

Apoptosis (The 1992 Frank Rose Memorial Lecture)

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Summary Apoptosis is a mode of cell death with characteristic structural features. These appear to result from a set of discrete cellular events that are regulated by gene expression. Oncogenesis and oncosuppressor genes are involved in this regulation. The role of *c-myc* is of particular interest, as it can act as a bivalent regulator, determining either cell proliferation or apoptosis, depending on whether free movement around the cell cycle is supported (by growth factors) or is limited by growth factor deprivation or treatment with other cycle-blocking agents. *In vivo*, *c-myc* expression may be associated with a 'high-turnover' state in which cell proliferation and apoptosis co-exist. Certain other oncogenes (e.g. *ras*, *bcl-2*) rescue cells from susceptibility to apoptosis and so convert this high-turnover state into rapid population expansion. One role of the oncosuppressor gene *p53* may be to initiate apoptosis by causing G 1/S arrest in cells expressing *c-myc*. Some aspects of resistance and sensitivity to chemotherapeutic agents can be explained on the basis of movement between the population-expansion and the high-turnover states, perhaps through modulation of the expression of these and other genes.

Apoptosis is a mode of cell death in which single cells are deleted in the midst of living tissue. The term derives from a Greek word used for the dropping off of leaves from trees. It is characterised by structural changes that appear with great fidelity in cells of widely different lineage, and presumably represent a pleiotropic effector response (Kerr *et al.*, 1972; Wyllie *et al.*, 1980; Arends & Wyllie, 1991). Apoptosis accounts for most or all of the programmed death responsible for tissue modelling in vertebrate development, for the cell loss that accompanies atrophy of adult tissues following endocrine and other stimuli, and – at least in some tissues – for the physiological death of cells in the course of normal tissue turnover. The extensive deletion of cells of the B and T lineages during negative selection in the immune response is effected by apoptosis as is a proportion of the deaths of the target cells of cell-mediated immune killing. Apoptosis occurs widely in tumours, although it is not the only mode of death adopted by tumour cells. It is often claimed that apoptosis is the most significant component of the well-established continuous cell loss of most tumours, although quantitative data to prove this are few (Sarraf & Bowen, 1988; Moore, 1987). Irradiation, chemotherapy and the appropriate hormone therapy all induce apoptosis in tumour cells. High doses of irradiation and chemotherapy may also cause cell destruction by other means (Searle *et al.*, 1975; Dyson *et al.*, 1986; Szende *et al.*, 1989; Eastman, 1990; Lennon *et al.*, 1990; Kyprianou *et al.*, 1990; Kyprianou *et al.*, 1991a,b; Martikainen *et al.*, 1991).

The *morphological changes* in apoptosis have been extensively reviewed elsewhere (Kerr *et al.*, 1972; Wyllie *et al.*, 1980; Kerr *et al.*, 1987; Arends *et al.*, 1990). Affected cells shrink in volume, lose contact with their neighbours and lose specialised surface elements such as microvilli and cell-cell junctions. Time lapse studies have shown that these changes occur rapidly and are accompanied by extraordinary surface convulsion and then the explosion of the cell into a series of membrane-bounded, condensed apoptotic bodies. The endoplasmic reticulum dilates and a series of crater-like cavities appear where the dilated cisternae fuse with the cell surface. Otherwise, cytoplasmic organelles are largely intact. Initially, and in contrast to cells dying by other means (e.g. necrosis), mitochondria are normal in structure. The most outstanding internal structural changes, however, occur in the nucleus. Chromatin condenses into dense granular caps under the nuclear membrane. Adjacent to these, nuclear pores are absent. The nucleolus dissociates to leave a shower of osmiophilic particles near the centre of the nucleus and the bare fibrillar centre, which usually lies close to the peripheral

condensed chromatin. Apoptotic cells do not induce an inflammatory reaction, even when present in large numbers, but they are targets of immediate phagocytosis, either by macrophages already present nearby, or by other adjacent viable cells. Within these, the compacted organelles and condensed chromatin of the apoptotic cells may be visible for a few hours but eventually reduce to large nondescript lysosomal residual bodies.

The *effector mechanisms* of apoptosis are still only incompletely understood. The nuclear changes are caused by activation of an endogenous calcium-magnesium sensitive nuclease (Arends *et al.*, 1990; Wyllie, 1980) which has not yet been fully characterised. This cleaves chromatin between nucleosomes, reducing the DNA of apoptotic cells to a series of fragments, integer size multiples of 180–200 base pairs, and thus producing a characteristic 'ladder' on agarose gel electrophoresis.

The swift phagocytosis is the result of recognition by the phagocytic cell of new molecular structures revealed on the surface of the apoptotic cell. Recognition of apoptotic rodent thymocytes can be blocked *in vitro* by N-acetyl glucosamine and its dimer N,N'-diacetyl chitobiose, suggesting that a component of the recognition signal may be a glycan rich in exposed N-acetyl glucosamine residues (Duvall *et al.*, 1985). The vitronectin receptor of human macrophages is responsible for binding apoptotic human neutrophils (Savill *et al.*, 1990). The distinctive recognition pathway used by macrophages for binding apoptotic neutrophils may represent a control point in the physiological termination of the acute inflammatory reaction (Savill *et al.*, 1989).

Many apoptotic cells express a new transglutaminase activity that cross-links cytoplasmic proteins (Fesus *et al.*, 1989; Piacentini *et al.*, 1991; Fesus *et al.*, 1991). Some of the shrinkage and distortion of contour of apoptotic cells may be attributable to activation of this enzyme, but the dramatic step-like increase in buoyant density shown by cells as they enter apoptosis (Wyllie & Morris, 1982) must be due in addition to net movement of fluid out of the dying cell. A possible mechanism to account for this profound fluid shift (responsible for loss of a third to a half of cell's volume within a few minutes) is inhibition of the sodium-potassium-chloride cotransporter system (Wilcock & Hickman, 1988).

The *cellular triggers* that initiate this pleiotropic response have proved elusive. Shortly before onset of the chromatin changes, at least in some cell types, free cytosolic calcium rises to sustained, but moderate levels of around 800 nM (McConkey *et al.*, 1989a). This appears to be important for the rest of the process, as blockade of calcium movement by pharmacological means can inhibit apoptosis. It is not known whether the sources of the calcium is external to the cell or internal (for example from mitochondria), although

this might have important implications for regulation. One type of surface receptor molecule (APO-1, *fas*) appears to be particularly involved in the triggering of apoptosis in some cell types including leukaemic cell lines (Trauth *et al.*, 1989; Itoh *et al.*, 1991). T-lymphocytes provide an example of how single receptor-ligand interactions can lead to strikingly different cellular responses. In the CD4 + , CD8 + immature cortical thymocyte, ligands that occupy the T-cell receptor initiate apoptosis, whereas in mature, post-thymic T-cells they initiate entry to S-phase (Smith *et al.*, 1989). Perhaps in a similar way, TNF can trigger apoptosis in appropriate cell types (Kyprianou *et al.*, 1991a; Laster *et al.*, 1988), although in other circumstances it may act as a growth factor.

In several circumstances, blockade of protein and RNA synthesis inhibits apoptosis (Wyllie *et al.*, 1984), but cycloheximide does not block – and indeed may initiate – apoptosis in some cell types. New transcription of genes that may be triggers for apoptosis has been sought for by a candidate gene strategy. There is a cascade-like induction of *c-fos*, *c-myc* and *hsp-70* in regressing prostate, for example (Buttayan *et al.*, 1988), and TGF β ₁ is induced during regression of a hormone-sensitive breast carcinoma cell line (Kyprianou *et al.*, 1991b), but it is difficult from experiments of this type to be certain that the new transcripts are integral to apoptosis as opposed to other (perhaps abortive) stress responses.

Subtractive hybridisation has also been used to identify genes whose transcription is uniquely associated with apoptosis. Several candidates are now known. Regressing secretory epithelia in mammary and prostatic glands transcribe a gene coding for a highly sulphated cell surface glycoprotein with complement-inhibitory properties (TRPM-2) (Monpetit *et al.*, 1986; Buttayan *et al.*, 1989), and several new transcripts appear in apoptotic lymphocytes (Owens *et al.*, 1991). The roles of all of these interesting new molecules have still to be established.

Regulatory genes influence cellular susceptibility to enter apoptosis. Some of these have been identified and are already familiar as oncogenes and oncosuppressor genes. At present, there are convincing data relating to *c-myc*, *bcl-2*, p53 and *ras*.

Expression of *c-myc* is of particular interest, as it seems to determine either continuous proliferation or apoptosis, depending on the availability of critical growth factors (Evan *et al.*, 1992). Cultured immortalised fibroblasts respond to the addition of serum growth factors by entering the proliferation cycle, and this is preceded by and apparently dependent upon transcription of *c-myc*. On withdrawal of serum growth factors, *c-myc* is down-regulated and the cells revert to a growth-arrested state in which they may remain viable for many weeks. In cells modified to express *c-myc* constitutively, however, the absence of serum growth factors is not accompanied by growth arrest. Instead, the cells remain in cycle – and some may successfully complete DNA and cellular replication – whilst substantial numbers die by apoptosis. This effect of serum starvation can be produced by other interventions that blockade some step in the proliferation cycle (for example leucine deprivation, thymidine-induced S-phase arrest or treatment with topo-isomerase II inhibitor (Bertrand *et al.*, 1991; Fanidi *et al.*, 1992)). Thus *c-myc* expression and the availability of critical growth factors (of which IGF-1 appears to be the most significant in fibroblasts) delineate three extreme cell states – *growth arrest* (*c-myc* off, growth factors absent), *population expansion* (*c-myc* on, growth factors present), and *apoptosis* (*c-myc* on, growth factors off). Study of cultured cells suggests the existence of an intermediate *high turnover state* in which susceptibility to apoptosis is high despite the fact that some cells may be competent to enter the proliferation cycle (Dive & Wyllie, 1992). Quantitative as well as qualitative consideration may determine cell transitions between these states.

Some cellular proto-oncogenes appear to 'rescue' cells from the high turnover state into the population expansion state. Amongst these is *bcl-2* (Hockenberry *et al.*, 1990; Nunez *et al.*, 1990; Bissonnette *et al.*, 1992; Fanidi *et al.*, 1992). An elegant demonstration of this is the resistance to

apoptosis of cortical thymocytes in which *bcl-2* is engineered for constitutive expression (Sentman *et al.*, 1991; Strasser *et al.*, 1991). Such cells fail to undergo apoptosis in response to a wide variety of stimuli to which normal thymocytes are sensitive. Activation of *bcl-2* is not unique in rescuing cells from apoptosis. High expression of the mutated *ras* oncogenes (Wyllie *et al.*, 1987) and exposure to many growth factors can have the same effect (Williams *et al.*, 1990; Koury & Bondurant, 1990) perhaps in a cell type dependent way.

Expression of wild type p53 appears to have the opposite effect, inducing apoptosis in susceptible cells (Yonish-Rouach *et al.*, 1991). Wild-type p53 is known to cause temporary G1 arrest in some cell types (Kastan *et al.*, 1991) and it is thus possible that this arrest co-operates with endogenous *c-myc* expression to initiate apoptosis.

It is not clear how these regulatory genes influence susceptibility to apoptosis. One obvious mechanism would be the induction or depletion of the effector proteins discussed earlier. In support of this, endogenous endonuclease activity is readily demonstrated in the nuclei of fibroblasts that constitutively express *c-myc*, but is absent from cells expressing mutated Ha-*ras* at high level (Arends, M.J.: unpublished observations). It is convenient to designate as *primed* those cells in which synthesis of the effector proteins of apoptosis has been induced, and so to distinguish them both from the unprimed cells that lack effectors and cannot immediately undergo apoptosis, and from cells in the process of entering apoptosis through activation of the effectors, which we call *triggered* (Arends & Wyllie, 1991). The concept that genes regulate dynamic transitions between susceptibility and resistance to apoptosis has important implications for our understanding of regulation of normal tissue kinetics and several aspects of the behaviour of tumour cells.

Thus, during affinity maturation of the immune response, virgin circulating B cells enter the follicle centre and are stimulated by local factors to rapid cell proliferation. However, the majority of these cells are destined for almost immediate death by apoptosis: they are in the high turnover state described previously complete with high *c-myc* expression. Only a small sub-population is selected for long-term survival (and B-cell memory) on the basis of the affinity of their surface immunoglobulin for the antigen, presented on the surface of dendritic cells in the follicle centre (Liu *et al.*, 1989). This 'rescue' is associated with induction of *bcl-2* in the surviving cells (Nunez *et al.*, 1991; Hockenberry *et al.*, 1991).

Although much less is known of the gene expression involved, an analogous situation exists in development of the nervous system. Motor neurones are generated in excess of eventual requirement, and deleted by apoptosis if their axons fail to make contact with muscle endplates, the source of growth factors which presumably rescue them from death. Rather similar processes appear to take place in the central nervous system in development of glia and the establishment of interneuronal networks in the central nervous system (Martin *et al.*, 1988; Raff, 1992).

One corollary of the hypotheses outlined above is that cells in the high turnover state include many that are primed for apoptosis and therefore susceptible to die by this means in response to a variety of lethal stimuli. Cells of the lymphoid follicle centre phenotype and at the base of intestinal crypts (another high-turnover, *c-myc*-expressing, *bcl-2* expressing population) (Liu *et al.*, 1989; Nunez *et al.*, 1991) are indeed susceptible to apoptosis engendered by agents with widely divergent modes of action (including many used in cancer chemotherapy) (Ijiri & Potten, 1987). There are obvious implications for toxicology and cancer chemotherapy if cell sensitivity to apoptosis can be modified by manipulation of a set of regulatory genes.

Similarly, there are implications in carcinogenesis. The genes discussed above as influencing apoptosis are all familiar because of their abnormal regulation in neoplasms. One important element in the early phases of carcinogenesis may be expansion of a target population of cells capable of subsequent genetic progression to malignancy, perhaps as a

result of further genetic events. This target population may normally be kept small through apoptosis. Inappropriate rescuing stimuli may therefore be oncogenic simply because they increase the number of cells available for mutagenesis. There are several potential examples, such as *ras* expression in premalignant hyperplasias of breast (Going *et al.*, 1992) and in colorectal adenomas (Williams *et al.*, 1985) and the

constitutive *bcl-2* expression of follicular lymphomas and the LMP-1-induced *bcl-2* expression of drug-resistant Burkitt's lymphoma cell lines (Clark *et al.*, 1992; Gregory *et al.*, 1991; Henderson *et al.*, 1991).

The pervasiveness of p53 mutation in human malignancies (Levine *et al.*, 1991) may be accounted for in a similar way.

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