cells in G₁ and 'B' is enriched for cells in G₂.

Fig. 9b Same fixed cells stained with PI, and an estimate of their cell cycle status. 'A' is enriched for cells in G₁ and 'B' is enriched for cells in G₂.

Fig. 9c Kinetics of cell death in the three groups, as determined by PI exclusion by flow cytometry. Each point is the mean of five readings and in all cases the standard deviation was less than 3% of the mean.

Fig. 10a

³H-thymidine incorporation by FDCP-2 cells on restimulation with IL3, after 24 h incubation in the absence of IL3, but presence of 0-1.25 mM hydroxyurea.

Fig. 10b

³H-thymidine incorporation by FDCP-2 cells after 24 h incubation with 0-1.25 mM hydroxyurea.

Fig. 10c

³H-thymidine incorporation by FDCP-2 cells on restimulation with IL3, after 24 h incubation in the absence of IL3, and presence of 0-0.06 mM aphidicolin.

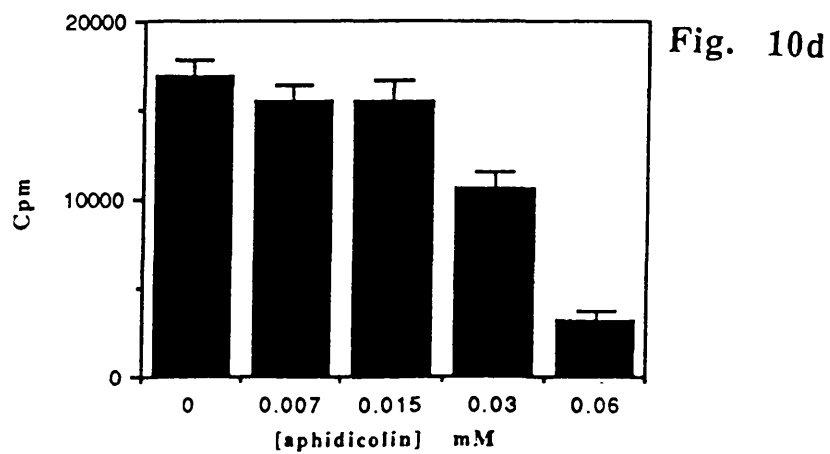
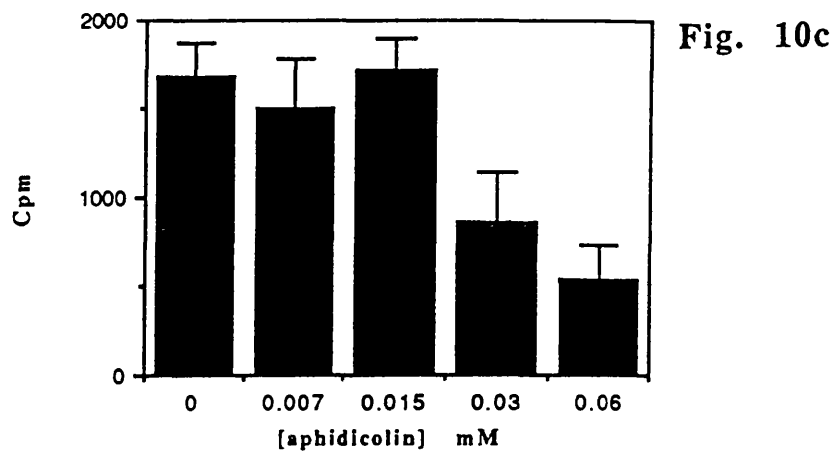
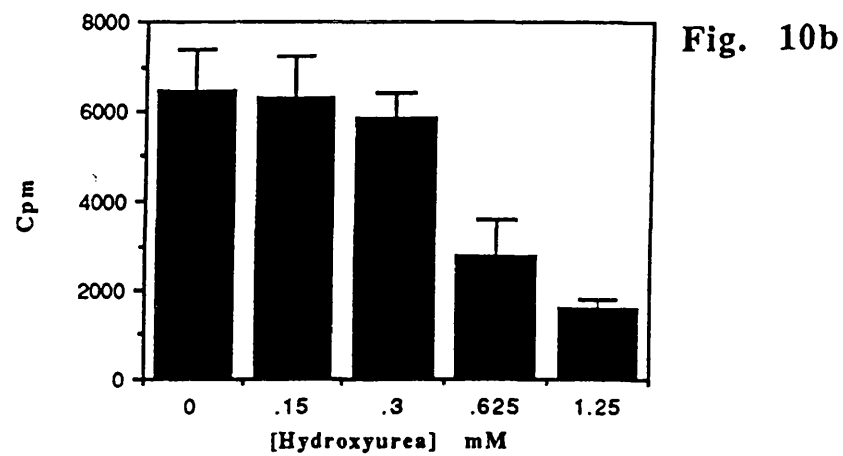
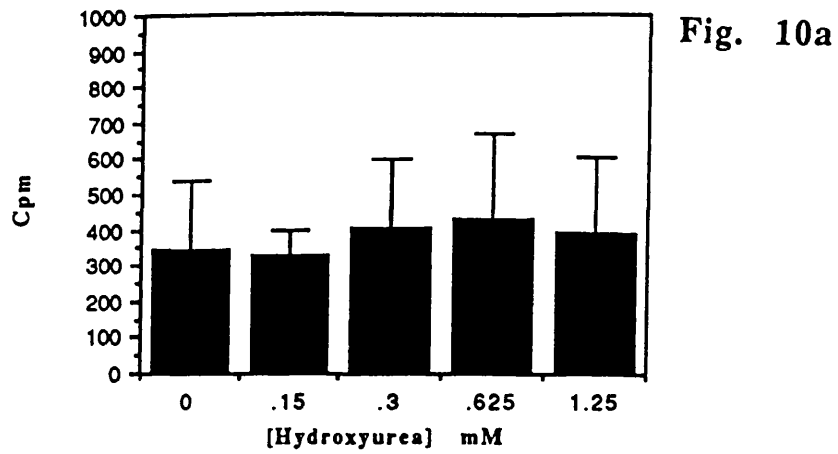
Fig. 10d

³H-thymidine incorporation by FDCP-2 cells after 24 h incubation with 0-0.06 mM aphidicolin.

Fig. 10e

Flow cytometry of FDCP-2 cells stained with anti-BrdU (FL1) and PI (FL2), analysed using "paint a gate" soft-ware. Cells painted blue are in G2/M. Cells were treated with 0-0.15mM aphidicolin for 4 h prior to staining.

(for key see fig. 8 legend)

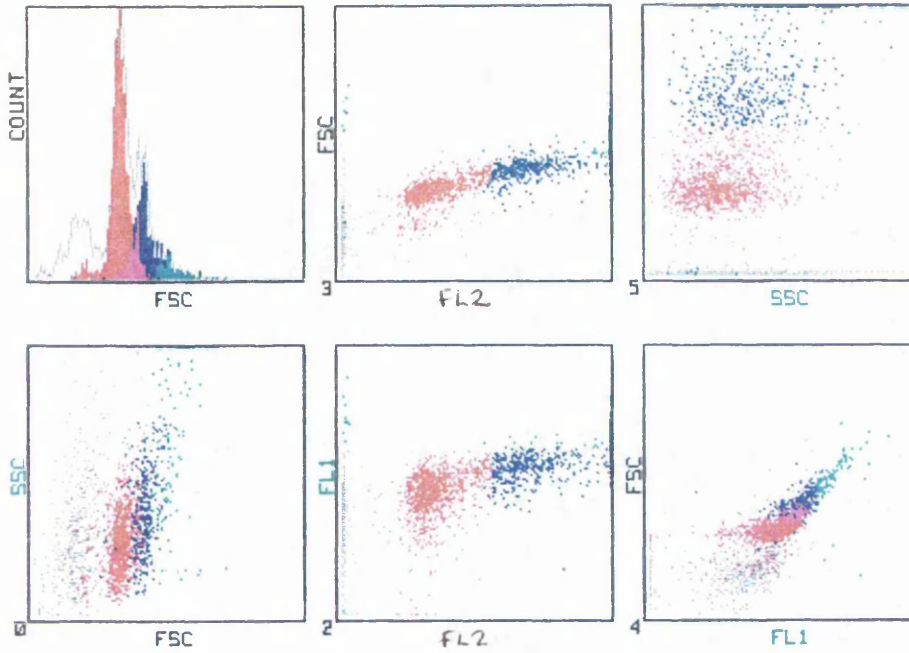


% = 51.0 0.9 21.4 0.4 4.6 0.0

RGB0 gate; +- mode; <> size

0-5 plot; FZH\$s

Fig. 10e



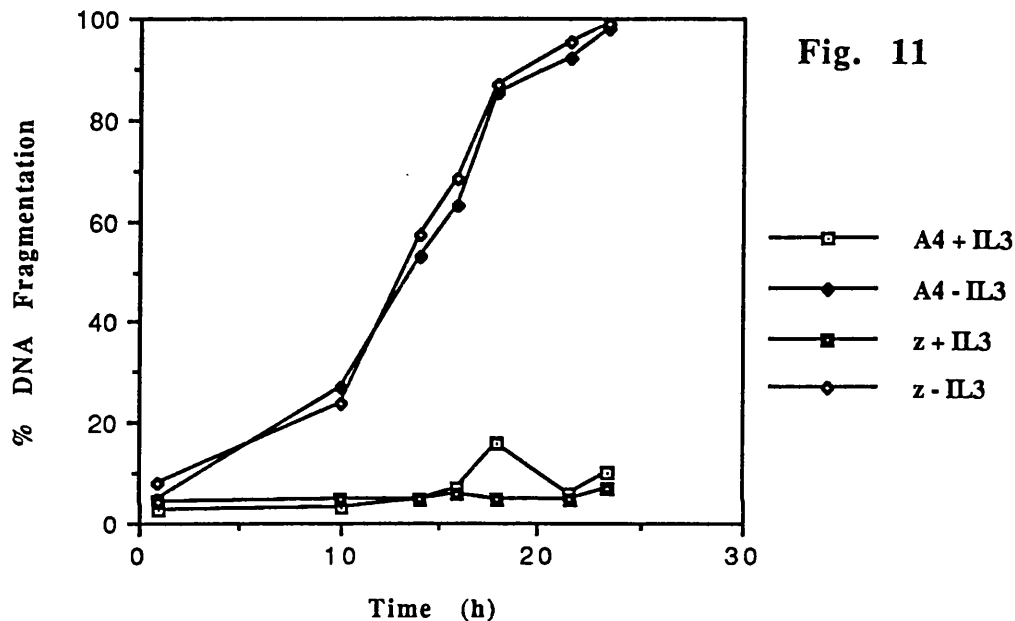


Fig. 11

Kinetics of DNA fragmentation by A4 cells, and by a population of A4 cells enriched for cells in G₂/M on a discontinuous percoll gradient (designated 'z'). The unfractionated population of A4 cells contained 54% cells in G₀/G₁ and 46% in G₂/M, whereas 'z' contained 85% cells in G₂/M. DNA fragmentation was determined by measuring the release of ³H-thymidine from pre-labelled cells, and is expressed as a percentage of total radiolabel present. Each point is a mean of 6, and σ_n was < 10% of the mean in all cases.

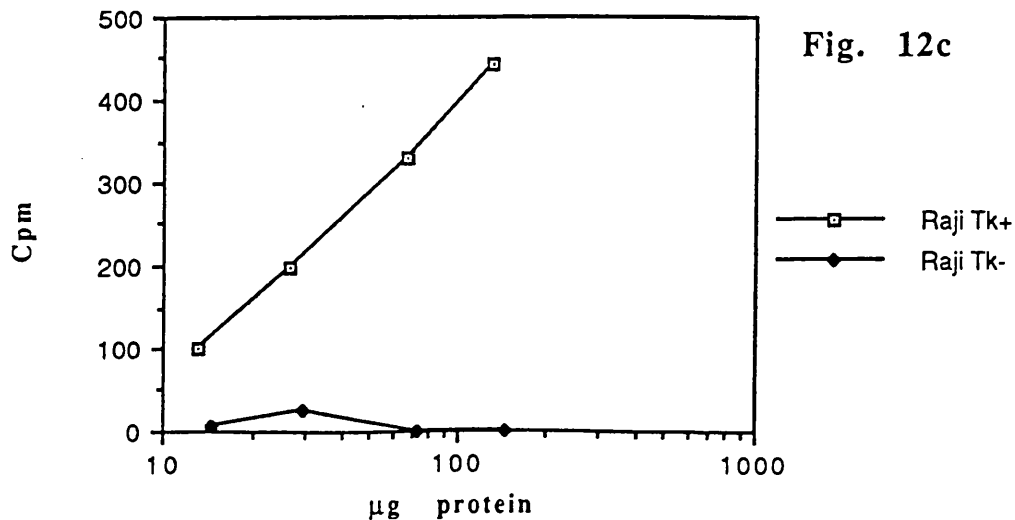
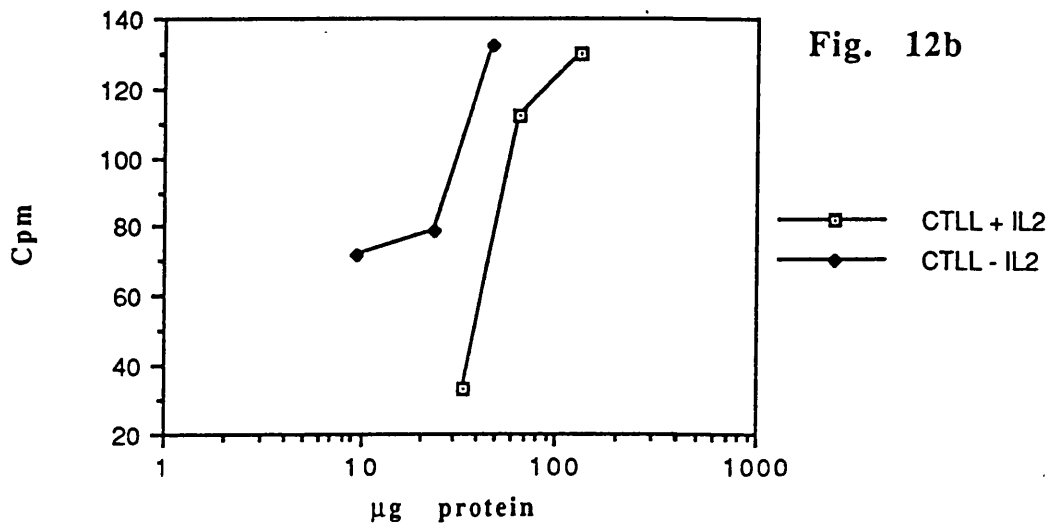
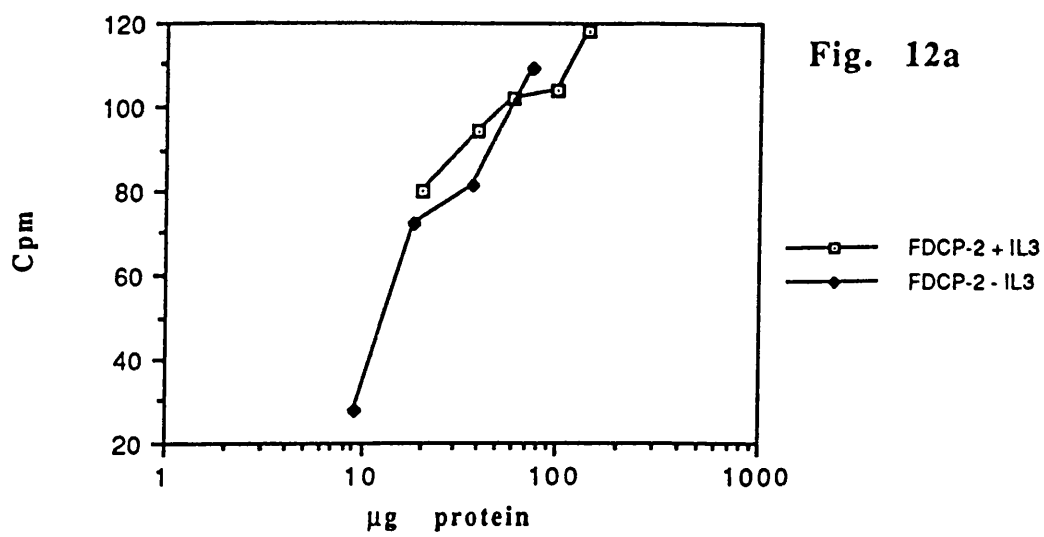


Fig. 12

Activity of O^6 -methylguanine-DNA methyltransferase in cellular extracts from FDCP-2 cells, cultured with or without IL3 for 15 h (Fig. 12a), CTLL cells, cultured with or without IL2 for 15h (Fig. 12b), and Raji Tk⁺ and Raji Tk⁻ cells, as positive control (Fig. 12c). Cpm shown are counts that the enzyme removed from a pre-labelled substrate.

DISCUSSION

There are several reported examples of programmed cell death being induced by withdrawal of a growth factor : IL2-dependent T cells die on removal of IL2 (Duke and Cohen 1986); cultured rat sympathetic neurons die on withdrawal of nerve growth factor (NGF) (Martin et al 1988); epithelial cells of the rat prostate die when androgen is withdrawn by castration (Stanistic et al 1978); and IL3-dependent FDCP-2 cells, A4 cells (this report), FDCP-1 cells and FDCP-mix cells (Williams et al 1990) die on removal of IL3. In all cases death is inhibited by the protein synthesis inhibitor cycloheximide, and this has been interpreted to mean that death is an active process that requires the synthesis of specific proteins essential for cell death. The finding that the removal of a signal causes the cell to commit suicide is surprising. Intuitively, one might think that growth factors stimulate cell proliferation and that their removal would lead to the cell withdrawing from the cell cycle; if death followed it might be due to a gradual decline in metabolism, rather than to active suicide. Is it possible, then, that there is an alternative explanation for the results obtained with cycloheximide?

In the case of proliferating cells, such as FDCP-2 cells, cycloheximide might, in principle, enhance survival by slowing the rate at which cells progress through the cell cycle. FDCP-2 cells die asynchronously on IL3 withdrawal (Fig. 1a), suggesting that death might be initiated at a specific point in the cell cycle, such as the "restriction point" (R). Cycloheximide might inhibit cell death by causing a proportion of the cells to arrest early in G₁ (Zetterberg and Larsson 1985), so that they never reach R during the timespan of the experiment. This does not seem to be true for FDCP-2 cells, however, as

synchronization of the cells does not alter the kinetics of cell death, suggesting that the cells are dying at different points in the cycle. It is still possible that FDCP-2 cells are incapable of going into G_0 so that R is the commitment point for either proliferation or death, but that after commitment to death, FDCP-2 cells take a varying amount of time to die. The fact that agents that cause cell cycle arrest such as hydroxyurea and aphidicolin do not seem to enhance survival on re-exposure to IL3 in the ^3H -thymidine incorporation assay suggests that this is not the case, as does the fact that cell cycle synchrony does not alter the kinetics of DNA fragmentation in the ^3H -thymidine release assay, even though for an individual cell this assay seems to be measuring an all-or-none phenomenon, rather than a gradual release of radio-label. In addition, transfection of the related IL3-dependent cell line FDCP-1, with the proto-oncogene *bcl-2* suppresses cell death on IL3 removal without stimulating proliferation (Vaux et al 1988), suggesting that these cells can become quiescent, and that the action of IL3 to promote survival is distinct from its ability to stimulate proliferation. Thus, cell cycle arrest does not seem to explain the inhibition of FDCP-2 cell death by cycloheximide.

The above arguments are not relevant to the action of cycloheximide in prolonging neuron survival when NGF is withdrawn. Cycloheximide increases survival of neurons in the absence of NGF *in vitro* (Martin et al 1988) and *in vivo* (Oppenheim and Prevet 1988) even though these cells do not proliferate. Perhaps, rather than preventing the *de novo* synthesis of proteins that kill the cell, cycloheximide acts to prolong the life of an essential mRNA, normally made when the cell is stimulated by growth factor. Stimulation of quiescent cells with growth factors activates a number of genes, such as *c-fos* and *c-myc*, and cycloheximide has been shown to superinduce the

mRNA levels of these and other genes, both by inhibiting the shut off of their transcription and by prolonging the life-times of the mRNAs, perhaps by inhibiting a labile RNAase (Lau and Nathans 1986, Greenberg et al 1985). Unfortunately, examination of *c-fos* and *c-myc* mRNA levels would not definitively distinguish between these two mechanisms for cycloheximide's effect in inhibiting cell death, as it has been demonstrated that *c-fos* and *c-myc* are activated when rat prostatic cells die in response to androgen withdrawal (Buttayan et al 1988).

The internucleosomal DNA cleavage observed in apoptosis has also been reported in forms of cell death that are not thought to be active, such as complement-mediated lysis of mouse B and T cells (Bachvaroff et al 1977). Exposure of isolated nuclei from T and B cells (Bachvaroff et al 1977), thymocytes (Cohen and Duke 1984), and FDCP-2 cells (this report) to high concentrations of Ca^{2+} and Mg^{2+} activates internucleosomal DNA cleavage, suggesting that the enzymes that catalyze the cleavage are always present in these nuclei and are not synthesized only on induction of apoptosis. Is DNA fragmentation, then, a secondary, non-causal phenomenon in apoptosis? The inhibition of death by the nuclease inhibitor ATC suggests that DNA fragmentation might mediate cell death in apoptosis. ATC blocks nuclease activity by inhibiting nucleic acid binding proteins (Blumenthal and Landers 1973). Therefore, it can also act as a general protein synthesis inhibitor by preventing the initiation of polypeptide synthesis (Stewart et al 1971). At the concentrations used in my experiments, however, the effect of ATC on overall protein synthesis was negligible (see Fig. 6d), suggesting that its effect on apoptosis resulted from nuclease inhibition. This interpretation is supported by the finding that cycloheximide, at concentrations that effectively prevented protein synthesis, had a much weaker effect than ATC in promoting cell

survival. ATC also inhibits death of thymocytes, induced by glucocorticoids or calcium ionophores (McConkey et al 1989).

The data presented here show that FDCP-2 cells die by apoptosis on IL3 removal and that DNA fragmentation probably causes death. Is this consistent with an earlier report that viability of FDCP-2 cells can be increased on IL3 withdrawal by addition of ATP to the culture medium (Whetton and Dexter 1983)? A theory of cell death which links ATP depletion to breaks in DNA, and so would explain the effects of both ATC and ATP to prolong survival of FDCP-2 cells, is the suicide hypothesis first proposed by Berger (1985). This postulates that it would be advantageous to an organism for there to be a mechanism by which cells with extensive DNA damage kill themselves, as the extra pressure placed on the DNA repair apparatus in cases of extreme DNA damage might increase the risk of error in repair, and associated mutagenesis. The theory suggests that the enhanced poly(ADP-ribosyl)ation of DNA that occurs under conditions of extreme DNA damage (Farzaneh et al 1982) actually functions to deplete cellular NAD^+ (Sims et al 1983). One of the consequences of this depletion of NAD^+ is a decrease in glycolysis (Berger et al 1986), and decline in the production of ATP. However, the function of poly(ADP-ribose) synthetase remains controversial (Gaal et al 1987) and some authors have suggested that poly(ADP-ribosyl)ation instead functions to stabilize the chromatin structure and that its action is directly antagonistic to programmed cell death (Wielckens et al 1987). In a study of glucocorticoid induced death of thymocytes Wielckens argues that death only occurs when this antagonistic potential is exhausted and that death can be regarded as a struggle between DNA repair enzymes and the endonucleases that cleave the DNA. Given that it is not clear if poly(ADP-ribose) synthetase is involved in DNA repair, I decided to look for evidence of increased activity of another well

defined DNA repair enzyme, O⁶methylguanine-DNA methyltransferase. No increase in activity of this enzyme was observed in the dying cells.

What is the physiological significance of the induction of apoptosis by growth factor withdrawal? The NGF-dependence of sympathetic neurons has been frequently described *in vivo*, and can be explained functionally, in that it facilitates the quantitative matching of targets with their sources of innervation.

The physiological role of interleukin-dependence is less well documented. IL2-dependence of activated T cells would in theory help dampen down an immune response when antigen is no longer present. When antigen is cleared, IL-2 production by T helper cells subsides and most effector cells disappear from the animal (MacDonald et al 1973). If all these effector cells became quiescent, they could potentially interfere with subsequent immune responses to other unrelated antigens (Moller and Sjoberg 1970) by competing for limiting concentrations of growth factors, and in addition they would use up energy with no advantage to the animal. It seems that the majority of antigen specific T cells do not merely cease dividing, but actually die on interleukin removal (Gillis et al 1978, Bishop et al 1985). Duke and Cohen (1986) have demonstrated IL2-dependence and active cell death *in vitro* in CD8⁺ T cell lines, MLR blasts and Con A blasts. They also demonstrate DNA fragments *in vivo* in lymph node cells draining a site of antigen administration. Apoptosis has been observed in lymph node (Searle et al 1982) and spleen (Swartzendruber and Congdon 1963). Taken together this evidence suggests that apoptosis induced by IL2 withdrawal does have a role in regulating the immune response.

Does apoptosis due to IL3 withdrawal have a function in the control of normal haemopoiesis? Normal somatic cells have a finite lifespan and in culture tend to undergo a limited number of cell

divisions before they reach a crisis point and die (Hayflick 1965). However an apparent exception to this inevitable cell death is the case of stem cells. Haemopoietic stem cells from aged mice can be repeatedly grafted into young mice, so that the cells proliferate and survive for at least five times the lifespan of a normal mouse, and the decline in transplantability that is finally observed may only be due to technical difficulties (Ross et al 1982). It is tempting to speculate that growth factor dependence might be the physiological control of this system of self-renewal. Normal haemopoietic cells rapidly die in culture in the absence of their appropriate colony stimulating factor (CSF) (Metcalf 1970). Haemopoiesis can be supported in culture by stromal cells in the absence of added IL3 or GM-CSF and, under these circumstances, the growth factors are not detectable in the culture medium (Roberts et al 1987), but it is likely that they are produced by the stromal cells and retained on their plasma membranes in association with the extracellular matrix (Roberts et al 1988). Thus it seems probable that the self-renewal and differentiation of haemopoietic stem cells *in vivo* is controlled by membrane bound CSFs produced by the bone-marrow stroma. It has not been possible to abrogate production of CSFs and demonstrate haemopoietic cell death *in vivo*, but elevation of serum levels of these factors for several days leads to dramatic increases in the numbers of precursor cells and mature cells in the bone marrow (Bronchud et al 1988, Gabilove et al 1988). This response is likely to be due to stimulation of proliferation of bone marrow cells, but may also at least in part be due to enhanced survival of the precursor population.

CHAPTER FOUR:
DO CTL KILLING AND GLUCOCORTICOID -INDUCED LYSIS SHARE A
COMMON PATHWAY?

INTRODUCTION

Cytotoxic T cells (CTL) control viral infections by killing infected cells (reviewed by Nabholz and MacDonald 1983). The killing is specific and occurs after recognition by the T cell receptor (TCR) on the CTL of a foreign peptide in association with self Class I MHC molecules on the target cell-surface (Townsend 1987). The molecular interactions of the recognition process are well characterized, but the mechanisms of killing remain controversial.

CTL-mediated lysis involves plasma membrane and nuclear damage (Russell 1983), following obligatory CTL-target cell contact up to delivery of the lethal hit, after which death proceeds in the absence of the killer cell (Golstein and Smith 1976 and 1977). CTL contain secretory granules (Podack and Konisberg 1984; Henkart et al, 1984), which in isolated form have strong calcium-dependent cytotoxicity. On CTL-target cell conjugation the CTL reorientates its Golgi apparatus (Kupfer et al 1985) and granules (Yanelli et al 1986) and secretes individual granules into the intracellular space between the two cells. Granules contain cytolytic proteins, the perforins (Podack and Dennert 1982; Dennert and Podack 1983; Masson and Tschopp 1985), serine proteases (Masson and Tschopp 1987; Hameed et al 1988) proteoglycans (Schmidt et al 1985), and cytotoxins homologous to TNF (Liu et al 1987).

Perforin is homologous to the C9 component of complement (Shinkai et al 1988) and is cytolytic by virtue of its calcium-dependent binding to phospholipids (Tschopp et al 1989, Yue et al 1987), membrane insertion and intramembraneous polymerization (Podack 1986). Thus it has been suggested that CTL-lysis is mediated by perforins, which cause plasma membrane lesions, in a manner analogous to the complement system (Young and Cohn 1986).

There are, however, several problems with this theory : (1) Some CTL, and particularly CTL *in vivo*, do not appear to have cytotoxic granules (Berke and Rosen 1987) and do not have detectable perforin activity (Allbritton et al 1988); (2) Even though serine esterases are presumed to be found in the same granules as perforin, in the absence of extra-cellular Ca^{2+} and after depletion of the killer cell's intracellular Ca^{2+} , serine esterase secretion is depleted, but lysis is not inhibited (Ostergaard and Clark 1987; Trenn et al 1987), and ; (3) Inhibitors of Ca^{2+} -dependent granule secretion, such as cyclosporin A, block both the constitutive and induced pathways of cellular secretion, yet only slightly affect CTL-mediated lysis (Clark et al 1988; Lanki et al 1989).

Current opinion remains divided between those who hold that CTL kill by a mechanism very similar to that of complement killing (reviewed by Podack 1989) and those who emphasize the differences between the two processes and who place importance on the nuclear lesion induced by CTL (reviewed by Martz 1989). There seems to be reasonable evidence that at least in some instances CTL killing does not involve perforin (Ostergaard and Clark 1989) and one alternative mechanism that has been suggested is that CTL kill by inducing a suicide mechanism in their target cells (Golstein 1987).

The evidence in favour of target-cell suicide came largely from the experiments of Ucker (1987), who reported a correlation between resistance to dexamethasone (dex)-induced lysis and resistance to cytotoxic T cell (CTL)-mediated killing in mutants of the thymoma, S49,4RD (Sibley and Tomkins 1974). Furthermore, he showed that a single step reversion could restore sensitivity to both lethal stimuli. These data strongly implied a common pathway of cell death and suggested that the genetic locus which restored sensitivity might

encode an element of an endogenous suicide pathway. The suggestion of a common pathway seemed attractive because CTL killing had been shown to induce the morphology of apoptosis in its targets (Kerr et al 1987), as had glucocorticoid-induced lysis of thymomas (Wyllie et al 1984). Both stimuli also lead to regular DNA fragmentation (Russell et al 1979, Wyllie et al 1984).

Unfortunately, Ucker's findings proved controversial because other groups were unable to repeat his work with the cells he provided, or with cells from the original source, supplied by Yamamoto's laboratory (E. Martz, personal communication) and Ucker's original cell line was subsequently lost. In an attempt to confirm the evidence for a common pathway of cell death, I decided to select independently for dex-resistant mutants from a sensitive parent cell line and test them for susceptibility to CTL-induced lysis. DNA fragmentation does not always occur in CTL-induced lysis (Gromkowski et al 1988) and it has been suggested that whether or not DNA fragmentation takes place might be dependent on a property of the target cells and not of the CTLs (Howell and Martz 1987a). It was therefore important to use a target cell line which does exhibit DNA fragmentation on CTL-induced lysis.

The murine mastocytoma P815 seemed an appropriate choice because it is well documented that this cell line does undergo DNA fragmentation when it is killed by CTL (Duke et al 1983, Russell et al 1979), and because the CTL clone CTL-P35:10 (Maryanski et al 1982), which is specific for P815, was available in our laboratory. P815 is of DBA/2 origin and is H-2^d. The subline used in this study was P815-X.

RESULTS

Cloning

A clone of P815-X, designated P815 α was isolated by a limiting dilution procedure. This clone was used in all subsequent experiments and was the parent from which dex-resistant clones were selected. Cloning efficiency was between 0.7-0.9.

Sensitivity of P815 α to dexamethasone

P815 α cells were dexamethasone sensitive and died after 3 days in culture in dexamethasone. Fig. 13a shows the death of P815 α cells in dexamethasone for 3 days, as measured by trypan blue exclusion. ^3H -thymidine incorporation after 3 days of culture in different concentrations of dexamethasone was used as an alternative measure of glucocorticoid sensitivity and is shown in Fig. 13b. This dose response to dexamethasone was then used to distinguish resistant from sensitive variants. An electrophoretic ladder was obtained when DNA prepared from P815 α cells incubated in 10^{-6} M dex for 2 days was run on an agarose gel (Fig. 14), confirming that the glucocorticoid induced cell death of these cells was apoptosis.

Sensitivity of P815 α to CTL killing

As was expected, P815 α was sensitive to killing by the CTL clone P35:10 and by CTL raised in a mixed lymphocyte reaction (MLR) of CBA spleen cells and irradiated Balb/c spleen cells (Fig. 15a and b respectively). DNA was fragmented and the release of ^{125}I -uridine on Triton X-100 permeabilisation (Duke et al 1983) preceded ^{51}Cr release at an Effector:Target (E:T) ratio of 10:1, suggesting that DNA fragmentation was an early event (Fig. 15c). The experiment shown in Fig. 15c was carried out using CTL from an MLR.

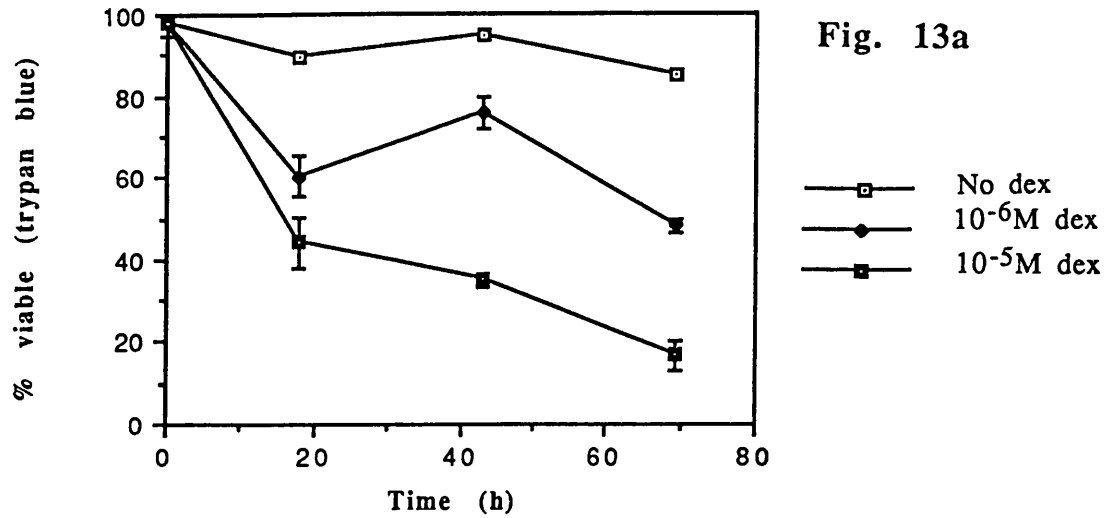


Fig. 13a
 Death of P815 α on culture in 10⁻⁵ M and 10⁻⁶ M dex. Viability is determined by trypan blue exclusion and each point is a mean of 5 readings.

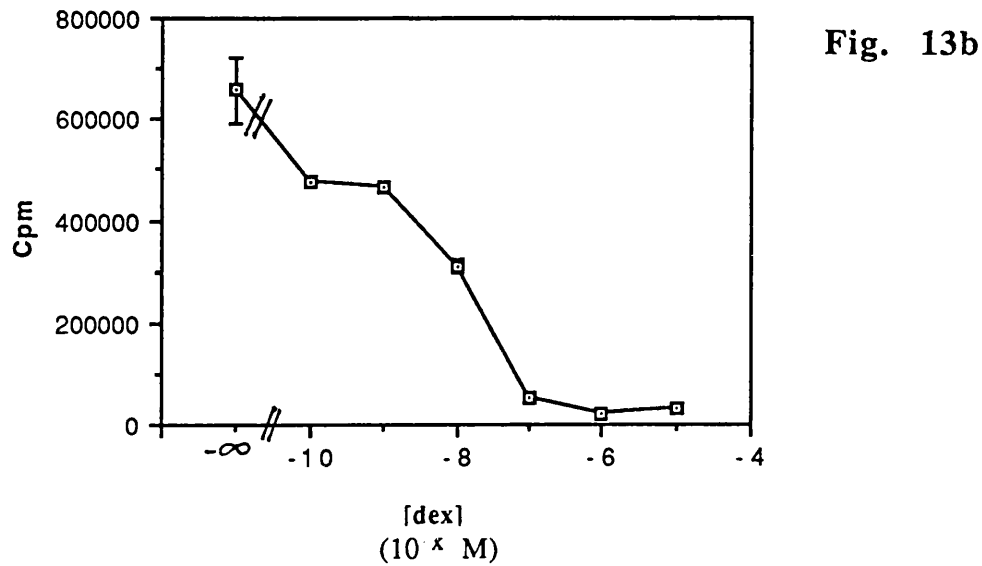


Fig 13b
 Proliferation of P815 α after 3 days culture in dex at concentrations from 10⁻⁵ M to 10⁻¹⁰ M. Proliferation is expressed as counts per minute (Cpm) and was measured by ³H-thymidine incorporation. Each point is a mean of 6.

Fig. 14

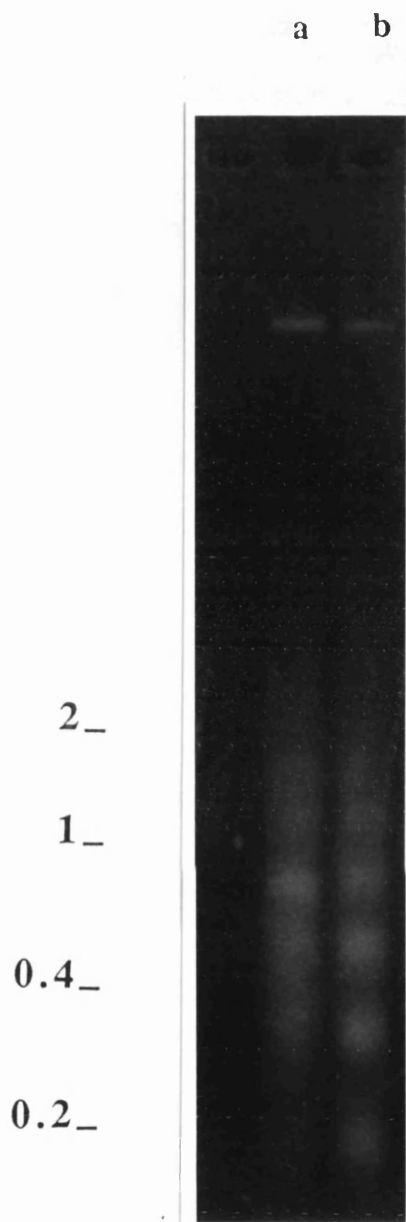


Fig. 14
Ethidium bromide stained 1% agarose gel showing DNA prepared from P815 α cells grown for 3 days in 10^{-7} M dex (track a) and 10^{-6} M dex (track b). Size is given in kilobases.

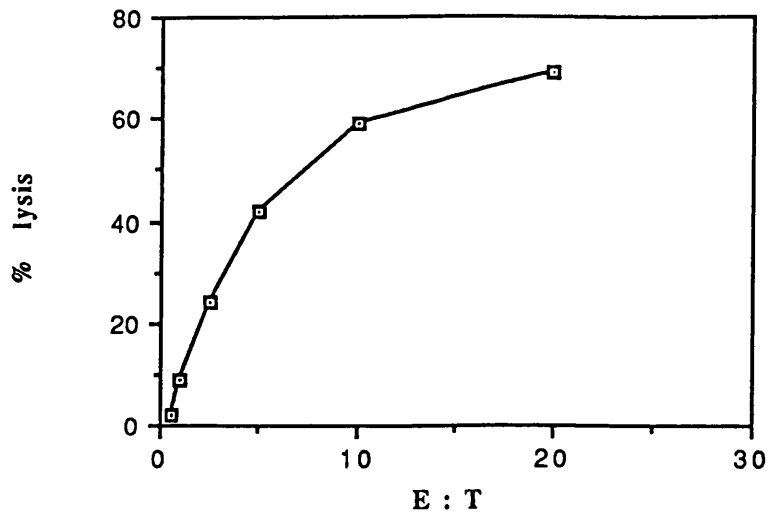


Fig. 15a

Fig 15a

Lysis of P815 α by CTL:P35:10. Lysis was determined by ^{51}Cr release. Each point is a mean of 3 with $\sigma_n < 5\%$ of the mean. Background release was less than 20% of total release.

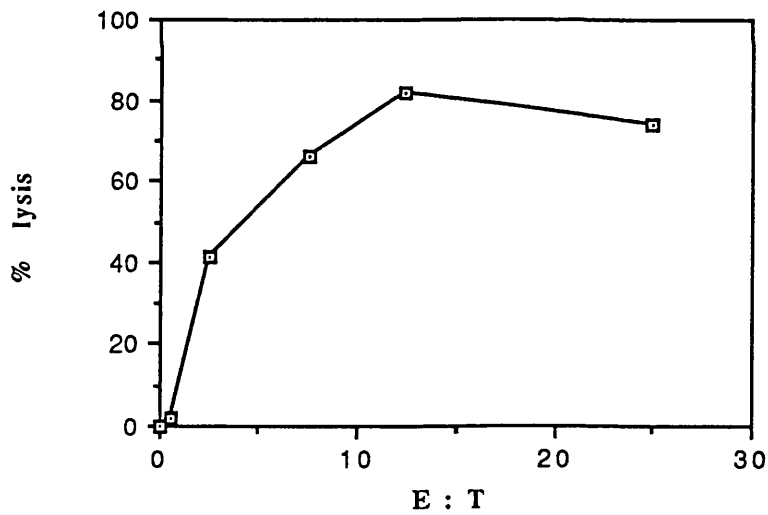


Fig. 15b

Fig 15b

Lysis of P815 α by CTL raised in a MLR, determined as in Fig 15a.

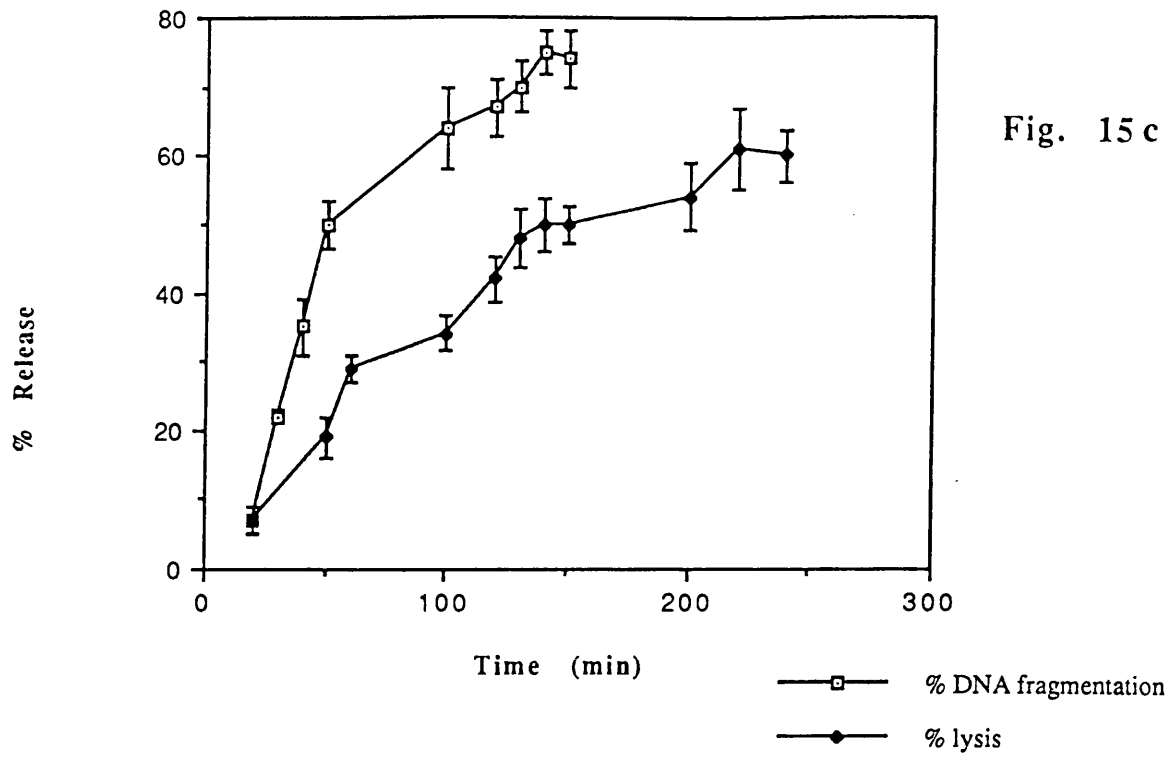


Fig 15c

The kinetics of lysis, as determined by ^{51}Cr release, and DNA fragmentation, as determined by ^{125}I -uridine release, in the killing of P815 α by CTL raised in an MLR.

Selection of dexamethasone-resistant clones

Dex-resistant clones were selected by two protocols. Either they were isolated by two rounds of limiting dilution cloning in 10^{-6} M dex, and were designated R1-R22, or they were cloned in dex from a bulk culture which had been first treated with the mutagen ethylmethane sulfonate (EMS), and were designated RA-RF. EMS treatment was carried out according to the protocol of Glimcher et al (1983). Cells were treated with a dose that caused about 40% toxicity for 16 h before washing and limiting dilution cloning in dex. Twenty-two dex-resistant clones were selected by the first method and six clones were selected by the second method. Resistant clones fell into two categories. Some showed no response to dexamethasone and six clones proliferated more in dexamethasone in a dose-dependent manner. The dose-response in the ^3H -thymidine assay of a representative clone from each category is shown in Fig. 16a. In selecting for dex-resistance it would seem very likely that one would obtain clones that have lost functional glucocorticoid receptors (Wyllie et al 1984), but this cannot be the case for those clones which proliferate more in dex, and resistant clones with functional receptors have been isolated from sensitive parents in other studies (Zawdyiwski et al 1983; Gasson and Bourgeois 1983). Approximately 20% of the resistant clones isolated showed a dose dependent response to dex, and this is the same proportion of resistant isolates with functional glucocorticoid receptors as has been reported in other studies (Sibley and Tomkins 1974). Increased proliferation is not surprising, as murine monocyte cell lines initially proliferate more when they are treated with dex (Norton 1989), and dex is known to induce the expression of multiple genes (Voris and Young 1981). Figs. 16b and 16c show the response to dex in the ^3H -thymidine incorporation assay of all resistant clones isolated without EMS treatment, and Fig. 16d

shows the response of clones isolated after EMS treatment. No increase in proliferation with dex was seen in any of the latter clones.

Sensitivity of dex-resistant clones to killing by CTL-P35:10

All dex-resistant clones were sensitive to killing by the cytotoxic T cell clone CTL-P35:10, and no differences in sensitivity between the resistant clones and the dex-sensitive parent were observed. Fig. 17a shows a representative experiment.

Sensitivity of dex-resistant clones to killing by CTL raised in a MLR

It has been suggested that there is more than one killing mechanism used by cytotoxic T cells, and that it is a perforin independent mechanism which causes DNA fragmentation in target cells (Ostergaard and Clark 1989). Culturing CTL clones in IL2-containing medium seems to favour the generation of perforin-containing cytoplasmic granules (Allbritton et al 1988) and perforin, being homologous to the C9 component of complement, is thought to act by permeabilizing the plasma membrane of the targets (Young et al 1986; Lowrey et al 1989). Granules derived from CTL clones can lyse targets without causing DNA degradation (Gromkowski et al 1988). Therefore, it seemed appropriate to test the sensitivity of the dex-resistant clones to CTL from another source. CTL were prepared in a 5-day MLR of CBA spleen cells and irradiated Balb/c spleen cells. Killing was specific against H-2^d and so was not mediated by NK or LAK cells, as inappropriate targets, such as Dab L cells transfected with H-2^k (a gift from H. Stauss) were not killed. All dex-resistant clones were killed and were as sensitive to killing as the dex-sensitive parent. A representative experiment is shown in Fig. 17b. These experiments

provide no evidence for the hypothesis that CTL and dex kill P815 cells by a common pathway, though clearly the limited number of dex-resistant clones tested does not rule out a common pathway.

Effect of E:T ratio on kinetics of DNA degradation

One of the arguments that is made in favour of the position that there is more than one way in which CTL can kill their targets, is that DNA degradation does not always occur, and that the cell whose DNA is fragmented dies in a fundamentally different way from the one whose DNA is not (Golstein 1987). DNA fragmentation is associated with the putative perforin-independent mechanism (Ucker 1987; Ostergaard and Clark, 1989).

This seems illogical. Just because DNA fragmentation has been shown to be causal in apoptosis induced by growth factor withdrawal (see Chapter 3) and in apoptosis in developing thymocytes (McConkey et al 1989, and Chapter 5), one cannot conclude that whenever it occurs it is necessary, and not just sufficient, for cell death. DNA fragmentation has occasionally been observed in killing by antibody and complement (Bachvaroff et al, 1977; Shipley et al 1971) and has recently been shown to occur in P815 cells killed by purified perforin (Hameed et al 1989). It seems possible that when death is mediated both by perforin and complement, whether DNA fragmentation takes place could be a function of the concentrations of perforin or complement + antibody and the speed of death. This suggestion is supported by the observation that at low concentrations a Ca^{2+} ionophore induced apoptosis and DNA fragmentation in immature thymocytes (Kizaki et al 1989), which other authors have shown to be inhibitable by ATC (McConkey et al 1989), whereas a higher dose of the ionophore caused cell lysis, but not DNA fragmentation or apoptosis. Thus, DNA fragmentation could be the

result of Ca^{2+} signalling which only takes place if the membrane lesion creates the appropriate Ca^{2+} flux to trigger apoptosis. If the Ca^{2+} flux is too great because the membrane lesion is greater, then, as in the situation with the higher dose of Ca^{2+} ionophore the cell would lyse without apoptosis being triggered. Kinetics of death would also be critical, as if the break up of the plasma membrane were very fast, soluble components, possibly including the relevant nucleases, would leak out of the cell before DNA degradation could occur.

In search of evidence in favour of this hypothesis, I looked at the kinetics of DNA fragmentation in P815 cells at different E:T ratios. There was no decrease in DNA fragmentation as E:T ratios were increased (Fig. 18a). I then measured release by target cells of ^{125}I -uridine and ^{51}Cr into the culture medium in parallel assays, after 1 h incubation with CTLs. Release of ^{125}I -uridine increased with increasing E:T ratio, up to an E:T ratio of 10, and thereafter declined (Fig. 18b), but ^{51}Cr release continued to increase with increasing E:T ratio (Fig. 18c). At high E:T ratios, where after 1 h the plasma membrane of about 35% of targets had disintegrated, the nuclear membranes had remained intact. Incubation of isolated nuclei in appropriate ion concentrations leads to DNA fragmentation (see Chapter 3) and so this could account for some of the DNA fragmentation observed in the experiment in Fig. 18a.

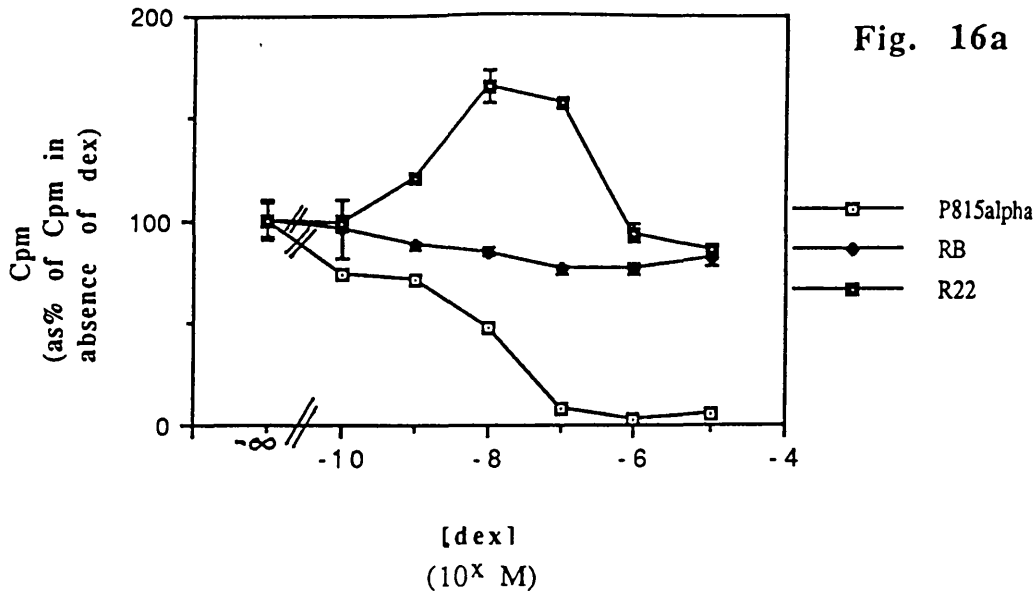


Fig. 16a
 Proliferation of clones of P815 after 3 days culture in dex at concentrations from 10^{-5} M to 10^{-10} M. Each point is a mean of 6. Proliferation was measured by ^3H -thymidine incorporation and is expressed as a percentage of proliferation in the absence of dex. Resistant clones were isolated by limiting dilution cloning.

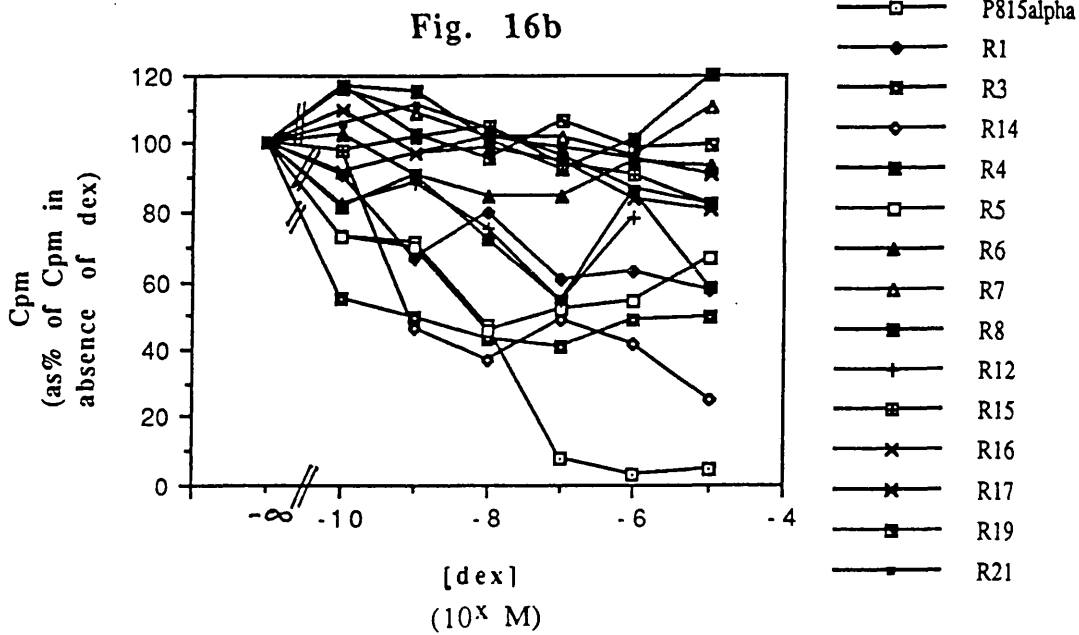


Fig 16b
 As above. Standard deviations are not shown, but in all cases they were less than 5 % of the mean.

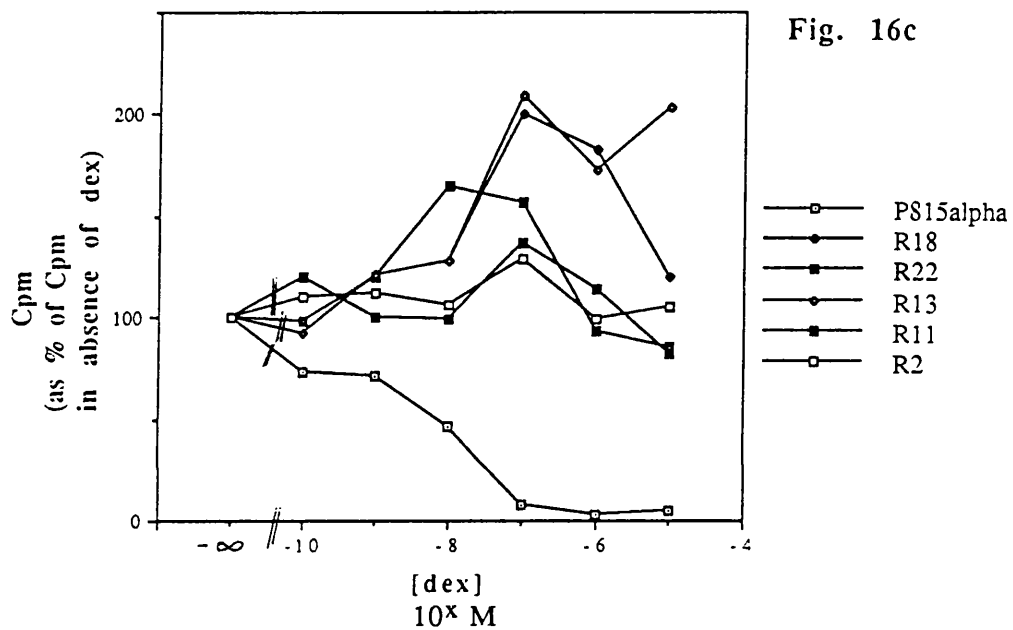


Fig. 16c

Proliferation of clones of P815 after 3 days of culture in dex at concentrations from 10^{-5} M to 10^{-10} M. Each point is a mean of 6, with $\sigma_n < 5\%$ of the mean. Proliferation was measured by ^3H -thymidine incorporation and is expressed as a percentage of proliferation in the absence of dex. Resistant clones were isolated by limiting dilution cloning.

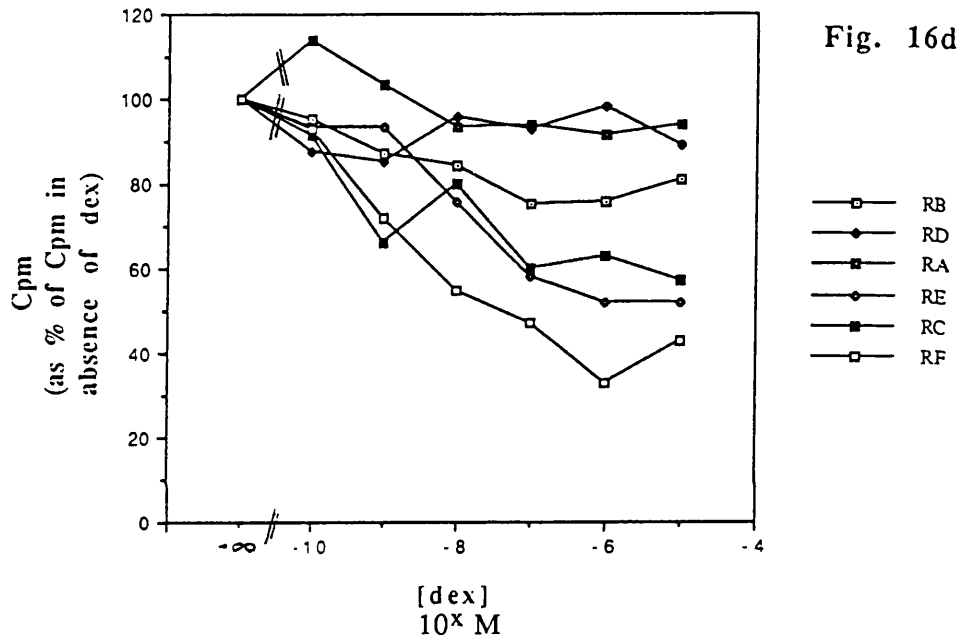


Fig. 16d

Proliferation of clones of PS15 after 3 days of culture in dex at concentrations from 10^{-5} M to 10^{-10} M. Each point is a mean of 6, with $\sigma_n < 5\%$ of the mean. Proliferation was measured by ^3H -thymidine incorporation and is expressed as a percentage of proliferation in the absence of dex. Resistant clones were isolated following EMS treatment.

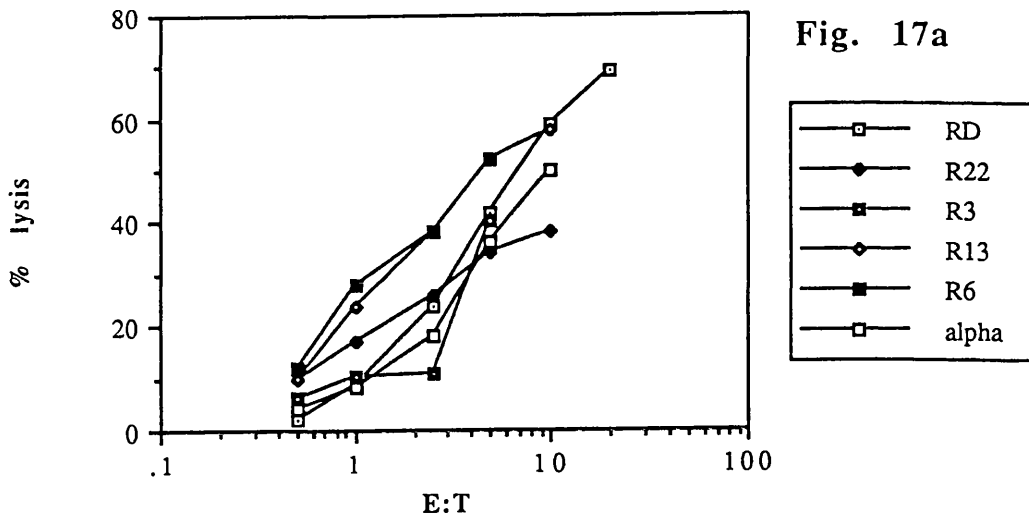


Fig. 17a

Lysis of clones of P815 by CTL:P35:10. Lysis was determined by ^{51}Cr release. Each point is a mean of 3, with $\sigma_n < 5\%$ of the mean. Spontaneous release was less than 20% of total.

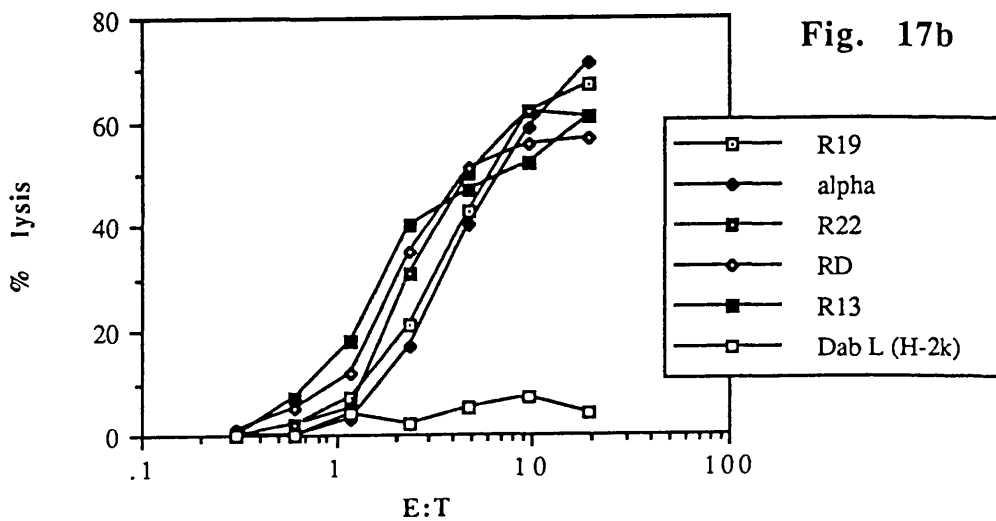


Fig. 17b

As above, but CTL were derived from an MLR.

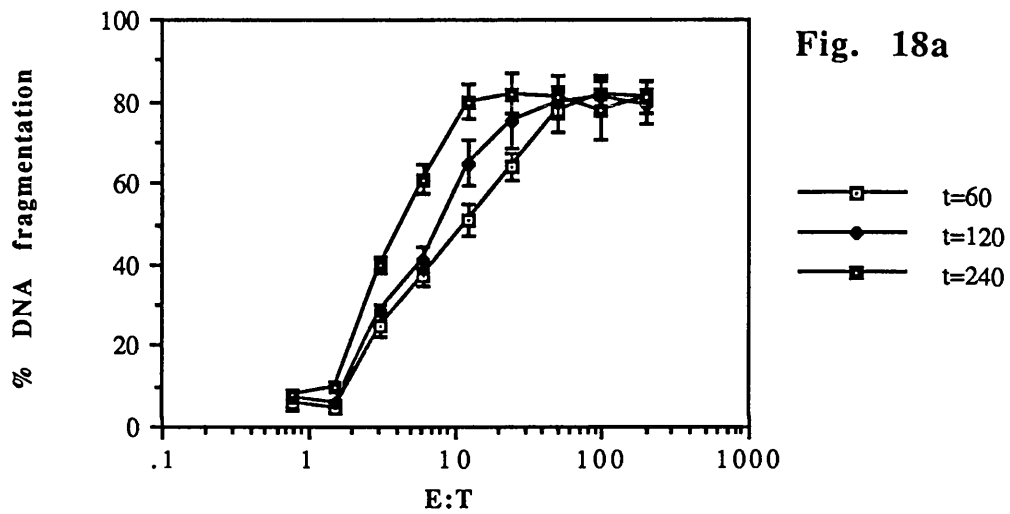


Fig 18a
 Kinetics of DNA fragmentation when P815 α is killed by CTL derived from an MLR. DNA fragmentation was determined by the Triton-X100 solubilization assay and is expressed as a percentage of total incorporated radiolabel. Each point is a mean of 6. Time is given in minutes.

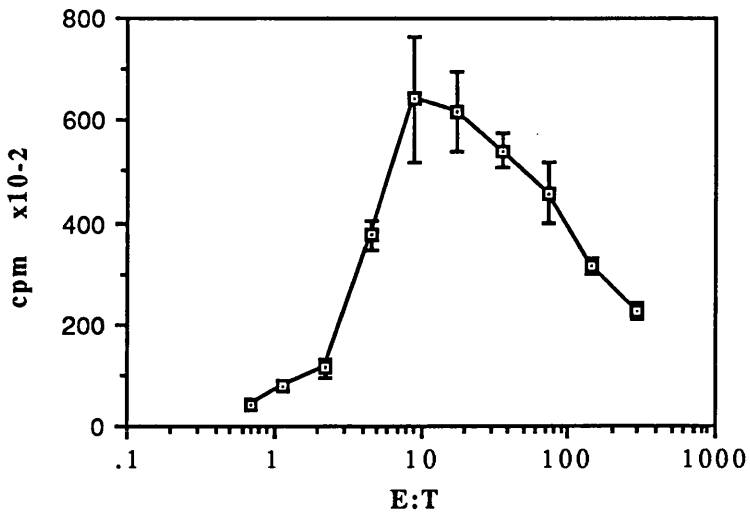


Fig. 18b

Fig 18b

Release of ^{125}I -uridine into the culture medium after 1 h incubation of P815 α with CTL derived from an MLR. Each point is a mean of 6.

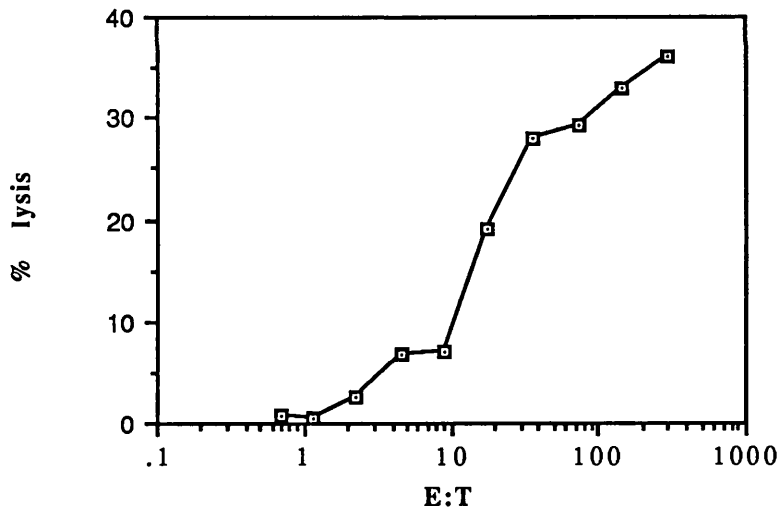


Fig. 18c

Fig 18c

Lysis of P815 α , as determined by ^{51}Cr release, after 1 h incubation with CTL derived from an MLR, carried out in parallel to the experiment shown in Fig. 18b. Each point is a mean of 3.

Effect of 5-azacytidine on P815 α clones

Treatment of cells in culture with the drug 5-azacytidine (5-azaC), an inhibitor of DNA methylation, has been shown to cause new gene expression (Groudine et al 1981), and in general, in eukaryotes, the DNA of inactive genes is more heavily methylated than that of active genes (reviewed by Cedar 1988). Treatment of glucocorticoid resistant lymphoid cell lines which have functional glucocorticoid receptors with 5-azaC has been shown to restore dexamethasone-sensitivity (Gasson and Bourgeois 1983) and spontaneous *de novo* methylation of these dex-sensitive cells is accompanied by the acquisition of the glucocorticoid resistant phenotype (Gasson et al 1983).

As dex-resistant clones were isolated from P815 α at a high frequency (cloning efficiency of P815 α in 10^{-6} M dex was reduced from 70-90% to approximately 1 in 2.3×10^3) it seemed possible that I had selected cells which had undergone a functional change due to an epigenetic or differentiatative event rather than a mutation in DNA sequence. To ask if dex-sensitivity might be restored to resistant clones by a decrease in DNA methylation, the dex-resistant clones were cultured in dexamethasone and 5-azaC for 5 days, according to the method of Gasson and Bourgeois (1983), and then bulk cultures were tested for glucocorticoid sensitivity. No lytic response was observed during the 5 day culture and Fig. 19a shows that after removal of 5azaC from the cultures there was no difference in their responses to dex in the ^3H -thymidine incorporation assay from the untreated cultures. No evidence in favour of the inactivation by methylation of a gene involved in lysis was found for any of the resistant clones.

Surprisingly, preliminary experiments showed that 5azaC treatment resulted in the acquisition of resistance by the sensitive parent P815 α . Fig 19b shows the dose response of P815 α in dex after 5

days 5azaC treatment and without treatment. In this experiment 5azaC treatment was carried out in the absence of dex, to exclude the criticism that resistance was acquired simply by selection in dex. Such bulk acquisition of dex-resistance was observed on several occasions. Cloning efficiency of P815 α in dex was increased 100-fold by 5azaC treatment, although treatment itself caused a reduction in cloning frequency to about 30%. The most straight forward interpretation of these data would suggest that in contrast to the lymphoid cell lines used in the work of Gasson et al, for P815 cells glucocorticoid resistance is an active function and not just acquired by the loss of a lysis capability. This would be in line with studies on the acquisition of resistance to apoptosis induced by tumour necrosis factor (TNF) (Laster et al 1988), in which TNF resistance is found to be dominant in cell fusion experiments (Nophar et al 1988). Clearly, to conclude this one would have to show that 5azaC was actually causing a decrease in DNA methylation; it is possible that, as 5azaC is itself toxic, it is selecting for cells that are more resistant to lysis, and not causing a bulk reversion to resistance by allowing new gene expression.

Northern blot analysis of glucocorticoid receptor mRNA levels

The cDNAs for the glucocorticoid receptor (GR) have been cloned in human, rat and mouse (Hollenberg et al 1985; Miesfeld et al 1986; Danielson et al 1986). The inactive glucocorticoid receptor is thought to be associated with the heat shock protein Hsp90 (Sanchez et al 1985), and in the presence of glucocorticoid hormones the Hsp90 dissociates and the receptor/steroid complex translocates to the nucleus and binds to the DNA at defined sequences, called the glucocorticoid response elements (GREs), thereby activating or inactivating specific gene

expression (reviewed by Gustafsson et al 1987; Yamamoto 1985). The hormone-binding and GRE-binding regions of the receptor have been defined by analysis of mutants (Okret et al 1986; Giguere et al 1986; Godowski et al 1987) and are at the C terminal of the receptor, separated by a short hinge region (Carlstedt-Duke and Gustafsson 1987).

In an effort to further elucidate the nature of the resistance to dex-lysis of the clones selected from P815 α , I carried out Northern blot analysis of the glucocorticoid receptor mRNA levels in the different clones, using a probe isolated from the plasmid pBS-0.7PR, which was a gift from Mike Jacobson. This probe is a 0.7kb GR cDNA fragment encoding the C-terminal region of the murine GR. Fig. 20a shows that this probe hybridized to two bands of molecular weights 7.2 kb and 5.2 kb in polyA⁺ RNA prepared from P815 α cultured in the absence of dexamethasone. These two different mRNA species have been reported previously and may be due to alternative polyadenylation sites (Rosewicz et al 1988; Kalinyak et al 1987).

Glucocorticoids are known to down-regulate GR mRNA levels by influencing gene transcription (Okret et al 1986; Rosewicz et al 1988). A possible explanation for the difference in sensitivity to dex of P815 α and the resistant receptor-positive sub-clones might lie either in their receptor levels or in their relative abilities to down-regulate GR mRNA expression on exposure to dex. Perhaps the sensitive cells fail to down-regulate their receptor levels and so over express genes that are induced by the hormone, which are then lethal to them over a period of days. Quantative comparisons of GR mRNA levels on exposure to dex was carried out by dot-blot analysis, using the 0.7kb GR cDNA probe. Poly A⁺ mRNA was prepared from P815 α , R19 (a resistant clone which has no response to dex) and R22 (a resistant clone which proliferates more in dex). Autoradiographs were scanned using a densitometer (Hoefer

Scanning densitometer GS-300) and integration of density curves was carried out using GS-370 electrophoresis data reduction system (Hoefer). A chicken β -actin probe (a gift from N. Pringle) was used as positive control and to make sure that equivalent amounts of RNA were compared.

Fig. 20b shows densitometer readings from a dot-blot, indicating the relative levels of GR receptor in R19 and P815 α and R22 at time points after addition of Dex. Units are an arbitrary measure of area and all figures are adjusted by comparison with actin mRNA levels from re-screening the same blot with an actin probe, to normalise mRNA concentrations. Both cell lines down-regulate their receptors at a similar rate, with R19 reaching one half its original level in 19 h and P815 α in 17 h. P815 α had about 2.6 times more GR mRNA than R19. R22, like P815 α , also had high levels of GR, which was down-regulated by one half in 17.9 h. When grown continuously in 10^{-6} M dex both R19 and R22 had GR mRNA concentrations similar to those after culture in the absence of dex, and after 48 h in dex [GR mRNA] in R19 is rising again.

Thus, these three cell lines manifest no difference in their abilities to down-regulate the GR on exposure to dex, but R19, a clone which does not respond to dex has strikingly less GR mRNA than R22 and P815 α .

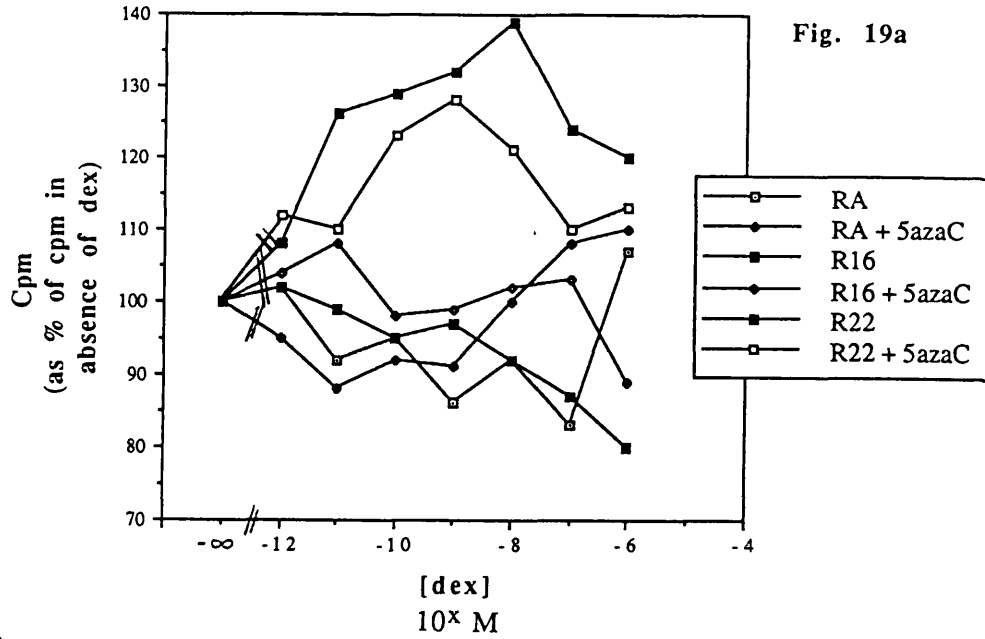


Fig 19a
 Proliferation of dex-resistant P815 clones after 3 days culture in dex. Clones have been treated with 5azaC. Proliferation was measured by thymidine incorporation and is expressed as a percentage of proliferation in the absence of dex. Each point is a mean of 6 with $\sigma_n < 5\%$ of the mean.

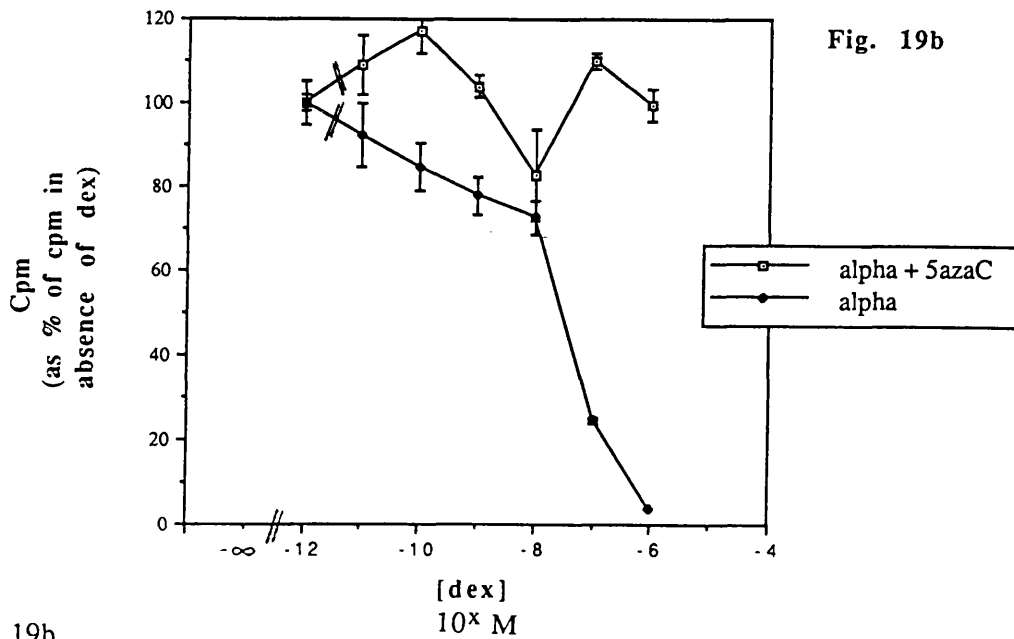


Fig 19b
 As above, but showing the response of the parent P815 α after 5azaC treatment.

Fig. 20a

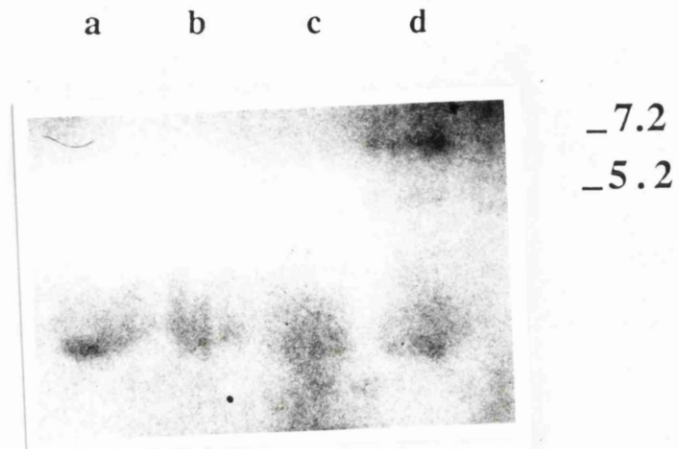


Fig. 20a

Northern blot of PolyA⁺ RNA prepared from RA (track a), RB (track b), RD (track c) and P815 α (track d), probed with a 0.7 kb GR cDNA probe. The probe hybridized to two bands of molecular weights 7.2 kb and 5.2 kb in track d (P815 α).

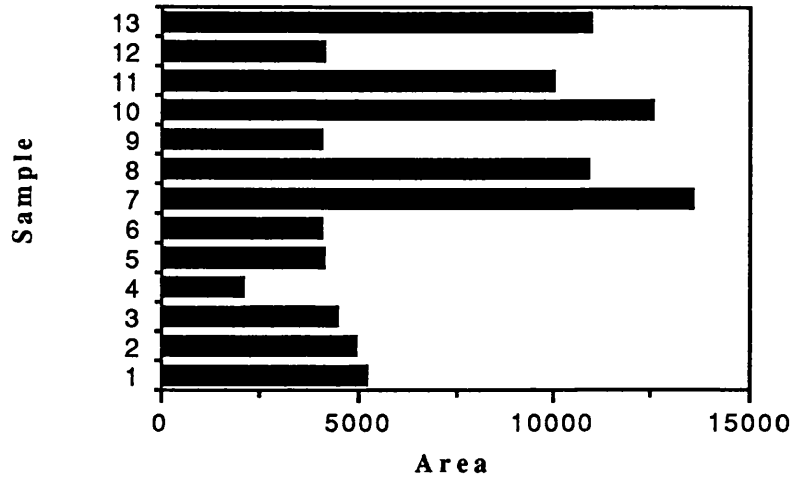


Fig. 20b

<u>Number</u>	<u>Sample</u>
1	R19, No dex
2	R19, 10^{-6} M dex, 2h
3	R19, 10^{-6} M dex, 4h
4	R19, 10^{-6} M dex, 24h
5	R19, 10^{-6} M dex, 48h
6	R19, 10^{-6} M dex, 2 weeks
7	P815 α , No dex
8	P815 α , 10^{-6} M dex, 4h
9	P815 α , 10^{-6} M dex, 24h
10	R22, No dex
11	R22, 10^{-6} M dex, 4h
12	R22, 10^{-6} M dex, 24 h
13	R22, 10^{-6} M dex, 2 weeks

Fig. 20b

The relative concentrations of glucocorticoid receptor mRNA in P815 α , R19 and R22 on exposure to dexamethasone. Units are an arbitrary measure of area, derived from integration of densitometer readings of an autoradiograph. Integration was carried out using the software GS-370 electrophoresis data reduction system (Hofer).

DISCUSSION

This study failed to provide evidence in favour of a common pathway of cell death induced by glucocorticoids and by CTL. None of the dex-resistant clones isolated showed a reduction in susceptibility to CTL lysis, indicating that the defects selected for were not part of a common suicide pathway, although it is possible that common elements in the death pathways exist downstream from these lesions. Other investigators have also been unable to demonstrate a common killing mechanism by analysis of mutants (Dennert et al 1988), which is a pity because a mutant cell line that is resistant to multiple forms of killing would be invaluable for investigating the molecular mechanisms of apoptosis. It always seems that a high percentage of dex-resistant mutants isolated in any study are defective in their glucocorticoid receptors (Sibley and Tomkins 1974; Wyllie et al 1984), which are unlikely to be involved in CTL killing. It might be possible to increase the probability of isolating a cell line with a mutation at a common point in a lysis pathway by first transfecting the dex-sensitive parent clone with multiple copies of the glucocorticoid receptor gene, thus reducing the chance of selecting a cell with defective receptor function.

The question remains, however, whether any cell is truly resistant to CTL lysis per se, if the need for target cell recognition by CTL is by-passed. In their search for a correlation between resistance to dex and resistance to CTL, Dennert et al examined several cell lines with reduced sensitivity to CTL-lysis and found in all but one case that these cells had reduced expression of MHC Class I; the sensitivity to CTL-lysis could be restored by increasing Class I expression. The only cell line where the failure to be killed could not be explained by lack of Class I expression was a subclone of the line S49-4RD, used in Ucker's study.

S49-4RD had normal levels of cell surface Class I but failed to induce the reorientation of the Golgi apparatus and microtubule-organising centre (MTOC) in the CTL, which is known to be a prerequisite for lysis (Kupfer and Dennert 1984; Kupfer et al 1985). S49-4RD's sensitivity to CTL was normal when the lectin ConA was added to by-pass the need for CTL recognition. This was interpreted to imply that the CTL must interact with another undefined molecule on the target cell surface in addition to Class I in order to reorientate its Golgi apparatus and MTOC. Other cells which have been reported to be resistant to CTL killing are neuroblastomas and gliomas (Main et al 1985). These cells have low levels of surface Class I expression, which can be increased with γ IFN treatment, but in some cases they remain resistant to CTL. However, when the need for adequate recognition is by-passed by the addition of lectins, these cells are killed (Main et al 1988), again implicating an undefined target cell-surface molecule in the recognition phase. Perhaps, previously reported CTL-resistant cells (Gasson and Bourgeois 1983) were deficient in such a cell surface molecule rather than in an element of a lysis pathway.

The final category of cells resistant to CTL-killing are CTL themselves (Kranz and Eisen 1987; Blakely et al 1987). The necessity for these cells to be resistant to their own lysis apparatus is obvious and it has been suggested that they have cell surface molecules which protect them from the membrane lesions induced by perforin (Zalman et al 1987; Muller-Eberhard 1988), in the same way that a homologous restriction factor (HRF) protects erythrocytes of a given species from injury by complement of that species (Zalman et al 1986). The role of HRF in protecting CTL remains controversial (Jiang et al 1989). Other authors have suggested that perforin must be activated by a cascade involving the granule-contained serine proteases, analogous to the

complement cascade, and that in the cell, the components of this cascade are sequestered within the granules (Masson and Tschopp 1987). The cytoplasmic granules themselves have T cell receptors on their surfaces, providing specificity in their lysis action (Peters et al 1989). An HRF-like protection mechanism would only protect CTL against a perforin-dependent mechanism of lysis. Authors who favour a perforin-independent killing process suggest that this type of killing occurs where the perforin-dependent mechanism fails (Ostergaard and Clark 1989). As CTL have been reported to be resistant to lysis not only by perforins (Shinkai et al 1988), but also by cytoplasmic granules (Verret et al 1987), and by CTL (Skinner et al 1987; Kranz and Eisen 1987; Blakely et al 1987), those in favour of an alternative mechanism of killing would have to postulate that CTLs are also resistant to this perforin-independent mechanism. If the alternative mechanism involves the triggering of an auto-destruct process of apoptosis (Golstein 1987), then CTL should be unable to undergo this process. This seems not to be the case: many CTL clones, although resistant to glucocorticoid-induced lysis (Nguyen and Nabholz 1985), are IL2-dependent (Gillis and Smith 1977) and die by apoptosis on IL2-withdrawal (Duke and Cohen 1986).

What is the mechanism of the resistance to glucocorticoids of the selected dex-resistant clones? Resistance has frequently been described in cell lines which have lost expression of functional glucocorticoid receptors (GR) (Sibley and Tomkins 1974), but this cannot be the explanation in all cases because some of the clones still show a response to dex, which increased their proliferation. Previous studies have indicated that there is little difference in the ligand affinity of the GR between different resistant and sensitive cell types (Schleche et al 1982;

Shipman et al 1983; Zawydiwski et al 1983) but degree of sensitivity may, correlate with the concentration of GR. As steroid hormones are used in the treatment of leukaemia, numerous studies looking for a correlation between GR levels and sensitivity to the hormone (and hence between GR levels and prognosis) have been carried out in humans. Some such studies report a good correlation (Lipman et al 1978; Costlow et al 1982), whereas others find no correlation (Mastrangelo et al 1980). A similar discrepancy exists between studies looking for a correlation between GR levels and the differential sensitivity of normal murine lymphoid cells (Bradley and Mishell 1982; Lippman and Barr 1976). This work measured GR concentration using ligand binding assays, an approach which has been criticised because of the difficulty of assuring a total exchange of receptor-bound unlabelled steroids for labelled hormone and of preventing the binding of labelled glucocorticoid ligand to heterologous receptors (Okret et al 1986). To avoid these criticisms I looked directly at GR mRNA levels in P815 α and two resistant sub-clones. R19, which shows no response to dex in proliferation assays, had about three times less GR mRNA than the sensitive parent or than R22, a resistant clone which undergoes increased proliferation in dex. This result suggests that in the case of R19 the lack of sensitivity to dex may simply be due to reduced expression of GR.

Ligand binding studies have suggested that GR concentration is regulated by the hormone (Cidlowski and Cidlowski 1981; Svec and Rudic, 1984), which also regulates GR mRNA concentrations (Okret et al 1986; Rosewicz et al 1988). Rosewicz's study of rat and human cell lines shows that corticosteroid-induced down-regulation of GR is caused by a decrease in the rate of gene-transcription, whereas other authors have also suggested that the hormone shortens GR half-life (McIntyre and Samuels 1985). Okret uses immunoprecipitation to analyse GR-DNA

interactions and shows that there are GR-specific binding regions within a GR cDNA clone, suggesting that GR down regulation might be due to interaction of the GR protein with its own gene. He also shows that down regulation is decreased by the protein synthesis inhibitor cycloheximide, implicating a trans-acting repressor protein. As 5azaC seems to convert dex-sensitive cells to dex-resistance, hinting that resistance might be the dominant state, it seemed possible that the difference between P815 α and the resistant clones might be the expression of such a trans-acting repressive factor. Therefore, I examined down-regulation of GR by R19, R22 and P815 α in 10^{-6} M dex. P815 α down-regulated its GR at the same rate as the resistant cells. The time for GR mRNA to decrease by one half was about 18 h. This is similar to the findings of Okret who showed that in rat hepatoma cells in culture [GR mRNA] was decreased by 50-95% in 24 h, whereas in Rosewicz's study the decrease was much faster, with a one-half time of 3 h for a human lymphocyte cell line and 6 h for a rat pancreatic acinar cell line. P815 cells in prolonged culture in dex re-express GR mRNA at their original levels. This concurs with Okret's study, which showed that levels return to normal after 72 h in dex, but Rosewicz found no return to the original level of expression.

The observation that 5azaC confers dex-resistance to the dex-sensitive parent cells needs further investigation, and suggests that resistance results from the acquisition of something which protects the cell from lysis or changes its response to glucocorticoids, rather than as a result of the loss of part of a lysis pathway. Unfortunately, this means that these cells were probably not appropriate to use in the search for a correlation between resistance to CTL and to dex (unless one believes that resistance to CTL is also active). Resistance to tumour necrosis factor (TNF) has been shown to be a positive function in some cells

(Nophar et al 1988) and heat shock proteins have been shown to protect WEHI-164 cells from apoptosis induced by TNF (Jaattela et al 1989). It would be interesting to examine levels of heat shock proteins in P815 cells in response to dex.

**CHAPTER FIVE:
STUDIES ON APOPTOSIS IN THE THYMUS**

INTRODUCTION

Possible roles for cell death in T cell development in the thymus.

Since the 1960s it has been known that there is massive cell death in the mammalian thymus (Matsuyama et al 1966; Metcalf 1966), but, until recently, the assumption had been that this cell death represented a dead-end pathway in development, and served no useful purpose (Shortman and Jackson 1974; Fathman et al 1975; Scollay et al 1984). However, a better understanding of the lineage relationships between sub-populations of thymocytes and of the molecular mechanisms that generate T cell receptor (TCR) diversity has radically changed this view.

About 80% of murine thymocytes express both the T cell accessory molecules CD4 and CD8 (Kisielow et al 1975; Mathieson et al 1979; Scollay and Shortman 1983), which on mature T cells are generally mutually exclusive (Dialynas et al 1983b; Swain 1981). It is these double positive cells which die in the thymus (reviewed by Scollay et al 1984; Rothenberg and Lugo 1985). Studies involving reconstitution of irradiated mice (Fowlkes et al 1985; Fowlkes and Mathieson 1985), abrogation of normal T cell development *in vivo* by the administration of monoclonal antibodies (mabs) (Smith 1987; MacDonald et al 1988a; Fowlkes et al 1988), and the generation of mice transgenic for TCR genes (Kisielow et al 1988a and b; Sha et al 1988) have suggested the following lineage in thymus development: Double negative ($CD4^-CD8^-$) cells to double positive ($CD4^+CD8^+$) cells to single positive ($CD4^+CD8^-$ and $CD4^-CD8^+$) cells. The double negative thymocytes lack expression of the CD3 $\alpha\beta$ TCR complex (Roehm et al 1984; Bluestone et al 1987), although a subpopulation express the $\gamma\delta$ TCR (Pardoll et al 1987). A proportion (about half) of the double positive thymocytes express low levels of the

CD3 $\alpha\beta$ TCR complex (Havran et al 1987; Crispe et al 1987) and, in humans, there is evidence that a small proportion (4-9%) are CD3^{high} (Blue et al 1987). The single positive thymocytes express the same levels of the CD3 $\alpha\beta$ TCR complex as T cells in the periphery (Snodgrass et al 1985; Cristanti et al 1986). A rapidly cycling CD8⁺CD3⁻ single positive population also exists, which is thought to represent the transition between the double negative thymocytes and expression of both accessory molecules (Paterson and Williams 1987; MacDonald et al 1988b). The CD3⁺ single positive thymocytes possess mature T cell function (Ceredig et al 1982 and 1983; Chen et al 1982) and are functionally and phenotypically indistinguishable from recent emigrants from the thymus (identified by intrathymic FITC injection, Scollay et al 1978 and 1984; Scollay 1982), whereas the double positives are not functionally mature (Adkins et al 1987).

The fact that the mature single positive thymocytes which leave the thymus are derived from the large double positive population has led to the suggestion that the cell death one observes in the double positive population reflects thymic selection procedures rather than a dead-end developmental lineage. The diversity of the T cell receptor repertoire is generated by genetic recombination events (reviewed by Kronenberg et al 1986) that produces self-reactive cells, which must be either deleted (Burnet 1962) or suppressed (reviewed by Howard and Mitchison 1975; Nossal 1983). Until recently no conclusive evidence for either deletion or suppression had been presented. Experiments that assay the primary T-cell responses of single positive thymocytes to MHC antigens *in vitro* had shown that these cells can respond to non-self, but not self MHC molecules, indicating that some tolerization of T cells occurs before they leave the thymus, suggesting either clonal deletion or inactivation in the thymus (Good et al 1983; Kruisbeek et al 1981).

Other work, however, favoured the maintenance of tolerance by suppressor T cells in the periphery. Many authors have claimed that some anti-self T cell reactivity can be measured *in vitro* (eg Smith and Pasternack 1978; Glimcher and Shevach 1982; Glimcher et al 1982) and it has been proposed that these self reactive cells are regulated by suppressor cells *in vivo* (Brondz et al 1984). Chen and Splitter (1983) found that Lyt1⁺2⁻ T cells, but not unseparated or Lyt1⁻2⁺ T cells, from nude mice grafted with normal neonatal thymuses gave a strong proliferative response *in vitro* to grafted thymus MHC-type stimulator cells, suggesting that tolerance to self MHC antigens is maintained *in vivo* by Lyt1⁻2⁺ suppressor T cells.

The observation that certain TCR V β domains are strongly correlated with reactivity to a particular antigen in the context of a defined MHC molecule (Kappler et al 1987a; MacDonald et al 1988e), and the availability of mabs to such V β domains, has made it possible to track the developmental fates of cells known to be self-reactive. In this way, clonal deletion as a mechanism of tolerance induction has now been demonstrated in several systems (Kappler et al 1987b; MacDonald et al 1988c; Kappler et al 1988; White et al 1989). That clonal deletion in the thymus is responsible for tolerance to some antigens does not exclude the possibility that other mechanisms such as suppression also occur.

Clonal deletion in tolerance induction has also been shown using mice transgenic for a TCR reactive to the H-Y antigen in the context of H-2D^b, backcrossed to *scid* mice, and hence expressing only the transgenic TCR. In the thymuses of the male transgenic mice (which express the H-Y antigen) there are virtually no single positive CD8⁺ cells and fewer than normal double positive thymocytes, indicating that tolerance in the thymus is caused by clonal deletion in the double positive population (Kisielow et al 1988a). Evidence that clonal deletion

occurs at the stage when T cell precursors are expressing both accessory molecules also comes from experiments in which the deletion of CD8⁺ single positive thymocytes, identifiable by their V β gene usage, is prevented by *in vivo* administration of mab against CD4 (MacDonald et al 1988a; Fowlkes et al 1988) and from histological analysis of where in the thymus cells that express a self-reactive receptor are absent (Hentgartner et al 1988).

The hypothesis I wish to consider in this chapter is that the mechanism of clonal deletion is apoptosis, induced by a ligand binding to the TCR of double positive thymocytes. This suggestion is supported by the work of Smith et al (1989) who show that addition of a mab against CD3 to the culture medium of foetal thymus organ cultures leads to an increase in cell death in the thymus organ culture, and that the dying cells show the characteristic morphology of apoptosis and DNA fragmentation.

This explanation for the death of double positive thymocytes is, however, complicated by the need for positive selection of the T cell repertoire. In 1975 the phenomenon of MHC restriction was discovered with the observation that cytotoxic T cells recognize antigens in association with self class I MHC molecules on the surface of target cells (Zinkernagel and Doherty 1975). Later MHC restriction was demonstrated to apply to T-helper cells also, although these are primarily restricted by class II MHC molecules (Sprent 1978). Experiments with chimaeric mice showed that T cell restriction is governed by the MHC type of the thymus in which T cells develop (Zinkernagel et al 1978; Fink and Bevan 1978). It was therefore postulated that developing T cells are selected in the thymus on the basis of their ability to bind to the MHC molecules of the thymus, such that cells which complete their maturation and exit to the periphery are

primarily restricted to thymus-type MHC antigens. Until recently this theory of positive selection had remained controversial: allo-restricted T cells, whose activity can be measured if animals are primed with antigen on allogeneic antigen presenting cells, were shown to exist (eg Wilson et al 1977; Matzinger and Mirkwood 1978; Ishii et al 1981). Experiments in which thymuses were grafted to nude mice showed that responses were restricted to nude MHC type rather than to that of the graft thymus (Kindred 1978; Zinkernagel et al 1980; Lake et al 1980). Moreover, the conceptual problem of how antigen-specific, MHC-restricted T cells can be selected in the thymus by MHC alone was unresolved.

Both the work with transgenic mice (Kisielow et al 1988b; Sha et al 1988) and the approach of following the fate of cells expressing particular V β gene products throughout their development have demonstrated positive selection in the murine thymus. In the case of the 'monoclonal' anti-H-Y transgenic mice produced by von Boehmer's group, female H-2D^b mice (which do not express H-Y) were found to have CD8⁺ single positives and double positives cells in their thymuses, whereas mice that did not express H-2D^b had double positives but no single positives (Kisielow et al 1988b). This suggests that an interaction between the TCR and MHC is necessary for differentiation from double positive to single positive and that this interaction determines the fate of the cell: since the transgenic TCR interacts with Class I, only CD8⁺ T cells are produced. In MacDonald's system (reactivity to the Mls^a gene product in the context of I-E correlates with V β 6 expression), the same Class II MHC loci which are required for deletion of V β 6⁺ cells in Mls^a-expressing mice, and which restrict Mls^a-reactive T cell clones and hybrids, control the frequency of V β 6⁺ cells among mature CD4⁺ T cells in mice lacking expression of Mls^a (MacDonald et al 1988d). This is

consistent with positive selection in which interaction of the TCR with MHC Class II is required for differentiation into a mature CD4⁺ single positive cell. The existence of positive selection is also supported by experiments in which the ratio of CD4⁺ to CD8⁺ mature thymocytes is skewed in fetal thymus organ culture by addition of hybrid antibodies against both one accessory molecule and CD3 (Zepp and Staerz 1988).

The need for positive selection to allow cells in the periphery to recognise antigen in the context of MHC clearly complicates an interpretation of the role of cell death in T cell development in the thymus. Perhaps all double positive thymocytes are programmed to die, unless rescued by a survival signal if their TCR has appropriate MHC-reactivity, and it is this that accounts for the cell death one observes in the double positive population.

Evidence for cell death in the murine thymus

The initial evidence for cell death in the murine thymus came from 'balance-sheet' studies in which an estimate of thymocyte proliferation, assessed by an autoradiographic analysis of ³H-thymidine (³H-TdR) incorporation, was compared with thymus weight gain and migration from the thymus. The extent of proliferation in the thymus could only be explained if most of the cells died *in situ*, as the population turnover time was about 3 days for thymocytes and yet the thymuses did not get larger and only a small percentage of labelled cells migrated to the periphery (Matsuyama et al 1966; Metcalf and Wladrowski 1966). Similar work in guinea pigs (Nossal 1964; Murray and Woods 1964) and rats (Goldschneider and McGregor 1968) also showed that most thymocytes die in the thymus and have a lifespan of 3 to 4 days

The extent of thymus cell death has been disputed, however, largely because of the difficulty of producing histological evidence

(Borum 1968, Michalke et al 1969; Sainte-Marie and Peng 1971; Poste and Olsen 1973). It was argued that if nearly all thymocytes die within 4 days of their birth then this cell death should be easy to visualize. Thymocyte cell death was demonstrated more conclusively by exploiting the difference in the ability of cells to incorporate the thymidine analogues, $^3\text{H-TdR}$ and $^{125}\text{I-uridine}$ ($^{125}\text{I-UdR}$) (Feinendegen et al 1973). $^3\text{H-TdR}$ is incorporated about six times more efficiently than $^{125}\text{I-UdR}$ (Baugnet-Mathieu and Goutier 1968) and so if thymocytes are pulse labelled with these precursors the relative rates of decline of the two isotopes will reflect the extent of local reutilization of thymidine, which should in turn mirror the degree of local cell death: If cells migrate, both isotopes should be lost in parallel, but if cells die and the nucleotides are reutilized locally by salvage pathways, then $^3\text{H-TdR}$ levels should be maintained about six times more efficiently than $^{125}\text{I-UdR}$ levels. Several studies (Feinendegen et al 1973; Laissue et al 1976; McPhee et al 1979) have demonstrated that about 60% of the injected $^3\text{H-TdR}$ is reused locally in the thymus and that the transit time from the last DNA synthesis until migration or cell death is about 3 days (Ernstroem and Larsson 1965). This work was still criticized because of the possible toxicity of $^{125}\text{I-UdR}$, but this criticism was excluded by McPhee et al (1979) (see Results) who estimated that a minimum of 60% of all thymocytes formed die in the thymus, both in adult mice and in 7-day old mice. Another criticism, that the observed cell death was induced by hydrocortisones released because of the stress of the experiment, was also excluded in McPhee's study, as the same estimate was obtained in adrenalectomised mice.

A final argument in favour of the contention that most thymocytes, and nearly all double positive thymocytes, die *in situ* can be made from the near impossibility of culturing dissociated double

positive thymocytes *in vitro*. In the absence of an intentional lethal stimulus from the experimenter all double positive thymocytes die within about four days in culture (Hopper and Shortman 1976). Where mature single positive cells are obtained from such cultures (eg Blue et al 1985, 1987) it has been argued that these are due to preferential expansion of contaminating single positive thymocytes, and limiting dilution cloning has suggested that very few double positive cells (<2%) can survive (Chen et al 1982 and 1987; Andrews 1985; Ceredig et al 1982). Recent experiments, in which the objection of contamination by single positive thymocytes was circumvented (by taking advantage of the fact that mature T cells bearing V β 6 are eliminated by tolerance mechanisms in the thymus of Mls^a positive mice, and by providing CD4⁺CD8⁺ thymocytes from such mice with a V β 6-specific stimulus) have suggested that about 3% of double positive thymocytes are clonable (Howe and MacDonald 1989). This fits well both with the theory that the double positive thymocytes are the pool on which both rounds of repertoire selection are carried out and with data from *in vivo* studies which indicate that about 1% of thymocytes migrate each day and 30% are born each day (Claesson and Hartman 1976; Scollay et al 1980; Scollay et al 1988). Thus most thymocytes die in the thymus.

The fact that this cell death is so difficult to see under the light microscope might be explained if thymocytes die by apoptosis. Apoptosis occurs when death is part of an organised tissue reaction, such as in embryogenesis, and is characterised by lack of scarring and rapid removal of dead cells, which do not elicit an inflammatory response (Wyllie 1981 and 1987). Apoptotic bodies are rapidly phagocytosed by adjacent cells (Duvall et al 1985), and it has been estimated that the half-time for which apoptotic cells remain visible by light microscopy is less than nine hours (Wyllie et al 1980; Ijiri and

Potten 1983). The speed of disappearance of apoptotic bodies from tissues *in vivo* indicates that their plasma membranes may be altered in a way that enhances phagocytosis, and abnormalities have been detected in the sugars exposed on their surfaces (Morris et al 1984; Wyllie 1985).

Apoptotic cells have been described in the thymus under normal conditions (Van Haelst 1967a; Fraker et al 1977; Joel et al 1977; Wyllie et al 1980) and glucocorticoid hormones are well known to induce apoptosis in thymocytes *in vivo* (Van Haelst 1967b; Umansky et al 1981; La Pushin and de Harven 1971) and in thymocytes *in vitro* (Wyllie 1980, Wyllie and Morris 1982).

RESULTS

Development of an assay for apoptosis *in vivo*

Strategy

The difficulty of visualizing cell death in the murine thymus, despite the convincing arguments suggesting that many cells must be dying at any point in time, led me to try to develop a way of detecting and quantifying apoptosis *in vivo*. Such a method would have to identify dying cells before their rapid phagocytosis and destruction and so ideally would rely on detection of a molecule that is expressed or up-regulated early in death. The molecule(s) might be the one whose synthesis is thought to be inhibited by cycloheximide, when it delays death by apoptosis (Williams et al 1990; Duke and Cohen 1986; Pratt and Greene 1976), or the sugars that change on the cell surface (Morris et al 1984; Wyllie 1985). Unfortunately the biochemistry of apoptosis has not been elucidated (Kerr et al 1987; Wyllie 1987) and so such probes are not available.

I tried, unsuccessfully, to raise monoclonal antibodies which distinguish between apoptotic and viable cells, by immunizing rats with either nuclei of apoptotic cells or whole apoptotic cells and screening hybridoma supernatants from a fusion by flow cytometry. The only mabs produced by this protocol which seemed hopeful, in that they stained a higher proportion of dex-treated thymocytes than fresh thymocytes, turned out to recognise a nuclear antigen, and the increase in their staining on the dying cells only reflected changes in plasma membrane permeability on death and hence suggested that my fixation and permeabilization protocol (D.H.Katz, personal communication) was inadequate. In addition, in collaboration with A.H. Wyllie, I immunized a mouse with an FPLC fraction containing endonuclease activity

obtained from a rat thymocyte nuclear extract. Hybridomas were screened by dot-blotting onto the nuclear extract, but none of the mabs obtained from this fusion convincingly stained more strongly on frozen sections of rat thymus treated with hydrocortisone *in vivo*, than on frozen sections of untreated rat thymus, or on permeabilized rat thymocytes treated with dex *in vitro* and analysed on the Facs, than on fresh permeabilized thymocytes.

As the antibody approach proved unsuccessful and it seemed unlikely that one would generate antibodies against something so specific when immunizing so crudely, (particularly given that the molecule must be in the thymus and so an animal would be very likely to be tolerant to it), I decided to try to adapt the DNA fragmentation assay used in CTL-mediated killing (Duke and Cohen 1983) to assess the extent of DNA fragmentation in a tissue at a given time. In principle, then, the plan was to label mice *in vivo* with a radioactive thymidine analogue ($^3\text{H-TdR}$ or $^{125}\text{I-UdR}$), to kill the mice and prepare cell suspensions from tissues of interest, and then to determine the degree of DNA fragmentation in the cells by partial lysis with Triton-X100 and centrifugation, to establish what proportion of the radiolabel was in different fractions of chromatin, as separated by size. As DNA fragmentation is a hallmark of apoptosis (Wyllie et al 1984) this approach to quantifying cell death should have the advantage that it measures apoptosis, but not necrosis. For this method to be successful the cells of interest would have to be proliferating in order to acquire the radiolabel (fortunately thymocytes are, Metcalf and Wladrowski 1966), and one would have to be certain that the radiolabel itself was not toxic to the cells (McPhee et al 1979).

Labelling the mice

Four week old male B10 BR mice were labelled with either ^3H -TdR ([6- ^3H]-thymidine, 22Ci/mmol, Amersham) or ^{125}I -UdR ([5- ^{125}I] iodo-2'-deoxyuridine, 5Ci/mg, Amersham). Doses were titrated to obtain sufficient counts in the thymus.

Labelling with ^3H -T d R

Mice were injected intraperitoneally (i.p.) with the ^3H -TdR in 0.4 ml PBS. As most thymocytes have a life span of about 3-4 days (Bryant 1972) and small cortical thymocytes (double positives) are thought to die about 3 days after their last DNA synthesis (McPhee 1979), each mouse was injected every morning for four days, in order for as many cells in the thymus to be labelled as possible, and not just one subpopulation or developmental stage to be labelled. To determine if the labelling was successful the mice were killed, cell suspensions of their thymuses were made and washed twice in MEM-H, and then 5×10^5 cells in 150 μl MEM-H were harvested on a Dynatech microtiter automash cell harvester. Filter paper was dried and each piece was emersed in 3 ml Optiscint scintillation fluid (LKB) and counted on a liquid scintillation counter (LKB Rackbeta 1214).

Fig. 21a shows the counts per 5×10^5 thymocytes after different labelling protocols. The largest increase in labelling achieved was between 50 μCi per day per mouse and 100 μCi per day per mouse, and as I wanted to obtain maximum intrathymic labelling with minimum cost, I decided to adopt a dose of 100 μCi per day for future experiments. At the highest doses used labelling appears to be approaching saturation point (for this ratio of Ci/mol) and so one can estimate that at 100 μCi per day about 2/3 of possible cells are labelled, assuming that there is not a large dose-dependent variation in counts per labelled cell. Higher

counts in the thymus on the day of killing might have been achieved by building up the dose over the four day period, but as far as possible it was preferable for thymocytes born on each day of the labelling period to incorporate equivalent amounts of $^3\text{H-TdR}$ and so to be exposed to the same dose of $^3\text{H-TdR}$. This dose ($100\mu\text{Ci}$ per day) is considerably more than other investigators have used: McPhee et al (1979) injected $25\mu\text{Ci}$ $^3\text{H-TdR}$ i.p. on one occasion only, Denizot et al (1986) injected $25\mu\text{Ci}$ $^3\text{H-TdR}$ i.p. on 6 consecutive days ($150\mu\text{Ci}$ total) and Ewing et al (1988) injected $100\mu\text{Ci}$ per mouse. Their studies assessed incorporation by autoradiography, but as I intended to count radiolabel in different chromatin fractions, I required higher labelling. The high dose used therefore made it particularly important to show that the $^3\text{H-TdR}$ was not itself toxic to the cells.

Fig. 21b shows the weights of the thymuses in the different groups. There is no decrease in weight at the higher doses, suggesting that these doses of $^3\text{H-TdR}$ were not toxic over the time of exposure. In addition, thymocytes from one mouse in each group were stained with mabs against CD4 and CD8. No difference in ratios of double positives to double negatives to single positives were found (approx. 73% $\text{CD4}^+\text{CD8}^+$, 9% $\text{CD4}^-\text{CD8}^-$, 4% CD8^+ and 14% CD4^+) between the different groups. One would expect double positives to be particularly susceptible to any potential toxin, so the fact that ratios were not changed also suggested that the $^3\text{H-TdR}$ was not toxic. The ratios I found in these mice are perhaps skewed towards double negatives; for example Havran et al (1987) reported 82% $\text{CD4}^+\text{CD8}^+$, 3% $\text{CD4}^-\text{CD8}^-$, 12% CD4^+ and 3% CD8^+ in 12 week old mice. This discrepancy may reflect the younger age (4 weeks) of my mice.

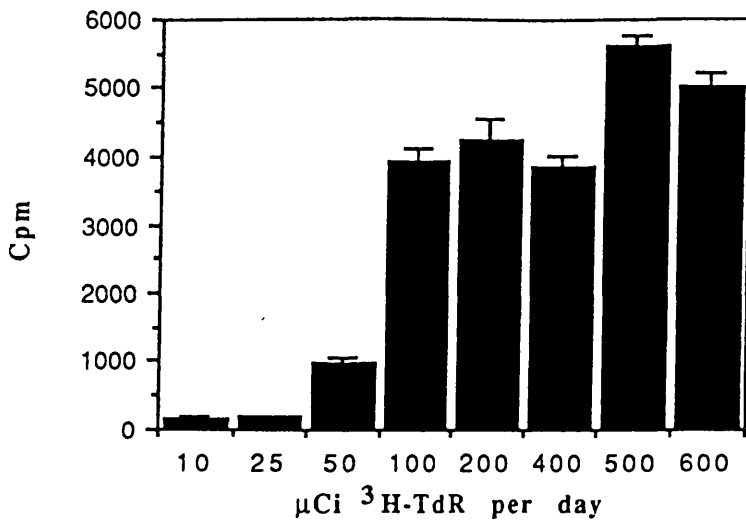


Fig. 21a

Fig. 21a

Cpm in 5×10^5 thymocytes after daily injection of $^3\text{H-TdR}$ in a dose range from $10 \mu\text{Ci}$ to $600 \mu\text{Ci}$ per day for 4 days. Each point is the mean of cpm from 3 mice, and the value for cpm for each mouse was a mean of 10 readings, with $\sigma_n < 5\%$ of the mean.

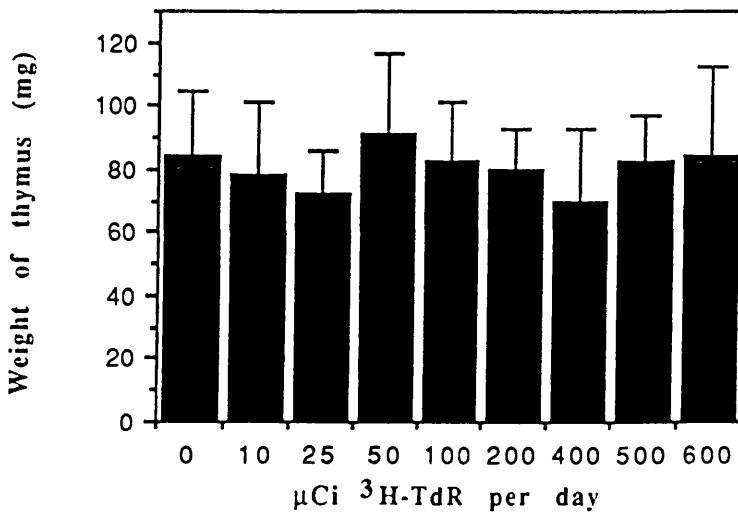


Fig. 21b

Fig. 21b

Weights of thymuses of mice which have been given a daily injection of $^3\text{H-TdR}$ in a dose range from $10 \mu\text{Ci}$ to $600 \mu\text{Ci}$ for 4 days. Each point is a mean of 3 mice.

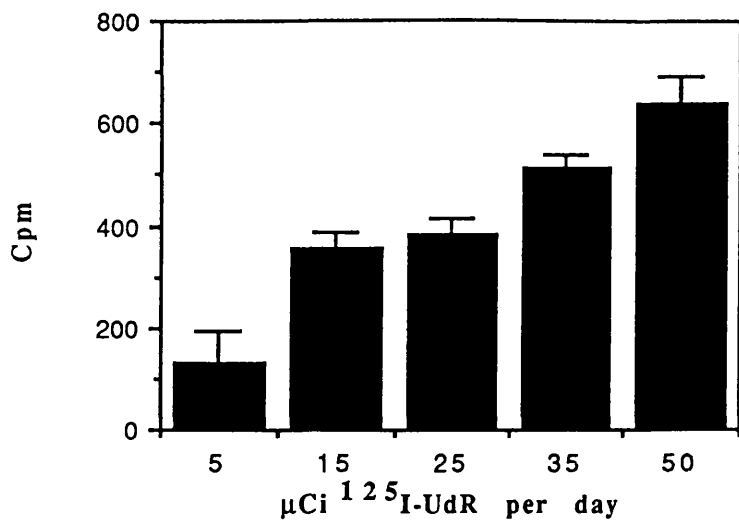


Fig. 21c

Fig. 21c

Cpm in 5×10^5 thymocytes after daily injection of $^{125}\text{I-UdR}$ in a dose range from $5\mu\text{Ci}$ to $50\mu\text{Ci}$ per day for 4 days. Each point is the mean of cpm from 3 mice, and the value for cpm for each mouse was a mean of 10 readings, with $\sigma_n < 5\%$ of the mean.

Labelling with ^{125}I -UdR

Mice were injected i.p. with ^{125}I -UdR in 0.4 ml PBS at doses ranging from 5 to 50 μCi per day for 4 days. Mice were killed and thymocytes prepared as above, but samples were counted on a gamma counter (Wallace LKB 80000 γ sample counter). Fig. 21c shows the cpm per 5×10^5 thymocytes from mice injected with the different doses. Thymocytes are particularly sensitive to damage, and the induction of apoptosis, by γ -irradiation (Sellins and Cohen 1987), and so although cpm per thymus was still increasing with dose of ^{125}I -UdR in the dose range assayed, it seemed advisable to stay within the doses that other investigators had shown to be non-toxic. McPhee et al (1979) injected mice with either 25 μCi 3H-TdR, or 25 μCi 3H-TdR together with 25 μCi ^{125}I -UdR, and showed that there was no difference in kinetics of the decline of βcpm between the two groups and hence that 25 μCi ^{125}I -UdR was not causing cell death. As in the case of labelling with 3H-TdR, there was no difference in the mean weight of thymuses between the groups of mice which had been labelled with the different doses, or in the percentages of the different thymocyte subpopulations, as defined by accessory molecule expression (data not shown).

Distribution of the radiolabel and the kinetics of its decline

Fig. 22a and b show the relative labelling of cells in the thymus, spleen and lymph nodes of mice labelled with 100 μCi ^3H -TdR and 35 μCi ^{125}I -UdR, respectively.

Fig. 23a and b show the decline of the two radiolabels in thymus and lymph nodes, respectively. Mice were labelled with one isotope only, because of the difficulty in counting two isotopes simultaneously in one sample, and hence the differences shown are from different mice of the same age, sex and strain. ^{125}I -UdR decline is much more

marked than $^3\text{H-TdR}$ decline in the thymus, suggesting that cells are dying and not migrating from the thymus. The difference is too great to be accounted for by the shorter half-life of ^{125}I than ^3H . The lesser decline in $^3\text{H-TdR}$ in the thymus must be due to local reutilization and not to incorporation of free precursor in the blood, as free precursor levels drop to <1% of their initial value within 1 day after injection (McPhee et al 1979, Feinendegen et al 1973).

Feinendegen et al (1973) calculated local TdR-reutilization (and hence cell death) based on the assumption that for each part of $^{125}\text{I-UdR}$ reutilized there would be approximately 5 parts $^3\text{H-TdR}$ reutilized. They give the amount of free TdR that is reutilized per unit time, in per cent of the amount of TdR that is, per unit time, liberated from the tissue DNA, (R), by the following equation:

$$R = \frac{1.2(\beta - \alpha)}{1.2\beta - 0.2\alpha} \cdot 100$$

where α is the regression coefficient for $^3\text{H-TdR}$ (proportion of $^3\text{H-TdR}$ liberated from tissue DNA during time) and β is the regression coefficient for $^{125}\text{I-UdR}$. From Fig. 23a it can be estimated that the gradient of the approximate-best fit (by eye) of decline between days 2 and 5 for $^3\text{H-TdR}$ is 10.67, and for $^{125}\text{I-UdR}$ is 23. At day 4, $\alpha=21.34$, and $\beta=46$. Therefore, $R=58\%$. As a minimum estimate this coincided reasonably with other studies. MCPhee et al (1979) estimated 61%; Feinendegen et al (1973) estimated 67%; Joel et al (1977) estimated only 28%.

In the case of the lymph nodes one would expect little cell death, (except after an infection, see Chapter 3), but one might expect cells to migrate. Fig. 23b shows that initially there was a decline in both radiolabels, suggesting some cell migration. If R is calculated from the slope of the first four days, it is 47%, which is surprisingly high and indicates thymidine reutilization and cell death. After the first four

days both values plateau, and R calculated from days 5-9 is 0, suggesting that no cell death occurred in the lymph nodes during that period. McPhee et al also found high thymidine reutilization in the spleen, estimated at 52%, compared to 61% for the thymus. They did not calculate a value for lymph nodes, but their graphs were not dissimilar to Fig. 23b, with an initial decline in both labels which then levels off. The fact that high levels of cell death were recorded in the spleen and lymph nodes is perhaps a little disconcerting, as it inclines one either to doubt the assay, or to doubt the contention that there is something special about cell death in T cell development in the thymus. The only other explanation I can see for the difference in the loss of the two radiolabels, if it is not due to selective reutilization of $^3\text{H-TdR}$ after cell death, is that $^{125}\text{I-UdR}$ is itself killing the cells in which it becomes incorporated, and this has been ruled out by McPhee et al (1979), and I could find no evidence for it myself.

Assay for DNA fragmentation

The assay frequently used to measure the degree of DNA fragmentation in CTL-mediated killing (eg Duke et al 1983; Gromkowski et al 1988; Ostergaard et al 1989, see Chapter 4) relies on pre-labelling targets with a radioactive DNA precursor and then assessing what percentage of the total incorporated radiolabel which is found in intact chromatin or in fragmented chromatin. This is achieved by measuring cpm in the culture supernatant, and then lysing the cells with 0.2% Triton-X100 in PBS and centrifuging the lysate at 15000g for 15 minutes in the cold, to separate intact from fragmented chromatin, and counting the supernatant. The sum of these two measurements, as a fraction of total incorporated counts, gives the percentage fragmentation (see Materials and Methods). This protocol was applied to thymocytes and

lymph node cells which had been labelled in vivo (with $100\mu\text{Ci } ^3\text{H-TdR}$ per day for 4 days, or $35\mu\text{Ci } ^{125}\text{I-UdR}$ per day for 4 days). Mice were killed, cell suspensions made and washed 2 x in MEM-H and aliquots of 5×10^5 cells were either harvested to obtain total incorporation, or lysed in 1 ml 0.2% Triton-X100 in PBS, centrifuged and the supernatants and pellets counted. When $^3\text{H-TdR}$ was the precursor used, $100\mu\text{l}$ supernatant was counted in 2 ml Aquasol (LKB) and pellets were also counted in 2 ml Aquasol to which was added $100\mu\text{l}$ MEM-H. The use of $^{125}\text{I-UdR}$ had the advantage that no scintillation fluid was required, making comparisons between the different fractions more straight forward. The counts from thymuses and lymph nodes of mice labelled with $^{125}\text{I-UdR}$, and the estimated percentage DNA fragmentation, are given in Tables 1a and 1b respectively. Tables 1c and 1d show the equivalent data from mice labelled with $^3\text{H-TdR}$, but total cpm when the cells were harvested are not given because these were counted using different scintillation fluid and are not directly comparable.

For $^{125}\text{I-UdR}$ labelled mice, the mean(%DNA fragmentation in the thymus) = 10.74, ($\sigma_n = 1.47$), and the mean(%DNA fragmentation in the lymph nodes) = 5.48, ($\sigma_n = 1.43$) Assuming that both means are of normally distributed, independent populations, one can test the hypothesis that there is no difference between the means (Hoel 1976). This hypothesis was rejected with 99.5% certainty, suggesting that the difference observed in the DNA fragmentation in thymus and in lymph nodes is statistically significant. In the case of $^3\text{H-TdR}$ labelled mice the mean(%DNA fragmentation in the thymus) = 9.82, ($\sigma_n = 1.30$), and the mean(%DNA fragmentation in the lymph nodes) = 6.24, ($\sigma_n = 0.91$). This difference is also statistically significant.

Are these values for DNA fragmentation reasonable? If one assumes that all but 3% of double positive thymocytes are going to die

within 3 days of their birth, that 73% of thymocytes in these mice are double positive, and that the mean time from the onset of a cell's death to its total disappearance is 9 hours, then one might predict that % DNA fragmentation at any instant in time would be: $(73-3) \times \frac{9}{72} \times 100 = 8.75\%$.

Clearly one has a problem in trying to assess the accuracy of an assay of this kind, because one has nothing with which to compare it directly. In order to check its sensitivity, therefore, I decided to see if the assay would pick up the increase in DNA fragmentation in the thymus that one would predict to occur on *in vivo* administration of hydrocortisones (Umansky et al 1981, Soffer et al 1952, Compton et al 1987).

Mice were injected with 35 μ Ci 125 I-UdR per day for 4 days and at the time of the last injection were also given 1mg hydrocortisone. The mice were killed at various times after their last injection and %DNA fragmentation in the thymus and lymph nodes was determined as described previously. Figure 24 shows the kinetics of DNA fragmentation. Increased DNA fragmentation was also detected in the lymph nodes, but this is not surprising: pyknotic nuclei have been observed in lymph nodes on glucocorticoid treatment (La Pushin and de Harven 1971); activated T cells seem to be glucocorticoid sensitive (Compton et al 1987) whereas single positive thymocytes are not (MacDonald et al 1989); and single strand nicks in DNA of cells in lymph nodes can be detected as an early event after injection of hydrocortisone to mice (H.R. MacDonald, personal communication).

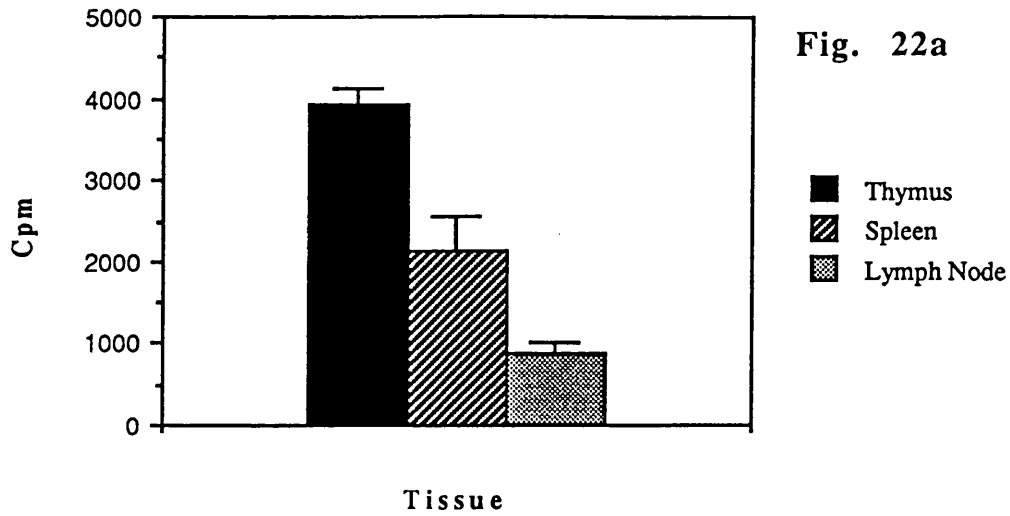


Fig. 22a

Cpm in 5×10^5 cells taken from thymus, lymph nodes and spleen of mice injected i.p. with $100 \mu\text{Ci } ^3\text{H-TdR}$ daily for 4 days. Each point is a mean of 3 mice, and the cpm of each tissue of each mouse was a mean of 10 readings with $\sigma_n < 5\%$ of the mean.

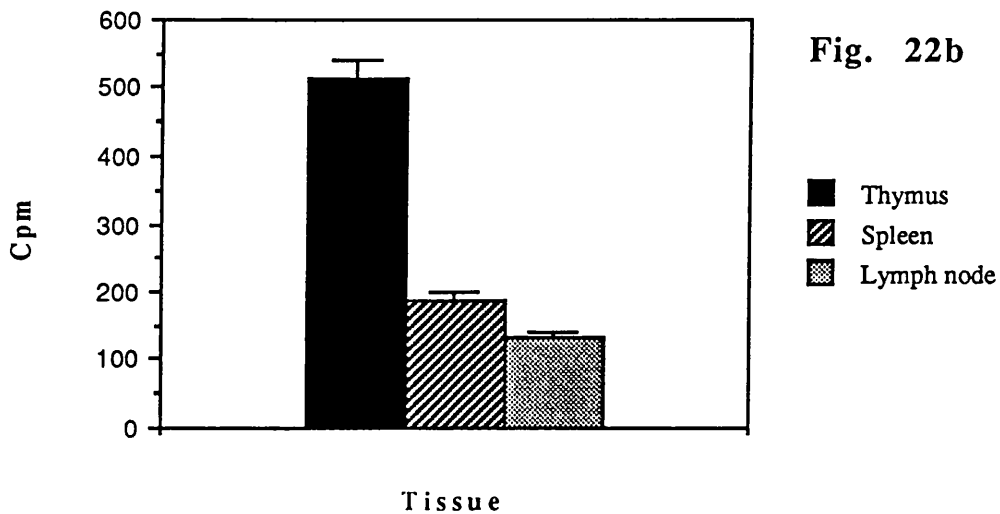


Fig. 22b

As above, but mice were labelled with daily i.p. injection of $35 \mu\text{Ci } ^{125}\text{I-UdR}$ for 4 days.

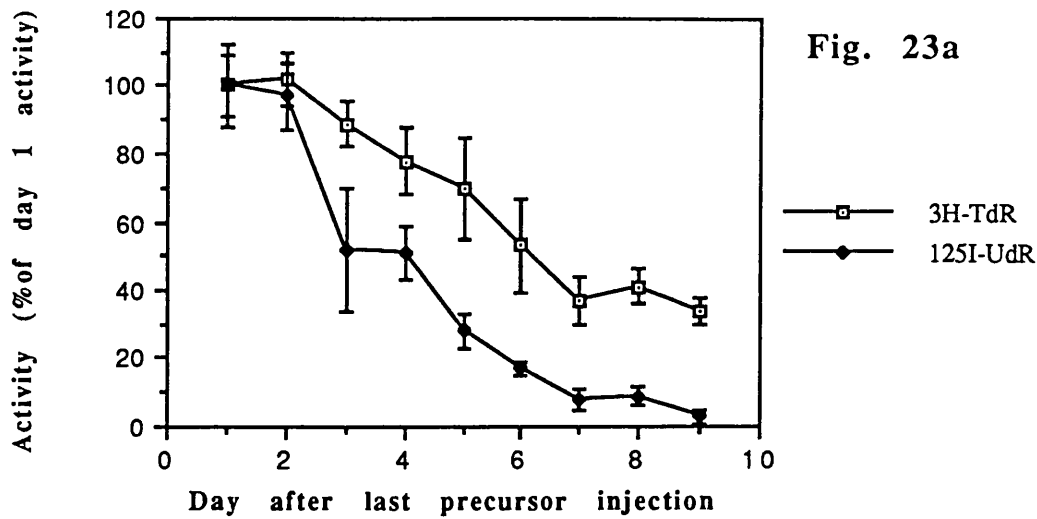


Fig. 23a

Decline of radiolabel in thymocytes of mice labelled with either daily injection for 4 days of either $100 \mu\text{Ci } ^3\text{H-TdR}$ or $35 \mu\text{Ci } ^{125}\text{I-UdR}$, expressed as a percentage of cpm on first day after labelling finished. Each point is a mean of 10 readings.

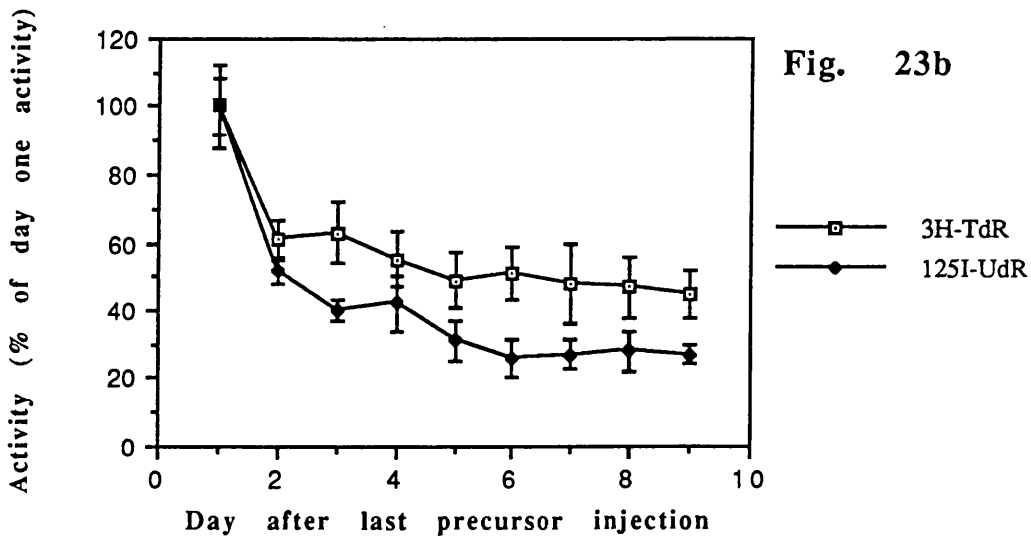


Fig. 23b

As above, but for cells taken from the lymph nodes.

Table 1a: Thymuses of ^{125}I -UdR labelled mice.

Total mean cpm (cell harvester)(σ_n)	Mean cpm in supernatant (σ_n)	Mean cpm in pellet (σ_n)	% DNA fragmentation
554 (26)	66.5 (9)	452 (24)	12.8
576 (19)	54 (8.7)	460 (18.7)	10.5
340 (10.2)	42 (12)	306 (15)	12.0
479 (22.9)	52 (6)	532 (47)	8.9
501 (38)	61 (9)	579(42)	9.5

Table 1a: Counts in thymocytes, harvested (column 1) or lysed in 0.2% Triton-X 100 (column 2 and 3). Each row represents a different mouse and each point is a mean of 10. Each measurement was made on 5×10^5 thymocytes. % DNA fragmentation is calculated from the value in column 2 divided by the sum of the values in column 2 and column 3, for that mouse (total cpm from harvester is given as a check on expected total counts).

Mean(%DNA fragmentation) = 10.74%, $\sigma_n = 1.47$

Table 1b : Lymph nodes of ^{125}I -UdR labelled mice.

Total mean cpm for 5×10^5 cells (harvester) (σ_n)	Mean cpm in supernatant from 3×10^6 cells (σ_n)	Mean cpm in pellet from 3×10^6 cells(σ_n)	% DNA Fragmentation
164 (7)	61.4 (3)	919.5 (67)	6.3
147.5 (15)	34.5 (9.1)	799.5 (54)	4.1
201 (32.9)	59.3 (4.7)	981 (63)	5.7
199.1 (27)	82 (9.3)	1002.5 (78.2)	7.6
157 (8.9)	37 (6.7)	961.4 (84)	3.7

Table 1b: Counts in lymph node cells, harvested (column 1) or lysed in 0.2% Triton-X 100 (column 2 and 3). Each row represents a different mouse and each point is a mean of 3 readings. % DNA fragmentation is calculated as above.

Mean(% DNA fragmentation) = 5.48%, $\sigma_n = 1.43$

Table 1c: Thymuses from $^3\text{H-TdR}$ labelled mice.

Mean cpm in supernatant (σ_n)	Mean cpm in pellet (σ_n)	% DNA Fragmentation
474.6 (29)	3531.6 (211.4)	11.8
416.7 (31.9)	4524 (197)	8.4
373.1 (12)	3463 (421.1)	9.7
536.9 (46.8)	4475.1(217)	10.7
409.3 (35.1)	4379.4 (316.2)	8.5

Table 1c: Counts in thymocytes, lysed in 0.2% Triton-X 100. Each row represents a different mouse and each point is a mean of 10. Each measurement was made on 5×10^5 thymocytes. % DNA fragmentation is calculated from the value in column 1 divided by the sum of the values in column 1 and column 2, for that mouse.

Mean(%DNA fragmentation) = 9.82%, $\sigma_n = 1.30$

Table 1d: Lymph nodes from $^3\text{H-TdR}$ labelled mice.

Mean cpm in supernatant (σ_n)	Mean cpm in pellet (σ_n)	% DNA Fragmentation
348.9 (22.6)	5256 (314.1)	6.2
315 (67.5)	4917 (210.7)	6.0
307.1 (73.2)	3587 (476.1)	7.9
261 (36)	4861 (295)	5.1
241.8 (27)	3791 (127.4)	6.0

Table 1d: Counts in lymph node cells, lysed in 0.2% Triton-X 100. Each row represents a different mouse and each point is a mean of 3. Each measurement was made on 3×10^6 cells. % DNA fragmentation is calculated from the value in column 1 divided by the sum of the values in column 1 and column 2, for that mouse.

Mean(%DNA fragmentation) = 6.24%, $\sigma_n = 0.91$

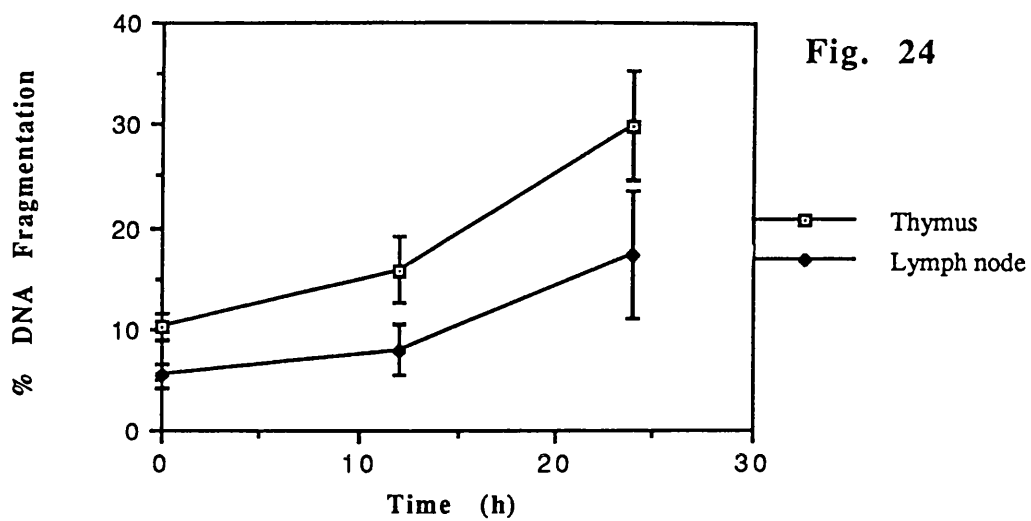


Fig. 24

DNA fragmentation in thymus and lymph nodes of mice after administration of hydrocortisone. Mice were labelled daily for 4 days with $35\mu\text{Ci } ^{125}\text{I-UdR}$ and at the time of the last injection also given 1 mg hydrocortisone, and killed at time intervals after hydrocortisone injection. Each point is the mean of 3 mice and the value for each mouse was a mean of 10 readings, with $\sigma_n < 5\%$ of the mean.

Effect of mab anti-CD3 on thymocytes *in vivo*

Smith et al (1989) have shown that addition of a mab against CD3 to fetal thymus organ cultures caused extensive apoptosis and DNA fragmentation within 18 h, and that the majority of the dying cells (83%) were of double positive phenotype. The same antibody causes proliferation in mature T cells (Bluestone et al 1987), but not in immature thymocytes (Havran et al 1987; Finkel et al 1987), although it does induce a transitory increase in cytoplasmic Ca^{2+} concentration in immature thymocytes (Finkel et al 1987). As changes in intracellular Ca^{2+} concentration can induce apoptosis in thymocytes (Wyllie et al 1984; McConkey et al 1988, 1989a and b), it seems possible that engaging the TCR-CD3 complex might, in immature thymocytes, signal the cells to die, and that this might be the mechanism of clonal deletion of self-reactive T cell precursors in the thymus.

Thymocyte DNA Fragmentation induced by mab against CD3 *in vivo*

Mice were labelled with ^{125}I -UdR as described previously and at the time of their last injection, were also injected with 0.25 mg protein-A-purified 2C11 (hamster IgG, anti mouse CD3, Leo et al 1987). The mice were killed 24 h later and the DNA fragmentation in the thymus, lymph nodes, and spleen was determined. Control mice were injected with either PBS or with 0.25 mg affinity-purified GK1.5. GK1.5 is a rat IgG anti mouse CD4 mab (Dialynas et al 1983a) and was used as a negative control, as CD4 is present on most thymocytes, and no hamster anti mouse IgG directed against a thymocyte cell surface molecule was available to me. Fig. 25 shows the %DNA fragmentation. Injection of 2C11 dramatically increased % DNA fragmentation in the thymus, from about 10% in control mice, to 47% in the treated mice, while it had no

measurable effect on DNA fragmentation in the lymph nodes. The fact that GK1.5 did not increase DNA fragmentation suggests that the effect of 2C11 is not due to a non-specific mechanism such as opsonisation or antibody-dependent killing involving other cells.

It would be very surprising if 2C11 were killing cells which did not express CD3, and so one would expect it to be acting on the CD3^{dull} double positive thymocytes, which make up about half of double positives, or on the CD3⁺ single positives. To determine which cells are dying, I stained thymocytes from 2C11-treated and normal mice with antibodies against CD4 and CD8. Fig 26a shows the Facs profile of staining with anti CD4 (FL2) and anti CD8 (FL1) on thymocytes from a 2C11-treated mouse 24 h after injection. Fig. 26b shows the equivalent profile from an untreated mouse. 2C11 treatment reduced the proportion of double positive thymocytes from about 75% to about 37%, and the proportions of the other three subpopulations defined by accessory molecule expression increased correspondingly, suggesting that all but the double positive thymocytes were resistant to death induced by 2C11 treatment.

Unfortunately one could not check that it was actually the CD3-expressing double positives which die, because after *in vivo* antibody treatment, 2C11 would be bound to CD3 on the cell surface and so mask the molecule in a staining assay. However, the antibody treatment did kill about the same proportion of double positives as express CD3. Fig. 26c shows staining with 2C11 on double positive thymocytes from an untreated mouse. The double positive thymocytes were purified by two rounds of panning with antibodies against CD4 and CD8 (YTA 156 and 2.43, Sarmiento et al, 1981). This protocol enriched the double positive population to 91% purity (see Fig. 26d) and so the 5.4% CD3^{high} cells that one can see in Fig. 26c are probably contaminating CD4⁺ single positives

(6.2%). Thus one can assume that the ratio of CD3⁻ : CD3^{dull} double positive thymocytes in these mice is 45.4 : 49.3 (ie 52% of double positives express CD3).

If all CD3⁺ double positives were induced to die by the 2C11 treatment one would expect about 39% DNA fragmentation. The discrepancy of 8% between this figure and the 47% mean DNA fragmentation measured could be due to the fact that not all of the approximately 10% of thymocytes that die in the non-treated mice necessarily express CD3, and so in the treated mice one might observe the death of all CD3⁺ double positives and in addition some death due to positive selection or to failure to assemble functional TCR genes. The high standard deviation (5.6) and small population size (3) in the DNA fragmentation assay mean that one cannot conclude too much from these data about DNA fragmentation in positive selection.

The antibody staining data does, however, inspire confidence in the assay for apoptosis. Where no increase in DNA fragmentation was found there were no changes in the pattern of CD4⁺ and CD8⁺ expression. At the time of making cell suspensions from the mice I also stained cells with Propidium Iodide (PI) (as a measure of plasma membrane integrity and hence viability). In the 2C11 treated mice 11% of thymocytes were stained as opposed to 6% in control mice. This suggests that the DNA fragmentation assay gives information that one would not obtain from more conventional assays of cell death. The difference between the two estimates of death may be due to the fact that DNA fragmentation can proceed loss of plasma membrane integrity (Duvall and Wyllie 1986), but may also be because the apoptotic cells and apoptotic bodies have already been phagocytosed, hence the reduced accessory molecule cell surface staining. As a final check on the assay, I prepared DNA from mice treated with 2C11 and from untreated mice,

and electrophoresed this on an agarose gel (See Fig. 27). The only track in which a ladder is seen is that containing the DNA from the thymus of a 2C11-treated mouse. Shi et al (1989) have also shown that a electrophoretic ladder is obtained from thymocytes treated with anti-CD3 antibody *in vivo*.

Apoptosis in immature thymocytes *in vitro*

As nearly all double positive thymocytes die rapidly in culture when dissociated, the effect of a potentially lethal stimulus such as an antibody against CD3, and also the effect of anything which might prolong survival in the presence of such a stimulus, are difficult to study. One can always argue that the cells would have died anyway despite the stimulus, and any surviving cells can be attributed to contamination by other thymocytes subsets. I attempted to look at the apoptosis induced by mab anti-CD3, and at agents which might prolong survival, in double positive thymocytes in culture. Double positives were prepared either by panning as described previously, which gave 91% double positives (See Fig. 26d), or by using thymocytes from embryonic day 20 (E20) embryos, which contained 93% double positives, and less than 3% single positives (See Fig. 28) The double positives from the fetal thymus expressed the same levels of CD3 as those from an adult, 4 week-old mouse (about 50% were CD3^{dull}) and were indistinguishable from those from an adult mouse in my experiments, and so I shall consider all ages together.

The effect of 2C11 on double positive thymocytes in culture

Double positive thymocytes were prepared and incubated either on 2C11-coated flat bottom 96 well plates, or on GK1.5-coated plates, or in

the absence of an antibody, at a density of 5×10^5 cells ml^{-1} in $200 \mu\text{l}$. In addition, the protein synthesis inhibitor cycloheximide and the nuclease inhibitor aurintricarboxylic acid (ATC) were added to some wells. At various time points wells were analysed for percentage viability by their ability to exclude PI, measured on the Facs. No difference was seen between thymocytes incubated with GK1.5 or with no antibody (data not shown), but cells given 2C11 did die more quickly. Fig. 29 shows a typical experiment. Initially, at $t=14$ (See Fig. 29a), there was no difference between wells containing mab anti-CD3 and those without it, and cycloheximide and ATC enhanced survival to a similar degree in both instances. By the third day in culture (Fig. 29b), however, there was a marked difference in the extent of cell death in the presence or absence of 2C11. About 20% more cells died when incubated with 2C11 and both inhibitors almost completely negated this difference. By day 4 in culture (Fig. 29d) almost all cells incubated with 2C11 were dead and the inhibitors were no longer effective at enhancing survival of these cells.

Although these data indicate that 2C11 does induce death in immature thymocytes *in vitro*, its effect is clearly much slower than *in vivo*, where Shi et al (1989) were able to observe a DNA 'ladder' 14 h after antibody administration, and I found disappearance of $\text{CD3}^+\text{CD4}^+\text{CD8}^+$ cells after 24 h. In fetal organ culture, increased apoptosis and DNA fragmentation were observed 18 h after incubation with anti-CD3 antibody (Smith et al 1989). It does not seem likely that this difference is due simply to dose of antibody, as the dose of 2C11 I used (pre-incubation of plates with $2 \mu\text{g ml}^{-1}$) was sufficient to cause proliferation of T cell hybridomas (data not shown). Other investigators have found that little anti-CD3-induced DNA fragmentation occurs when double positive thymocytes are dissociated *in vitro*, despite the fact that

these are the cells believed to be responsible for the fragmentation seen on *in vivo* antibody treatment (Tadakuma et al, 1990). The discrepancy seems unlikely to be the result of a slower death programme as such, since these cells die very quickly in 10^{-6} M dex (See Fig. 30). Thus one is tempted to speculate that, in addition to triggering through CD3, some other interaction, which is present in the thymus *in vivo*, and in organ culture, may be necessary to induce apoptosis in double positive thymocytes. The TCR-transgenic mice (Kiselow et al 1988; Sha et al 1988) have indicated that both positive and negative selection are dependent on a ligand-TCR interaction, and unless the difference between the two outcomes is determined simply by the affinity of the interaction, then other molecules must be involved. If treating a thymus with mab anti CD3 mimics the induction of clonal deletion, then, it is not surprising that other interactions supplied by the thymic environment are also required.

That cycloheximide and ATC prolong survival suggests that this cell death is an active process and that DNA fragmentation is causal. Other interpretations of the action of these inhibitors are discussed in Chapter 3.

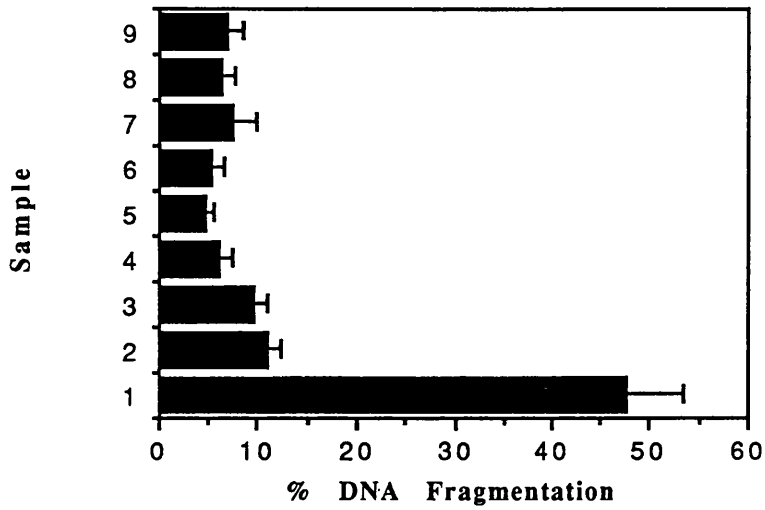


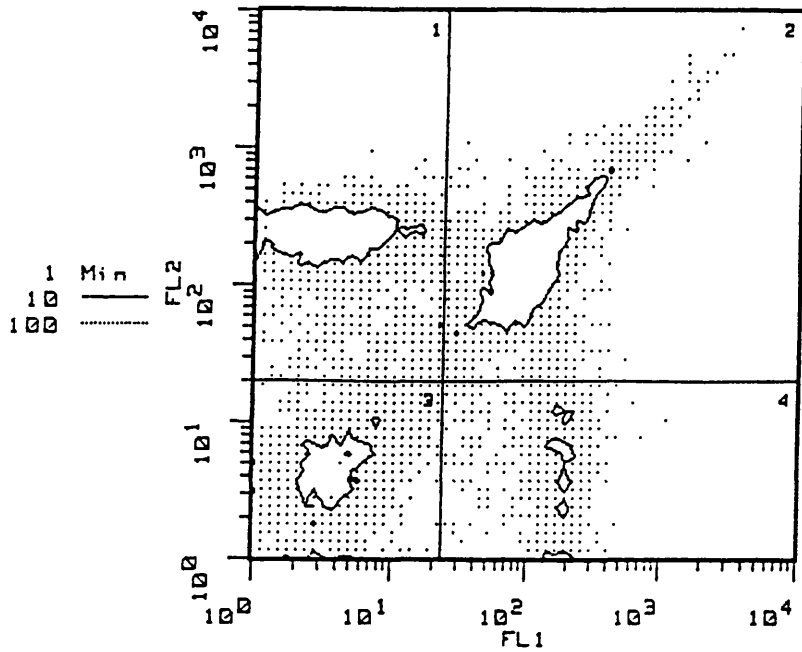
Fig. 25

<u>Number</u>	<u>Sample</u>
1	Thymus + 2C11
2	Thymus + GK1.5
3	Thymus + PBS
4	Lymph node + 2C11
5	Lymph node + GK1.5
6	Lymph node + PBS
7	Spleen + 2C11
8	Spleen + GK1.5
9	Spleen + PBS

Fig. 25

% DNA fragmentation in thymus, lymph nodes, and spleen of ^{125}I -UdR labelled mice, injected with PBS, or with 0.25 mg 2C11 or GK1.5. Each point is a mean of 3 and standard deviations are given.

Fig. 26a

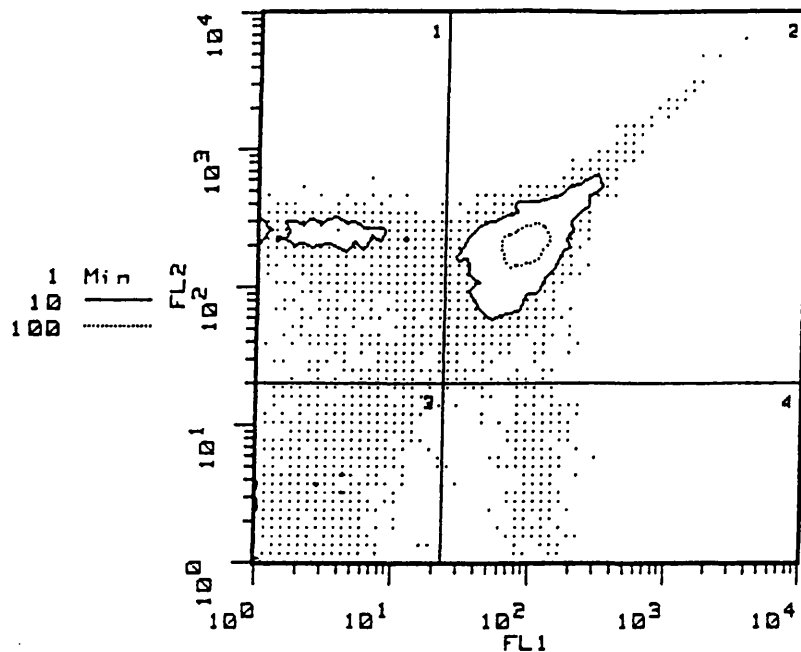


<u>Subpopulation</u>	<u>%</u>
CD4 ⁺ single positive	31.2
CD8 ⁺ single positive	10.03
CD4 ⁺ CD8 ⁺ double positive	36.7
CD4 ⁻ CD8 ⁻ double negative	22.07

Figure 26

Fig. 26a Facs profile of staining with directly conjugated anti CD4 (FL2) and anti CD8 (FL1) (Beckton Dickinson) on mouse thymocytes 24 h after i.p. injection of 0.25 mg 2C11.

Fig. 26b

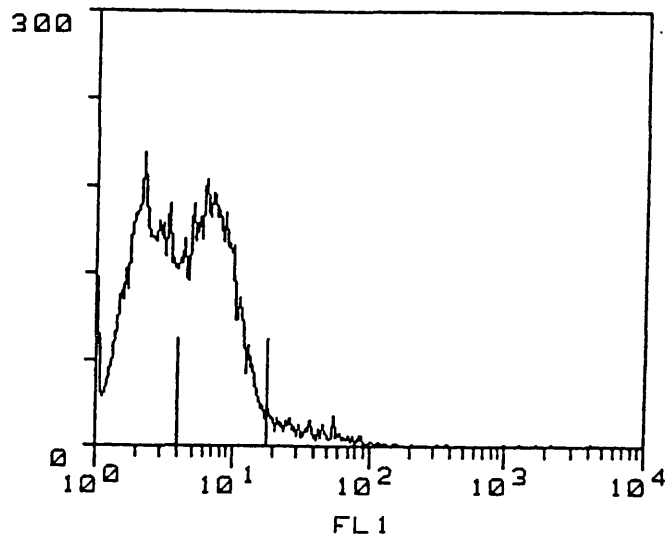


<u>Subpopulation</u>	<u>%</u>
CD4 ⁺ single positive	14.19
CD8 ⁺ single positive	3.02
CD4 ⁺ CD8 ⁺ double positive	74.32
CD4 ⁻ CD8 ⁻ double negative	8.47

Figure 26

Fig. 26b Facs profile of staining with directly conjugated anti CD4 (FL2) and anti CD8 (FL1) (Beckton Dickinson) on mouse thymocytes 24 h after i.p. injection of 200 μ l PBS.

Fig. 26c

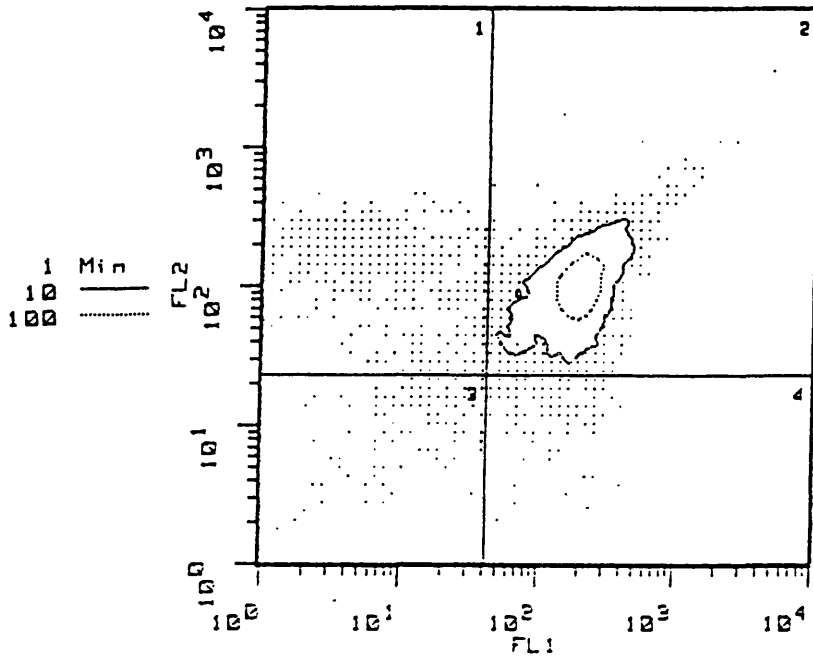


<u>Subpopulation</u>	<u>%</u>
CD3 ⁻	45.4
CD3 dull	49.3
CD3 ^{high}	5.4

Figure 26

Fig. 26c Facs profile of staining with directly conjugated 2C11 (anti CD3) on mouse thymocytes enriched for double positives to 91% purity with two rounds of panning with YTA 156 and 2.43 (See Fig. 26d).

Fig. 26d



<u>Subpopulation</u>	<u>%</u>
CD4 ⁺ single positive	6.29
CD8 ⁺ single positive	1.21
CD4 ⁺ CD8 ⁺ double positive	91.16
CD4 ⁻ CD8 ⁻ double negative	1.34

Figure 26

Fig. 26d Facs profile of staining with directly conjugated anti CD4 (FL2) and anti CD8 (FL1) (Beckton Dickinson) on mouse thymocytes, enriched for double positives with two rounds of panning with YTA 156 and 2.43.

Fig. 27

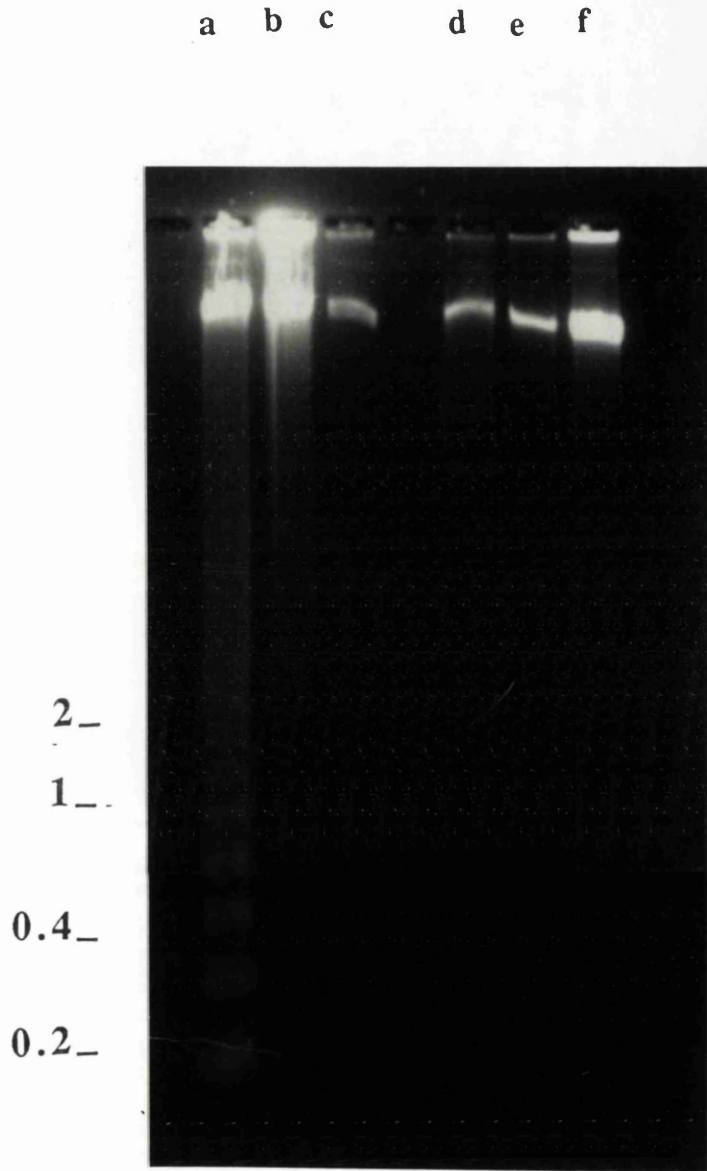


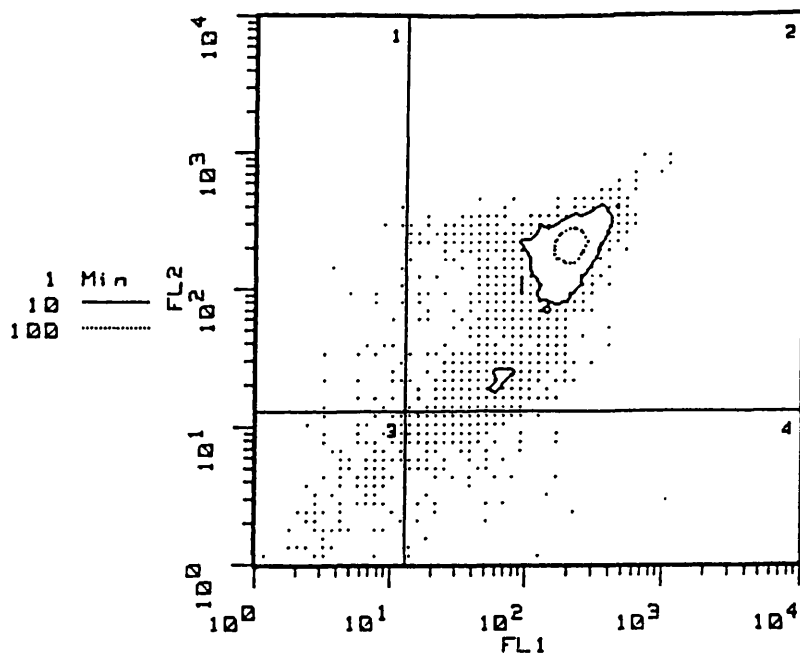
Fig. 27

Ethidium bromide stained 1% agarose gel showing DNA prepared from mice 24 h after injection with 0.25 mg 2C11 (tracks a-c) or 0.25 mg GK1.5 (tracks d-f). Size is given in kilobases.

Track a thymus + 2C11
Track b spleen + 2C11
Track c lymph node + 2C11
Track d thymus + GK1.5
Track e spleen + GK1.5
Track f lymph node + GK1.5

In other gels where loading was equivalent, no ladder was seen in any track but a.

Fig. 28



<u>Subpopulation</u>	<u>%</u>
CD4 ⁺ single positive	0.54
CD8 ⁺ single positive	2.49
CD4 ⁺ CD8 ⁺ double positive	93.37
CD4 ⁻ CD8 ⁻ double negative	3.6

Figure 28

Fig. 28 Facs profile of staining with directly conjugated anti CD4 (FL2) and anti CD8 (FL1) (Beckton Dickinson) on E20 mouse thymocytes.

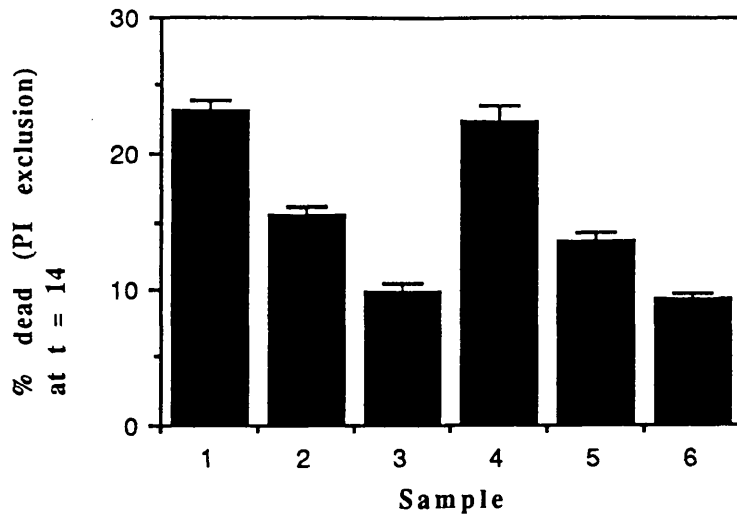


Fig. 29a

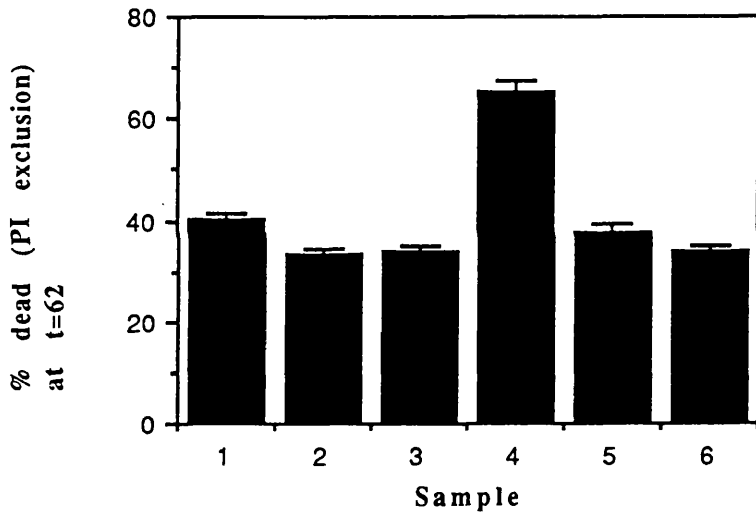


Fig. 29b

Number	Sample
1	double positives only
2	+ 2 μgml^{-1} cycloheximide
3	+ 30 μgml^{-1} ATC
4	+ 2C11
5	+ 2C11 + 2 μgml^{-1} cycloheximide
6	+ 2C11 + 30 μgml^{-1} ATC

Fig. 29

% dead thymocytes, determined by PI exclusion on the facs, after culture in conditions stated for 14 h (Fig. 29a) and 62 h (Fig. 29b). Each point is a mean of 5.

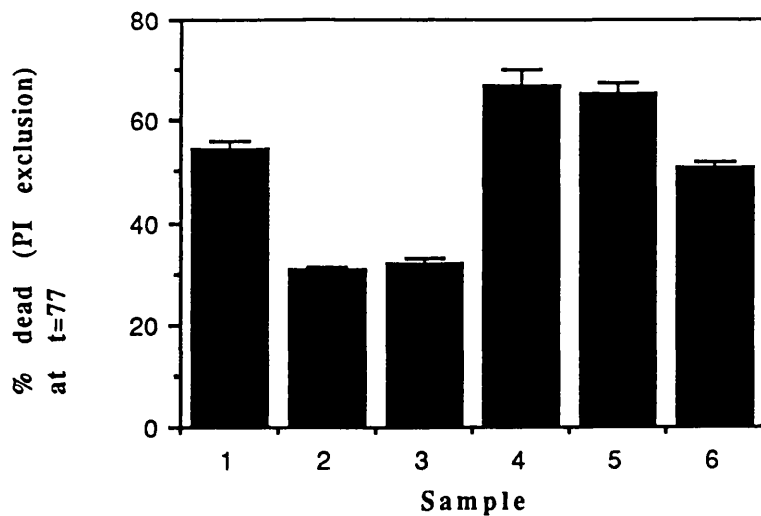


Fig. 29c

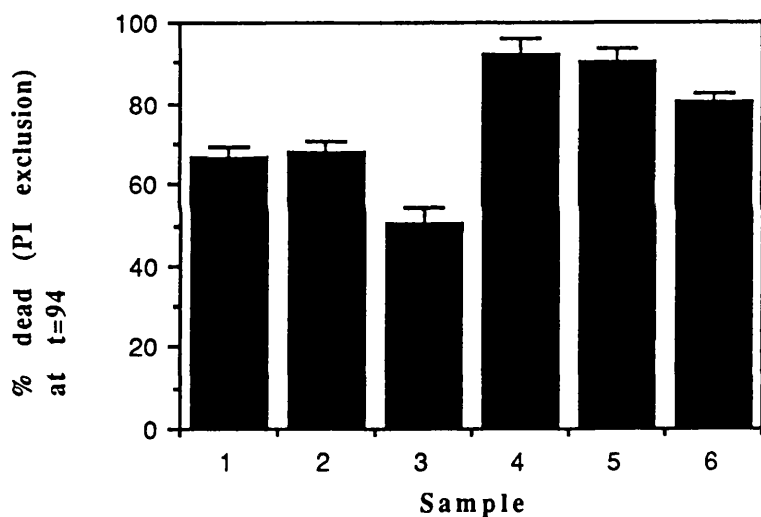


Fig. 29d

Number	Sample
1	double positives only
2	+ 2 μgml^{-1} cycloheximide
3	+ 30 μgml^{-1} ATC
4	+ 2C11
5	+ 2C11 + 2 μgml^{-1} cycloheximide
6	+ 2C11 + 30 μgml^{-1} ATC

Fig. 29

% dead thymocytes, determined by PI exclusion on the facs, after culture in conditions stated for 77 h (Fig. 29c) and 94 h (Fig. 29d). Each point is a mean of 5.

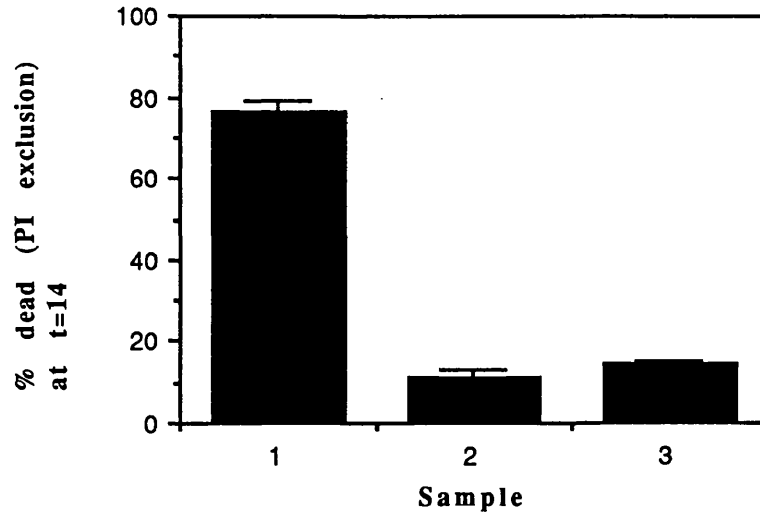


Fig. 30

<u>Number</u>	<u>Sample</u>
1	+ 10^{-6} M dex
2	+ 10^{-6} M dex + $2\mu\text{g ml}^{-1}$ cycloheximide
3	+ 10^{-6} M dex + $30\mu\text{g ml}^{-1}$ ATC

Figure 30

Death of double positive thymocytes incubated in 10^{-6} M dex with or without cycloheximide and ATC, as determined by their loss of ability to exclude PI, measured on the Facs. Each point is a mean of 5.

DISCUSSION

From the point of view of understanding clonal deletion, an attractive explanation for the death of thymocytes induced by mab anti CD3 *in vivo* is that by binding to CD3^{dull} double positive thymocytes, the antibody induces an increase in $[Ca^{2+}]_i$, which directly triggers apoptosis. This is supported by the observations that an elevation of $[Ca^{2+}]_i$, induced by a calcium ionophore, is necessary and sufficient to induce apoptosis in immature thymocytes (Kizaki et al 1989; McConkey et al 1989) and that antibodies to CD3 increase $[Ca^{2+}]_i$ to similar levels in immature thymocytes as they would in mature T cells (Finkel et al 1987). Thus it is possible that the antibody mimicks the action of a self-peptide + MHC in triggering the cell to commit suicide.

There are, however, several problems with this interpretation:

- (1) It has not been shown conclusively that it is the CD3-expressing double positives cells that die in response to anti-CD3 treatment; the reduction in the proportion of double positive thymocytes shown by Facs analysis might conceivably be due to down regulation of accessory molecule expression induced by the antibody treatment (eg Blue et al 1987b) and not due to preferential death of that subpopulation.
- (2) Neither this study nor published data (Smith et al, 1989; Shi et al 1989) have excluded the possibility that the action of anti-CD3 in promoting double positive cell death is indirect, via another CD3⁺ cell type (double negative CD3⁺ $\gamma\delta$ TCR⁺ or single positive CD3⁺ $\alpha\beta$ TCR⁺) that might either produce something that is toxic to immature thymocytes or stop making something that is essential for their survival.
- (3) There is no known case in which a T cell is activated physiologically by a ligand binding exclusively to CD3, without also engaging the $\alpha\beta$ TCR. It has recently been demonstrated that, in immature thymocytes,

binding to the $\alpha\beta$ TCR and signal transduction through CD3 are uncoupled (Finkel et al 1989). Cross-linking with an antibody to CD3 produced a Ca^{2+} signal of similar magnitude in immature and mature T cells, but a pan anti- $\alpha\beta$ TCR mab produced a markedly smaller Ca^{2+} in immature thymocytes than in mature T cells, as did mabs that recognize specific V β gene products. This difference is corroborated by the observation that *in vivo* administration of mab KJ16 (anti-V β 8) prevented the emergence of mature single positive thymocytes expressing the KJ16 epitope, but did not reduce the proportion of, or cause the death of, KJ16⁺ double positive thymocytes (McDuffie et al 1986).

The first objection seems merely formal, but the second is perhaps supported by the delayed death response to anti-CD3 mab *in vitro*. One might argue that this is because of the absence of a mediator produced by other thymocyte subpopulations. Tadekuma et al (1990) also observed a reduced response to mab anti-CD3 *in vitro*, as assessed by measurement of DNA fragmentation, in a population of Facs-sorted double positive thymocytes. However, the kinetics of death were not altered when I did not enrich for double positive thymocytes (data not shown) and so it seems more likely that the difference is due to the disruption of the thymic microenvironment by dissociation of the cells, as rapid cell death has been reported in fetal thymus organ culture (Smith et al 1989). Earlier work from Owen's laboratory did suggest that mab anti-CD3 in fetal thymus organ culture abrogated T cell development by interfering with a putative 'nurse' cell function of $\gamma\delta^+CD3^+$ double negative thymocytes (Owen et al 1988 and 1989). Kyewski et al (1989) have demonstrated reduced production of mature T cells after *in vivo* treatment with antibodies against CD3 or TCR. They attributed this to interference in the interactions of the double positive

thymocytes with dendritic cells and epithelial cells and not to cell death, although they did not look for evidence of apoptosis immediately after antibody treatment. It would be interesting to look at the ability of mab anti-CD3 to induce apoptosis *in vivo* during fetal thymus development, where one could rule out the possibility that the action of the antibody results from its effect on other CD3⁺ cell types, since Finkel et al (1989) have shown that there are very few $\gamma\delta^+CD3^+$ cells until birth and CD3⁺ $\alpha\beta$ TCR⁺ single positives are absent until E18 and infrequent until after birth (Kisielow et al 1984; Ceredig et al 1983).

The observation that both stimulation with antigen and with antibodies to CD3 cause apoptosis in T cell hybridomas also supports the view that the action of mab anti-CD3 is direct (Ashwell et al 1987; Mercep et al 1989 and 1990; Shi et al 1989; Sussman et al 1988). T cell hybridomas are the product of a fusion between antigen-specific peripheral T cells and a thymoma cell line, and, as such, their response to antigen may be representative of the response of an immature thymocyte. Shi et al (1989) have shown that cyclosporin A, which is known to interfere with the process of deletion of autoreactive clones and thereby to cause autoimmune disease (Sakaguchi and Sakaguchi 1988; Gao et al 1988) inhibited cell death induced by mab anti-CD3 in T cell hybridomas *in vitro* and in the thymus *in vivo*, suggesting a common mechanism of induction of death. T cell hybridomas, therefore, seem to be an appropriate model with which to study the mechanism of thymocyte cell death, having the advantage of being a homogeneous population.

The third objection remains unanswered and implies that the phenomenon observed on injection of anti-CD3 mab *in vivo* and in fetal thymus organ culture may have little relevance to T cell development, or at least may not give much information about at which

developmental stage self-reactive cells are deleted. Such experiments may give insight into the mechanism of death distal to receptor occupancy, but double positive thymocytes have been shown to be particularly sensitive to the induction of apoptosis by numerous other lethal stimuli, such as glucocorticoids (Wyllie 1980), calcium ionophores and phorbol esters (Kizaki et al 1989), environmental contaminants such as TCDD (McConkey et al 1988) and γ -irradiation (Sellins and Cohen 1987), any of which could be used to study the mechanism of death.

If signal transduction and receptor occupancy are not linked in double positive thymocytes, then it is perhaps more likely that these are the cells on which positive selection operates. Presumably, most of the cells which die when treated with anti-CD3 mab have not reached the stage at which they would be deleted were they self-reactive. As tolerance induction has been shown to occur at the stage of double positives, however, there must be a small population in which binding of ligand to the TCR does trigger a Ca^{2+} signal via CD3, but perhaps these were too few to be detected in Finkel's study. (Alternatively, the theory that ligand-binding to the TCR results in deletion of self-reactive clones by apoptosis triggered through an increase in $[\text{Ca}^{2+}]_i$ might be wrong). Schneider et al (1989) have shown that in $\text{Mls}^{\text{a}+}$ neonatal mice some single positive self-reactive $\text{V}\beta 6^+\text{CD}4^+$ cells do leave the thymus, but that they die in the periphery within a few days of birth, suggesting that the signal for self-reactive cells to die may be a very late event in T cell development.

GENERAL CONCLUSION

The work presented here provides evidence that growth factor dependent cell lines die actively on withdrawal of their growth factor, and that DNA fragmentation is causal in their death. In addition it suggests that immature thymocytes die by the same mechanism on ligand-binding to their surface CD3, and hence implicates apoptosis in thymic tolerance induction.

The consensus of opinion on the mechanism of apoptosis seems to be that an increase in $[Ca^{2+}]_i$ signals new gene expression which leads to the activation of nucleases already present in the cell, which cleave the chromatin into nucleosome sized pieces, and this kills the cell. The molecular biology remains obscure, but two strategies might enable one to identify genes involved in the process:

(1) Subtractive hybridisation of cDNA libraries prepared from viable cells and from cells initiating apoptosis. A growth factor dependent cell line would be a convenient source of mRNA from which to prepare libraries because cells would be clonal, and hence any unique sequences in the library from apoptotic cells would be directly related to withdrawal of the growth factor. Cycloheximide blocking studies might facilitate the identification of an optimal time window after growth factor withdrawal from which to prepare the library.

(2) An alternative approach might be to look for mammalian homologues of the *C. elegans ced* genes. *Ced-4* is cloned and sequenced, and *ced-3* and *nuc-1* are likely to soon be available. Unfortunately the nematode genome contains many more C and G residues than the vertebrate genome, and so a direct search for homologues by screening a mammalian cDNA library with nematode probes is unlikely to succeed, even at very low stringency hybridisation. However, once the

sequence of the nematode genes are available one might screen mammalian cDNA libraries with short oligonucleotide probes, synthesized to compensate for the discrepancy in base usage between the two genomes.

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