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Cell

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The generation of cells in the human body has been difficult to study and our understanding of cell turnover is limited. Extensive testing of nuclear weapons resulted in a dramatic global increase in the levels of the isotope ^{14}C in the atmosphere, followed by an exponential decrease after the test ban treaty in 1963. We show that the level of ^{14}C in genomic DNA closely parallels atmospheric levels, and can be used to establish the time point when the DNA was synthesized and cells were born. We use this strategy to determine the age of cells in the cortex of the adult human brain, and show that whereas non-neuronal cells are exchanged, occipital neurons are as old as the individual, supporting the view that postnatal neurogenesis does not take place in this region. Retrospective birth dating is a generally applicable strategy that can be used to measure cell turnover in man under physiological and pathological conditions.

Many cells have a shorter life span than the organism and are continuously replaced. Cells exposed to a harsh environment, such as in the skin or intestine, are often very short lived. In other tissues there may be less cell turnover under physiological conditions, but regeneration may be activated in response to injury. For many cell types, however, it is largely unknown whether they turn over at all once development is completed.

Cell generation is often studied by analysis of molecular markers of proliferation. This provides a good view of the number of cells in cycle at a given time, but it does not provide insight into the number of mature cells that are generated or added to the tissue. Administration of labeled nucleotides such as ^{3}H-thymidine or BrdU allows prospective labeling of newborn cells and can reveal the generation and integration of mature cells in an organ. It is, however, difficult to detect rare events and there are several technical caveats with a risk of both false positive and negative results, giving room to controversy (Nowakowski and Hayes, 2000; Rakic, 2002a). Moreover, it is not possible to retrospectively determine cell turnover in collected material and the toxicity of labeled nucleotides limits its use for studies in man.

Much of our view on cell turnover in the adult human body is inferred from studies in rodents, which in most cases are only a few months old at the time of analysis. This may not be an ideal model for man, who can live for a century, and can potentially have a greater need to replace cells over the lifespan. Whereas it may be easy to conceptualize that for example a neuron in the brain can live for months, is it possible for the same cell type to be maintained and function for many decades?

Whether a specific cell type is exchanged, and at what rate, is a fundamental question that may have important implications for how we view the human body under physiological

and pathological conditions. Alterations in cell turnover is a key feature in several diseases, such as decreased erythrocyte production in aplastic anemia or increased keratinocyte turnover in psoriasis. Distorted cell turnover has been implicated in the pathogenesis of many diseases, for example decreased neurogenesis in depression (Duman, 2004; Santarelli et al., 2003; Sheline et al., 1996) and impaired production of cardiomyocytes in heart failure (Sussman and Anversa, 2004), but it has remained controversial and difficult to study.

Much of the impetus in stem cell research and regenerative medicine is fueled by the prospect of promoting cell replacement. Stimulating blood cell production with erythropoietin or G-CSF are successful and established therapies (Richard and Schuster, 2002), and it has been suggested that similar pharmacological therapies may be developed to influence cell replacement in other organs (Ding and Schultz, 2004; Lie et al., 2004; Lindvall et al., 2004). Without knowing if a specific cell type is renewed in the healthy or pathological situation, it remains uncertain whether it may be realistic and rational to modulate this process.

The lack of methods to study cell turnover in man prompted us to develop a novel strategy to approach this issue. Inspired by ^{14}C-dating in archeology, we sought to develop a way to retrospectively determine the age of cells without the need of delivering any chemical to the individual prior to the analysis. ^{14}C levels on earth have remained relatively constant over long time periods, and the radioactive decay of the isotope is used to retrospectively date biological material in archeology. The resolution in modern time is poor due to a half-life of 5730 years. However, extensive above ground testing of nuclear weapons between the mid 1950s and early 1960s resulted in the generation of

large quantities of ^{14}C (Figure 1A), which rapidly distributed evenly in the atmosphere around the globe (De Vries, 1958; Nydal and Lovseth, 1965). Since the test ban treaty in 1963, there has been no high yield above ground nuclear detonation leading to significant ^{14}C production (Levin and Kromer, 2004). Thus, the levels have dropped thereafter exponentially, not primarily because of radioactive decay, but due to diffusion and equilibration with the oceans and the biosphere (Figure 1A), resulting in a slope decreasing 50% approximately every 11 years after 1963 (Levin and Kromer, 2004).

We have taken advantage of the drastically altered atmospheric ^{14}C levels in modern time to develop a strategy to retrospectively birth date cells in the human body. We use this method to address whether cortical neurons are renewed in the adult human brain, and find that these neurons are as old as the person, arguing against adult neurogenesis in this region. This is a generally applicable strategy that can be used to analyze cell turnover in man under physiological and pathological conditions.

Results

^{14}C in genomic DNA reflects the age of cells

^{14}C in the atmosphere reacts with oxygen and forms CO_2, which enters the biotope through photosynthesis. Our consumption of plants, and of animals that live off plants, results in ^{14}C levels in the human body paralleling those in the atmosphere with a short lag for seasonal growing and harvest cycles (Harkness, 1972; Libby et al., 1964).

Most molecules in a cell are in constant flux, with the unique exception of genomic DNA, which is not exchanged after a cell has gone through its last division. The level of ^{14}C integrated into genomic DNA should thus reflect the level in the atmosphere at any given time point and we hypothesized that determination of ^{14}C levels in genomic DNA could be used to retrospectively establish the birth date of cells in the human body.

Atmospheric ^{14}C levels have been monitored over time at several locations. As there may be some local variation in ^{14}C levels in different geographical regions, we first established the atmospheric levels of ^{14}C in recent years in the geographical region of the studied population. We dissected year rings from Swedish pine from 1962 to present, as well as several rings from the pre-bomb time. The ^{14}C content of each tree ring was measured by accelerator mass spectrometry. A tree ring is laid down annually and the cellulose is not changed thereafter, thus giving an accurate reflection of the ^{14}C levels in the atmosphere for a specific year. The levels in Sweden closely matched the mid-latitude northern hemisphere levels (Figure 1B, C, Supplemental Table 1), in line with the rapid distribution of ^{14}C in the atmosphere. Since our local data closely corresponded to the extensive material of mid-latitude northern hemisphere measurements collected in Germany (Levin and Kromer, 2004), we related all our following analyses to this data.

We next asked whether cells generated at different time points had ^{14}C levels in genomic DNA that correspond to the time they were generated. The sensitivity of accelerator mass spectrometry is rapidly increasing and ^{14}C levels can today accurately be established with samples containing as little as 30μg carbon, which corresponds to genomic DNA from 15 million cells. It is critical when extracting the genomic DNA for this application to keep contamination with non-DNA carbon sources to a minimum and not to introduce exogenous carbon that could be isolated with the DNA and thus skew the analysis. We therefore modified established DNA extraction protocols to minimize the risk of carbon contamination (see experimental procedures). DNA samples were analyzed for purity in several ways; in addition to spectrophotometric analysis, the contents of all samples were analyzed by HPLC and the amount of total carbon (^{12}C, ^{13}C and ^{14}C) was determined during graphite preparation for isotope analysis by accelerator mass spectrometry. The knowledge of the amount of DNA (with a known proportion of the mass accounted for by carbon) and total carbon in each sample allows very sensitive detection of carbon contamination, irrespective of the source, and any sample in which the total carbon content was higher than calculated from the amount of DNA was excluded from further analysis.

Depletion of hematopoietic stem and progenitor cells by irradiation results is the rapid loss of leukocytes, demonstrating their short life span. We analyzed ^{14}C levels in DNA from nucleated blood cells, representing a population of cells known to be newborn. The measured ^{14}C values were compared to the recorded atmospheric levels to establish at which time point they corresponded. The strategy to establish the age of a cell population by relating ^{14}C concentrations in genomic DNA to atmospheric levels is schematically

depicted in Figure 2A, B. The levels of ^{14}C in leukocyte DNA did indeed correspond to the contemporary atmospheric levels at the time when the sample was taken (Figure 2C, D). We next asked whether cells generated at a known time point much earlier could be accurately dated. To this end, we analyzed DNA from early postnatal brain tissue collected many years earlier. Since the tissue was from postmortem infants, there is a narrow time frame when the cells could have been generated. ^{14}C levels in DNA from early postnatal brain tissue corresponded to the time shortly after birth (Figure 2E, F), in line with brain cells being born both prenatally (mostly neurons) and postnatally (mainly glial cells, which form the majority). This analysis of cells generated at known time points confirm that ^{14}C levels in DNA can be used to establish when cells are born.

Establishing the age of cells in adult human organs

We next birth dated cells in different adult organs. We selected intestine, skeletal muscle and two brain regions, based on the assumption that these tissues have different rates of cell turnover. Intestinal epithelial cells have an average life span of about 5 days (Marshman et al., 2002), whereas many non-epithelial cells in the gut are likely to be long lived. There is thought to be very little cell replacement in the cerebral cortex and cerebellum. All tissues contain blood, but nucleated cells only account for about 1/1000 of cells in peripheral blood, and their effect on the average age of cells in an organ will be negligible. ^{14}C birth dating revealed that the average age of cells in the intestine (jejunum) is 10.7±3.6 years (mean±SD from 3 individuals of average age 34.8 years, Figure 3). We quantified the proportion of epithelial cells to other cells in histological sections of jejunum and found that in average 42±3% (N=5 individuals) of all cells in the specimen

were epithelial. Assuming that all epithelial cells are contemporary, the average age of the non-epithelial cells is 15.9 years. Measurement of the level of ^{14}C in DNA from intercostal skeletal muscle from two individuals (37 and 38 years old) indicated an average age of 15.1 years.

The average age of cells in the grey matter of the cerebellum was almost as old as the individual (born at the age of 2.9±1.2 years, Table 1), whereas cells from the occipital cortex grey matter were substantially younger (Figure 3), indicating more cell turnover in the cerebral cortex than in the cerebellum. Analysis of multiple samples from the same individuals revealed a precision of ±2 years (1 SD) for the dating procedure, and a high degree of reproducibility between individuals (Table 1).

An average cell age slightly younger than the individual, as seen for cerebellum, could reflect that the generation of cells continued for a short time postnatally and then stopped, or that most cells were generated before birth but a subpopulation of cells turnover in adulthood. These two possibilities can be distinguished by analyzing tissue from individuals born before the nuclear bomb tests, as schematically depicted in figure 4A. The strategy to birth date cells builds on the steep slope of ^{14}C decline in the atmosphere after the nuclear bomb tests, and the resolution in time before the bomb tests is very poor. However, the low levels of ^{14}C before the bomb-pulse makes the detection of a small population of cells born during or after the bomb tests especially sensitive, and we determined that we could detect such a population constituting down to 1% of the total cell population. Analysis of individuals born pre-bomb demonstrated ^{14}C levels in cerebellar grey matter that correspond to atmospheric levels prior to 1955 (Figure 4, Table 1). The cerebellar grey matter consists of approximately 92% neurons

(Supplemental Figure 1), thus this data reflects primarily the average neuronal age. This indicates that cerebellar neurogenesis is completed in the postnatal period and also that there is limited turnover of glial cells. In contrast, analysis of ^{14}C levels in genomic DNA from occipital cortex in individuals born before the nuclear bomb tests revealed substantial cell turnover in this region of the brain (see below).

Isolation of cell type specific DNA from archival material

The analysis of ^{14}C in genomic DNA gives an average age of cells in a tissue. Most tissues are complex and composed of many cell types, and in order to study the potential turnover of a specific cell type, we wanted to separate cells prior to analysis. We focused on the human brain, since there is little known about the potential turnover of neurons, and alterations in neurogenesis have been implicated in human disease.

Fluorescence activated cell sorting (FACS) using antibodies against specific cell surface epitopes is commonly used to purify distinct cell types. However, the complex morphology of neurons makes it difficult to isolate intact cells from brain tissue. This, together with the lack of pan-neuronal cell surface proteins, prompted us to modify this strategy and instead sort cell nuclei. Nuclei were first isolated from dissociated tissue and then incubated with directly conjugated antibodies to NeuN (Figure 5A-F), a well-established neuron specific epitope mainly localized to the nucleus (Mullen et al., 1992). This enabled FACS isolation of neuronal nuclei with high specificity (Figure 5G, H). Re-analysis of sorted nuclei revealed that we could obtain >99% neuronal nuclei.

A significant advantage of the method to sort nuclei, rather than whole cells, is that the nuclear sorting is less sensitive to post-biopsy or post-mortem interval, and most

importantly, works equally well on fresh tissue and frozen archival material. This makes it possible to study material already collected in biobanks.

Cortical neurons are as old as the individual

Contrary to the long-standing dogma that neurons cannot be generated in the adult brain, it is now firmly established that neurogenesis continues in discrete brain regions throughout life in all studied mammals (Altman and Das, 1965; Eriksson et al., 1998; Gould et al., 1998; Kaplan and Hinds, 1977). The establishment of a strategy for the retrospective birth dating of cells together with FACS isolation of neuronal nuclei makes it possible to study neuronal turnover in the adult human brain.

Technical difficulties have contributed to conflicting data regarding the distribution and extent of adult neurogenesis in experimental animals. One of the most controversial issues is whether neurogenesis persists in the cerebral cortex. Studies in several species have indicated that this may occur under physiological or pathological conditions (Chen et al., 2004; Dayer et al., 2005; Gould et al., 1999; Gould et al., 2001; Kaplan, 1981; Magavi et al., 2000), whereas other studies have failed to detect adult cortical neurogenesis (Kornack and Rakic, 2001). It has been suggested that some positive results were due to technical shortcomings including unspecific labeling with BrdU or mistaken co-localization due to low resolution microscopy (Kornack and Rakic, 2001; Nowakowski and Hayes, 2000; Rakic, 2002b). Perhaps the strongest indication of adult cortical neurogenesis under physiological conditions, from a technical point of view, comes from electron microscopic detection of ^{3}H-thymidine labeled neurons in the occipital cortex of the rat (Kaplan, 1981).

We therefore set out to retrospectively determine the age of neurons in the adult human occipital cortex, to establish whether there is any appreciable addition of neurons in this brain region postnataly. ^{14}C levels in unsorted total occipital cortex showed an average age substantially younger than the individual, pointing to cell turnover (Figures 3 and 6). To specifically analyze the age of neurons and non-neuronal cells, we isolated NeuN-positive and –negative cells by flowcytometry. ^{14}C levels in NeuN-positive neurons from individuals born after the bomb-pulse demonstrated levels corresponding to the average age of the cells being as old as the individual (Figure 6A, B). We can currently establish the age of a cell population with a precision of ±2 years and the time of birth of the individual was within this error margin in all measurements of NeuN-positive neurons from occipital cortex. The NeuN-negative cells, in contrast, were substantially younger (Figure 6A, B). We additionally analyzed cells from individuals born before the bomb-pulse, which provides a very sensitive measure of postnatal cell turnover. The ^{14}C levels in genomic DNA from NeuN-positive neurons corresponded to those in the atmosphere prior to the nuclear bomb tests (Figure 6C, D), not lending support to adult neurogenesis in this region.

Discussion

Cell turnover may be necessary under physiological or pathological conditions to maintain certain organs, yet our knowledge regarding this process in most human tissues is scarce due to a lack of means to study this process. We describe here a general strategy to study cell renewal in man. The dramatic increase in atmospheric ^{14}C levels and the subsequent exponential decline have resulted in different amounts of ^{14}C being integrated into the DNA of cells depending on the time point the DNA was synthesized. We all therefore have a date-mark in our DNA, and we show here that this can be used to establish the age of cells.

DNA as a time capsule

Most molecules in a cell are in constant flux and DNA is likely to be the most stable molecule after a cell has undergone its last mitosis. It is important to consider the stability of DNA for the validity of the current technique, since turnover of nucleotides in the absence of cell division would give a false impression of a cell population being younger than its actual age. DNA damage, followed by nucleotide exchange, mainly occurs during DNA replication (Nouspikel and Hanawalt, 2002). Since DNA repair during cell division will not influence the current analysis, it is most important to consider the potential turnover of DNA in very rarely dividing or postmitotic cells. DNA repair in postmitotic cells is limited to transcribed genes, and untranscribed DNA in terminally differentiated cells, including human neurons, does not appear to be repaired even after massive experimental damage (Nouspikel and Hanawalt, 2002). Nucleotide exchange, even in transcribed DNA, appears limited in terminally differentiated cells. The mutation rate of

transcribed genes in rarely dividing human lymphocytes has been measured using different techniques and estimated to be 1.4-2/10^9 per day and locus, which corresponds to 5.2–7.3/10^5 events over a century (Bridges, 1997; Green et al., 1995; Morley, 1996). Since these frequencies are obtained for transcribed genes, the rate is likely to be substantially lower in total DNA. Thus, available data indicate extremely little nucleotide turnover in rarely dividing and postmitotic cells, well below levels that would influence the current method. Our finding that cerebellar cells and cortical neurons have ^{14}C levels corresponding to the time of birth of the person corroborates that nucleotide exchange in postmitotic cells is very limited and below the detection level with the method employed.

Another source of carbon exchange in the genome is methylation, which constitutes an important mechanism in transcriptional regulation (Bird, 2002). Methylation is restricted to cytosine residues 5' to guanosine in CpG stretches, and the degree of methylation varies in different organs between 0.7-1% of nucleotides in DNA (Ehrlich, 1982). Even if all methyl groups were contemporary, addition of one carbon atom by methylation of 1% of nucleotides (which contain in average 9.75 carbon atoms) could maximally skew the analysis by about 1‰, and is thus negligible.

Sensitivity of retrospective birth dating

How many cells have to be generated postnatally for turnover to be detected? The resolution in time and number of cells depends on when the person was born in relation to when the new cells were generated. In an individual born just before the nuclear bomb tests, the relative difference in ^{14}C concentration is highest between the time of birth and the period of and just after the nuclear tests, and dropping thereafter. The sensitivity for

detecting cell generation is therefore highest for the childhood period. A person born 20 years before the bomb pulse will instead have the largest relative difference in ^{14}C levels between the time up to adolescence and early adulthood. In contrast, analysis of cells from a person born after the bomb tests will have the highest sensitivity for the latest born cells. Taking these differences into account, the highest total sensitivity is reached by analysis of several individuals born at different time points in relation to the nuclear bomb tests. This allows for the detection of relatively small additions of new cells, and may also provide information as to when in time a cell population is generated. The detection limit, when comparing time points with the largest difference in ^{14}C levels with the current sensitivity of accelerator mass spectrometry, is about 1% newborn cells within a population of old cells.

The current method provides an average age for a cell population. The sensitivity of accelerator mass spectrometry is increasing rapidly, making it likely that successively smaller populations can be analyzed in the future. Single cell resolution will, however, never become possible, since there is only one ^{14}C atom in the DNA of less than every 15^{th} cell ($6.4x10^{10}$ carbon atoms in nucleotides of the human genome and 1 out of 10^{12} C is ^{14}C).

The current analysis provides qualitatively different type of information than with ^{3}H-thymidine and BrdU in experimental animals. Labeled nucleotides are given in a short pulse and analysis of labeled cells at different time points provides information at the single cell level about newly generated cells of a certain phenotype. Since the labeled nucleotide is given as a pulse it is difficult to detect rare events as well as to gain a view of the proportion of cells that are exchanged over a longer time period. The current

method is unique in that it provides information over the whole life-span of the individual, rather than at a single time point, which can give good resolution even for rare events. For example, if 1/100 000 cells would be replaced per day in a certain structure, it would be far from reliably detectable by labeled nucleotides, but over a decade it would amount to 3.65% of the cells, which is easily detected with the current methodology.

Atmospheric levels of ^{14}C rapidly equalized around the globe after the nuclear bomb tests, making the method generally applicable in different countries. ^{14}C levels may, however, be slightly lower in extremely polluted industrialized regions due to excessive burning of ^{14}C depleted fossil fuels such as coal, oil and natural gas (Pawelczyk and Pazdur, 2004). If an individual lived mainly off food derived from the directly polluted area, ^{14}C values could be depressed and cell age underestimated. Our measurement of ^{14}C in tree rings in the region where the individuals studied in our analysis lived excluded pollution skewing our results, but this may be important to consider in more heavily industrialized areas.

The age of cortical neurons

The cerebral cortex is the site of the highest cognitive functions. There is clearly a considerable degree of plasticity in the cortex, enabling memory formation and adaptation to new conditions (Chklovskii et al., 2004). Much of the plasticity can be accounted for by modulating pre-existing connections, but there are also structural changes in the adult human cortex in response to certain conditions resulting in detectable changes in volumes in distinct areas (Draganski et al., 2004). It is important to understand if neuronal turnover may contribute to cortical plasticity.

The cerebral cortex spans a large area, and although structurally similar, different cortical areas have distinct functions. We selected to study the occipital cortex since the strongest evidence, from a technical point of view, for neurogenesis in animals under physiological conditions have been reported from this area (Kaplan, 1981). Our analysis revealed that neurons from the adult human occipital cortex have ^{14}C levels in their genomic DNA corresponding to the time when the individual was born, lending little support to postnatal cortical neurogenesis in man.

Kaplan (1981) reported 1/10 000 cortical neurons in the adult rat and Gould and colleagues (1999) (Nowakowski and Hayes, 2000) found approximately 1/100 000 labeled cortical neurons in the adult primate being newborn after single injections of labeled nucleotides. It is difficult to infer the rate of cell replacement over time from pulse labeling with ^{3}H-thymidine or BrdU, but even with conservative estimates these frequencies would amount to a large fraction of neurons (Nowakowski and Hayes, 2000), very easily detectable by retrospective birth dating, being generated during adulthood. Our data establish that neuronal turnover of this magnitude leading to long term stable integration of new nerve cells does not occur in the adult human occipital cortex. This does, however, not rule out the possibility of neurogenesis in other cortical areas or that neurogenesis may be induced in response to injury (Chen et al., 2004; Magavi et al., 2000).

Applications for retrospective birth dating

The rapid development of accelerator mass spectrometry has made sensitive ^{14}C analyses increasingly accessible and affordable, enabling scientists in many fields to use it to

answer specific questions. The steady decrease of ^{14}C in the atmosphere will make retrospective birth dating less sensitivite with time, and limits the time period in which this technique may be used on new material. However, the existence of tissue banks, where material has been collected from many pathologies, and the applicability of the method on archival material, allows for analyses of already collected material. In some regards though, the technique becomes even more powerful in the coming decades; as people born around the nuclear bomb tests get older, its usefulness for the study of age-related pathologies, such as dementia, will increase.

The possibility to determine the age of cells can give us a map of the human body from a cell renewal perspective. The stability or turnover of cells in different tissues is a fundamental feature that may influence the response of different organs to insults and the aging process. Analysis of cell turnover in different pathologies may further the understanding of certain diseases.

Experimental procedures

Tissue collection

Tissues were procured from cases admitted during 2003 and 2004 to the Department of Forensic Medicine, Karolinska Institute for autopsy, after consent from relatives. Ethical permission for this study was granted by the Karolinska Institute Ethical Committee. Five individuals born before and five born after the nuclear bomb tests were included in this study. Tissues were frozen in 1 g samples and stored at –80°C until further analysis.

Nuclei isolation

Tissue samples (1g) were defrosted and Dounce homogenized in 10 ml lysis buffer (0.32 M sucrose, 5 mM $CaCl_2$, 3 mM magnesium acetate, 0.1 mM EDTA, 10 mM Tris-HCl (pH 8.0), 0.1% Triton X-100, 1mM DTT). Homogenized samples were gently suspended in 18 ml of sucrose solution (1.8 M sucrose, 3 mM magnesium acetate, 1 mM DTT, 10 mM Tris-HCl (pH 8.0)), layered onto a cushion of 10 ml sucrose solution and centrifuged at 30 000 g for 2.5 hours at 4°C. The isolated nuclei were resuspended and stored overnight at 4°C.

Immunohistochemistry

Brain tissue was immersion fixed in 4% formaldehyde in PBS and cut on a cryostat. Tissue sections were incubated overnight at 4°C with mouse monoclonal antibodies against NeuN (Mullen et al., 1992) at a dilution of 1:1000.

Flowcytometry

Neuronal nuclei were isolated by FACS of nuclei labeled with the neuron-specific monoclonal antibody NeuN. NeuN antibodies were directly conjugated with Zenon mouse IgG labelling reagent (Alexa 488, Molecular Probes) as follows: 10 μl of Alexa 488 conjugate was added to 100 μl blocking mix (PBS/0.5% BSA/10% NGS) and 300 μl NeuN mix (6μl NeuN in 1.5ml PBS) and incubated for 5 min at room temperature (RT). One ml of nuclei mix (cerebellum, 83 mg starting tissue/ml; all other brain regions, 167 mg starting tissue/ml) was added to NeuN-conjugated mix and incubated at 4°C for a minimum of 45 min.

To ensure that only single nuclei were sorted (and not aggregates), nuclei were stained with a red-fluorescent cell-permeable DNA probe, DRAQ5, according to manufacturer's instructions (Biostatus). Single nuclei were easily discerned from doublets, triplets and potential higher order aggregates based on their fluorescence intensity (FL1), and a gate was set so that only single nuclei were sorted. Using this technique it was calculated that 98% or more of all nuclei are singlets. DRAQ5 binds tightly to DNA, and therefore becomes a source of carbon-contamination to the extracted DNA. To avoid this problem an aliquot of nuclei was labeled with DRAQ5 and the singlet population plotted as a function of forward scatter width (FSC-W) versus forward scatter height (FCS-H). Using these parameters it is easy to determine single nuclei from doublets, triplets and potential higher order aggregates as well as background noise (Wersto et al., 2001). Selective isolation of single-nuclei events was performed for every sort using this technique.

Nuclei were sorted based on purity, and the purity of all sorts confirmed by re-analyzing the sorted populations. Nuclei pellets were collected by centrifugation and frozen at -

80°C in readiness for DNA extraction. All FACS analysis and sorting was performed using a FACS Vantage DIVA (BD).

DNA extraction

The following extraction protocol was optimized for minimal introduction of carbon and maximal DNA yield and purity. Two ml of 1% SDS, 5 mM EDTA-Na_2, 10 mM Tris-HCl (pH 8.0) and 100 μl of protease solution (2 mg/ml, Sigma) was added to each sample of isolated nuclei and the tube was inverted several times and incubated at 65°C for 40 min (tubes were inverted periodically). After this incubation, 20 μl RNAse cocktail (Ambion) was added to each sample. The samples were inverted again, and incubated 20 min. Three ml of sodium iodide solution (7.6 M NaI, 20 mM EDTA-Na_2 , 40 mM Tris-HCl (pH 8.0)) was added to each sample followed by repeated inversion, after which 6 ml filtered 99.5% ethanol was added and tubes inverted repeatedly until the DNA precipitated (Wang et al., 1994). The DNA was washed in 70% ethanol for 15 min, and this was repeated three times. Finally, the DNA was quickly rinsed in a water bath, for 5 to 10 seconds, and transferred to a glass vial. Once the DNA sample had dried, it was resuspended in water and left in the incubator at 65°C for at least three days, with constant inversions, in order to fully dissolve the DNA in the water. DNA was quantified using spectrophotometry and purity was analyzed by spectrophotometry and HPLC.

For DNA isolation from whole tissue, fresh or defrosted tissue was minced and mechanically dissociated using a Stomacher-80 Biomaster in plastic bags containing 1.2 ml digestion buffer (100 mM NaCl, 10mM Tris-HCl pH8, 25mM EDTA pH8, 0.5% SDS, 0.1 mg/ml proteinase K) per 100 mg tissue. Samples were incubated shaking at 50°C for

3–12 hrs, until fully digested. Nucleic acids were extracted at RT using an equal volume of phenol/chloroform/isoamyl alcohol and centrifuged for 10 min at 1700 g in a swinging bucket rotor. This step was repeated 2-6 times as necessary (as determined by achieving a protein-free interface between the aqueous upper phase and the phenol-protein containing lower phase). The aqueous layer was transferred to a new tube and DNA precipitated by adding half the volume of 7.5 M ammonium acetate and 2 volumes (of the original amount of top layer) of 100% ethanol. DNA was washed thoroughly in 70% ethanol, air dried and re-suspended in nuclease-free DDH_2O.

DNA purity for all samples was analyzed by spectrophotometry and HPLC. A minimum of 15 million cells is required for ^{14}C analysis with the current sensitivity of accelerator mass spectrometry. The amount of tissue that is required for an analysis varies from region to region, depending upon region-specific cell densities.

Accelerator mass spectrometry

All accelerator mass spectrometry analyses were performed blind to age and origin of the sample. Purified DNA samples suspended in water and whole tissue samples were transferred to quartz combustion tubes and evaporated to dryness in a convection oven maintained at 90-95°C. Excess copper oxide (CuO) was added to each dry sample, tubes were evacuated and sealed with a H_2/O_2 torch. Tubes were placed in a furnace set at 900°C for 3.5 h to combust all carbon to CO_2. The evolved CO_2 was purified, trapped, and reduced to graphite in the presence of iron catalyst in individual reactors (Vogel et al., 1987). Large CO_2 samples (> 500 μg) were split and $\delta^{13}C$ was measured by stable

isotope ratio mass spectrometry. Graphite targets were measured at the Center for Accelerator Mass Spectrometry at Lawrence-Livermore National Laboratory.

Few of the DNA samples were large enough to get $\delta^{13}C$ splits, but those measured ranged from –19 to –23 per mil, values similar to the whole tissues. We used a $\delta^{13}C$ correction of –21 +/-2 for all samples. Corrections for background contamination introduced during sample preparation were made following the procedures of Brown and Southon (Brown and Southon, 1997). The measurement error was determined for each sample and ranged between ±2-10‰ (1 SD) $\Delta^{14}C$. All ^{14}C data are reported as decay corrected $\Delta^{14}C$ following the dominant convention of Stuiver and Polach (1977). This convention established for reporting radiocarbon data in chronological and geophysical studies was not developed to deal with post-bomb data, but it is the most common pending the adoption of a standard nomenclature for post-bomb data (Reimer et al., 2004).

Preparation of tree rings

A wedge was sliced from each cross section of pine tree, and the surface was sanded to remove surface conntamination. Year rings were counted inward from the outer edge. For years of interest, a subsample was selected which integrated a whole growth year. Wood samples were prepared by rinsing with dilute acid-base-acid followed by distilled water and then dried as described by Love et al. (2003). The samples were placed in quartz tubes with excess CuO, sealed and combusted to CO_2. The CO_2 was then reduced to graphite over iron catalyst and analyzed by accelerator mass spectrometry.

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Case #	DOB of person	N	$\Delta^{14}C$‰ Mean (SD)	Cell birth date (SD)	Average birth date of cell after DOB
ND014	1968.2	4	462 ± 95	1972.6 ± 3.3	4.4
ND004	1972.6	10	382 ± 42	1975.1 ± 1.9	2.5
ND009	1973.2	17	357 ± 48	1976.2 ± 1.5	3
ND002	1973.8	4	373 ± 4	1975.4 ± 0.8	1.6
				Average (SD)	**2.9 ± 1.2**
ND017	1952.0	2	-8.9	1955.0 ± 1.5	3
ND018	1953.4	3	0.5	1955.8 ± 1.2	2.4
ND007	1955.0	2	-8.5	1955.5 ± 0.2	0.5
ND008	1958.1	2	381	1962.6 ± 2.2	4.5
				Average (SD)	**2.6 ± 1.7**

Table 1 Resolution and reproducibility of retrospective birth dating

Accelerator mass spectrometer analysis of genomic DNA from cerebelli from individuals born after (upper half) or before (lower half) the nuclear bomb tests. N indicates the number of independent analyses of different samples for each individual. The cell birth date is the time point when the measured $\Delta^{14}C$ corresponded to the atmospheric value. The resolution before the nuclear bomb tests is in general very poor, with the exception of the years just before the testing. DOB is date of birth.

Figure legends

Figure 1 ^{14}C levels in the biotope

The levels of ^{14}C in the atmosphere have been stable over long time periods, with the exception of a large addition of ^{14}C in 1955-1963 as a result of nuclear bomb tests (A, data from (Levin and Kromer, 2004; Stuiver et al., 1998). ^{14}C levels spanning the last decades in the geographical area of the study (Sweden) were measured in cellulose taken from annual growth rings of local pine trees (B) which were subjected to accelerator mass spectrometry, and were found to closely correspond to mid-latitude northern hemisphere ^{14}C levels (C). Only a fraction of representative measurements are displayed. ^{14}C levels from modern samples are by convention given in relation to a universal standard and corrected for radioactive decay, giving the $\Delta^{14}C$ value (Stuiver and Polach, 1977).

Figure 2 The level of ^{14}C in genomic DNA reflects when a cell was born

(A, B) Schematic images depicting the strategy to establish the birth date of cells. The individual in A is born after the period of nuclear bomb tests and the individual in B is born before. The time of birth of the person is indicated by a vertical line in each plot. First, the ^{14}C concentration in genomic DNA from the cell population of interest is established by accelerator mass spectrometry. Second, the measured ^{14}C value is related to the recorded atmospheric levels to establish at what time point they corresponded (indicated by red dot). Third, the year is read off the X-axis, giving the birth date of the cell population. All the following data is presented in this way, with each plot representing one individual. (C, D) ^{14}C levels in genomic DNA of nucleated peripheral blood cells, which are very short lived with a high turnover rate, correspond to

contemporary atmospheric levels at the time of sampling (2004), irrespective of when the person was born (indicated by vertical line). The levels of ^{14}C in genomic DNA of cells known to be older (brain cells from archival specimen from sudden infant death syndrome patients, SIDS) correspond to the time when the cells were generated (E, F). The error bars for the accelerator mass spectrometry readings are too small to be visualized in this and the following graphs. Each graph represents one individual.

Figure 3 Cell age in different adult human organs

Analysis of ^{14}C levels in genomic DNA from cerebellar grey matter, occipital cortex grey matter and small intestine (jejunum) from three representative individuals (A-C) born at different times (indicated by vertical lines), reveal the differing turnover rates of cells in different tissues.

Figure 4 Analysis of tissues from individuals born before the nuclear bomb tests

(A) Schematic representation of how the integration of information from individuals born before and after the nuclear bomb tests can provide further information on the kinetics of a population. A ^{14}C value corresponding to the generation of a cell population shortly after birth (red dot) in an individual born after the nuclear bomb tests (red vertical line indicates birth date) can arise in several ways. The two extreme possibilities are that either (scenario 1) all cells are born up to short after birth and no cells are generated after that, or (scenario 2) that one cell population is generated prenatally and another population is born substantially later. Analysis of ^{14}C in genomic DNA of cells from individuals born before the nuclear bomb tests (indicated in green in A) offer a sensitive

way to detect postnatal generation of cells and can distinguish these possibilities. (B-D) Cells from cerebellar grey matter have ^{14}C levels corresponding to the time before 1955, indicating no or very limited generation of cells in this region after the perinatal period. Each graph represents one individual and are representative examples.

Figure 5 Isolation of neuronal nuclei from the adult human brain

Immunohistochemical identification of neurons with antibodies against the neuron-specific epitope NeuN in tissue sections (A-C) and nuclear isolates (D-F) from adult human cerebral cortex. All nuclei are labeled with DAPI. (G, H) Shows specific isolation of NeuN+ neuronal and NeuN- non-neuronal nuclei by FACS sorting.

Figure 6 Cortical neurons are as old as the individual

The ^{14}C levels in genomic DNA of FACS-isolated NeuN+ neurons and NeuN- non-neuronal cells from occipital cortex of individuals born after (A, B) or before (C, D) the period of nuclear bomb tests indicate specific exchange of non-neuronal cells, and no or minimal turnover of neurons.

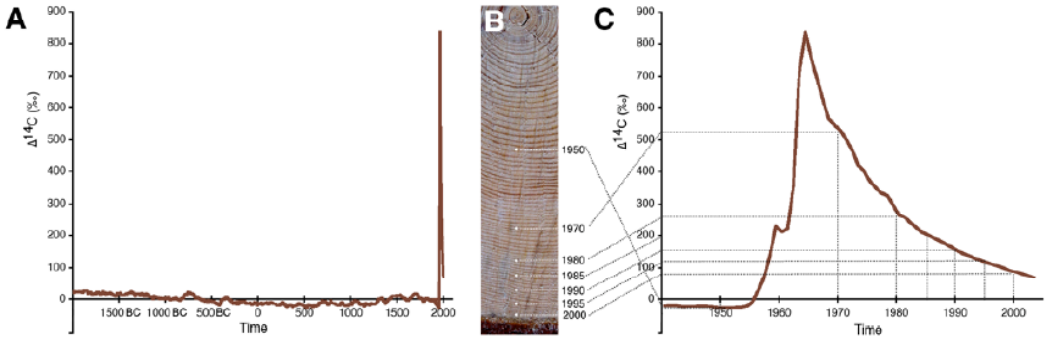
A
B
C
Δ14C (‰)
Time
1500 BC
1000 BC
500 BC
0
500
1000
1500
2000
1950
1970
1980
1985
1990
1995
2000

Figure 1

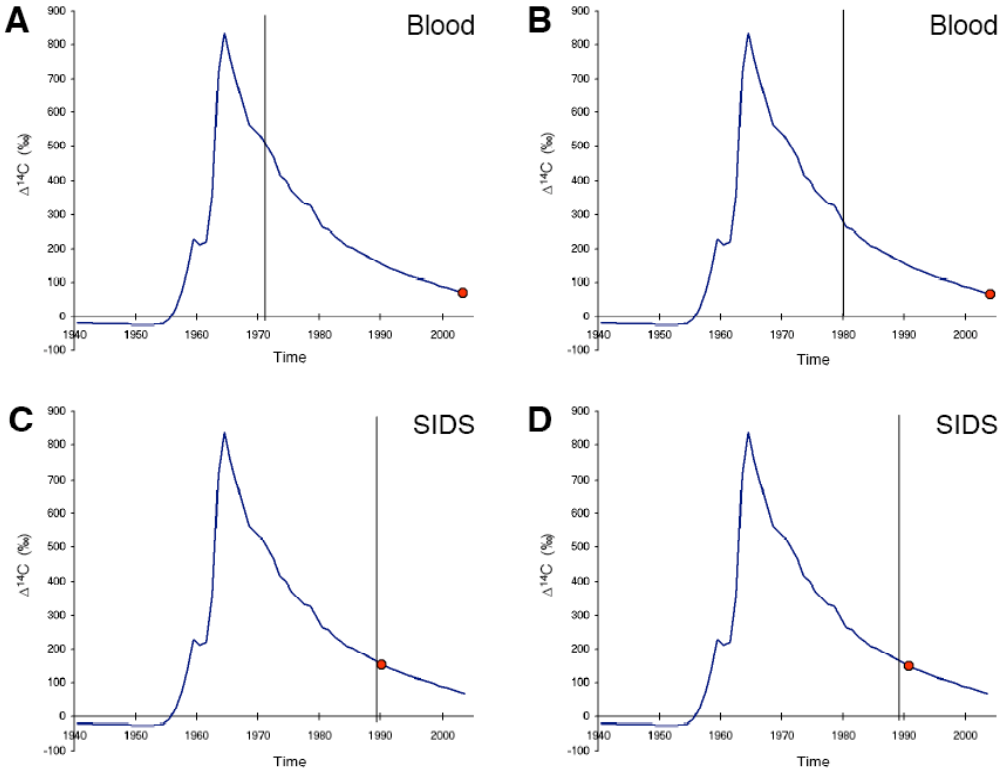
A
Blood
B
Blood
C
SIDS
D
SIDS
Δ14C (‰)
Time
900
800
700
600
500
400
300
200
100
0
-100
1940
1950
1960
1970
1980
1990
2000

Figure 2

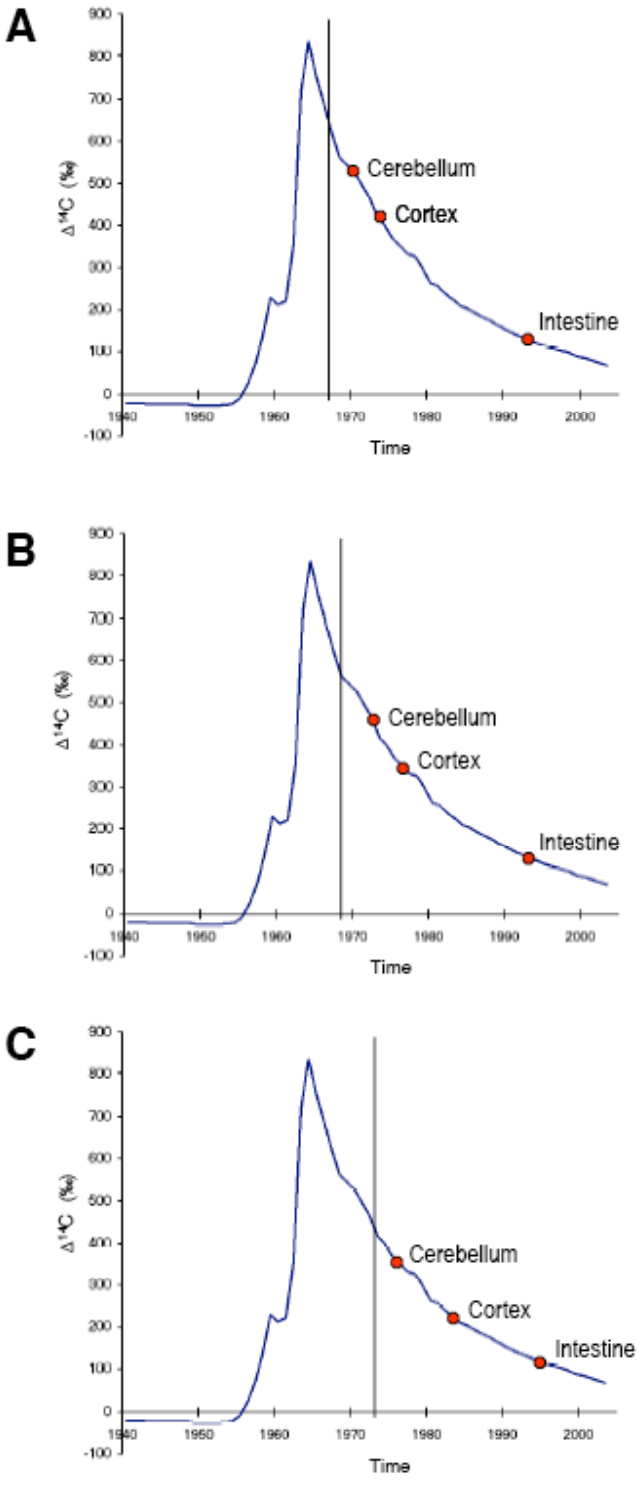
A
B
C
Δ14C (‰)
Time
Cerebellum
Cortex
Intestine
900
800
700
600
500
400
300
200
100
0
-100
1940
1950
1960
1970
1980
1990
2000

Figure 3

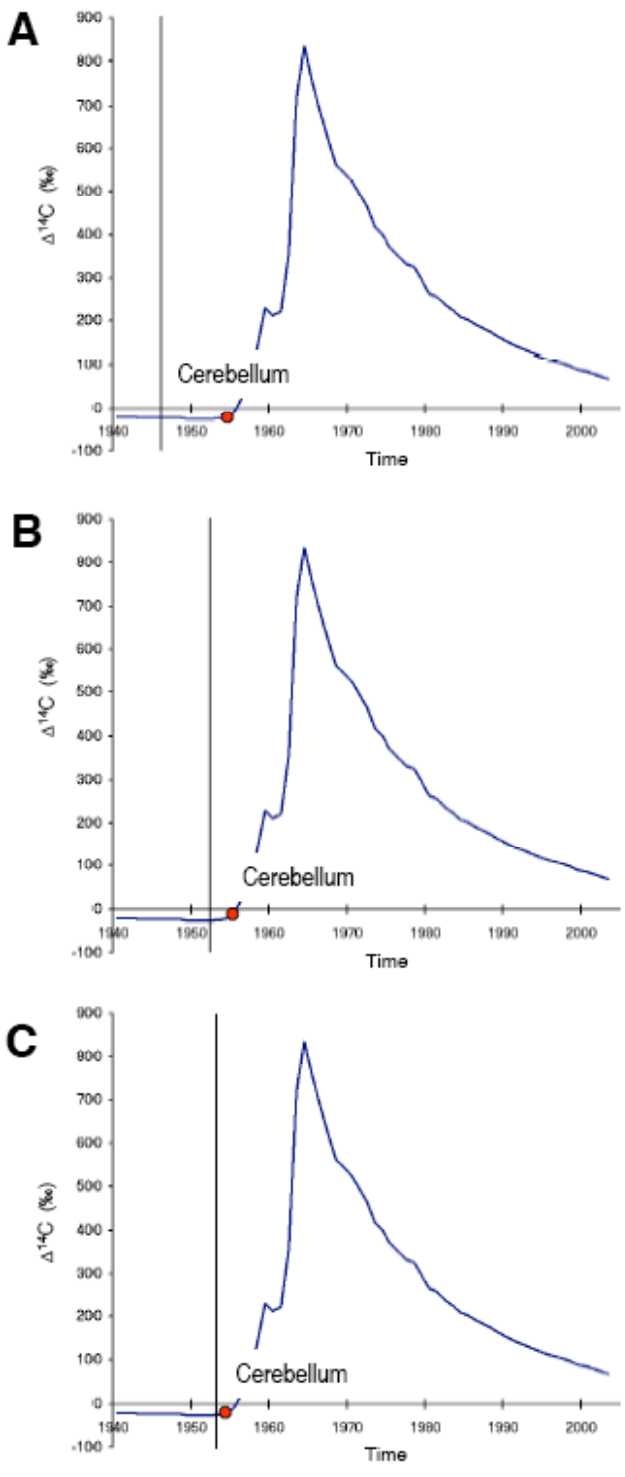
A
B
C
Δ14C (‰)
900
800
700
600
500
400
300
200
100
0
-100
1940
1950
1960
1970
1980
1990
2000
Time
Cerebellum

Figure 4

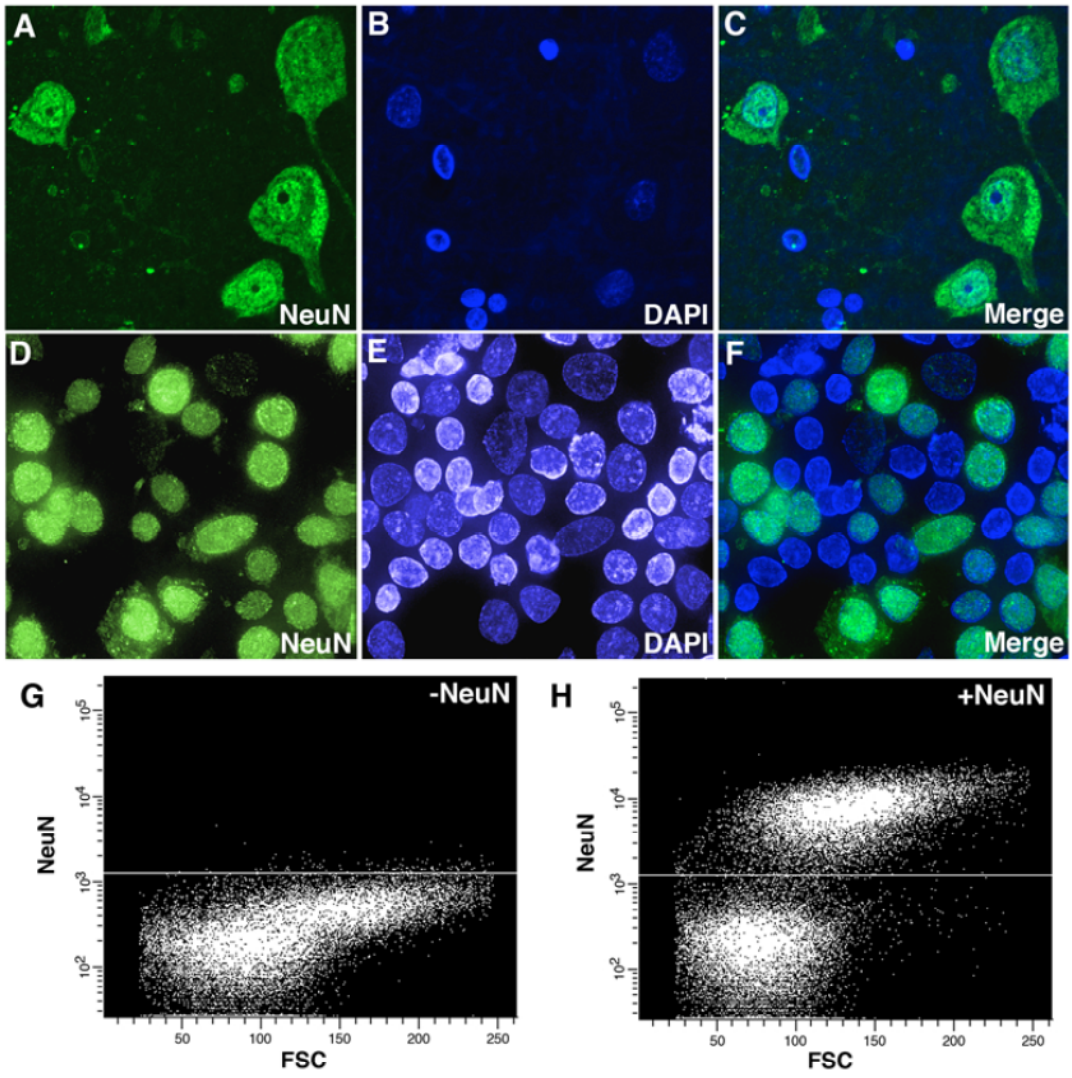
A
NeuN
B
DAPI
C
Merge
D
NeuN
E
DAPI
F
Merge
G
-NeuN
NeuN
FSC
H
+NeuN
NeuN
FSC

Figure 5

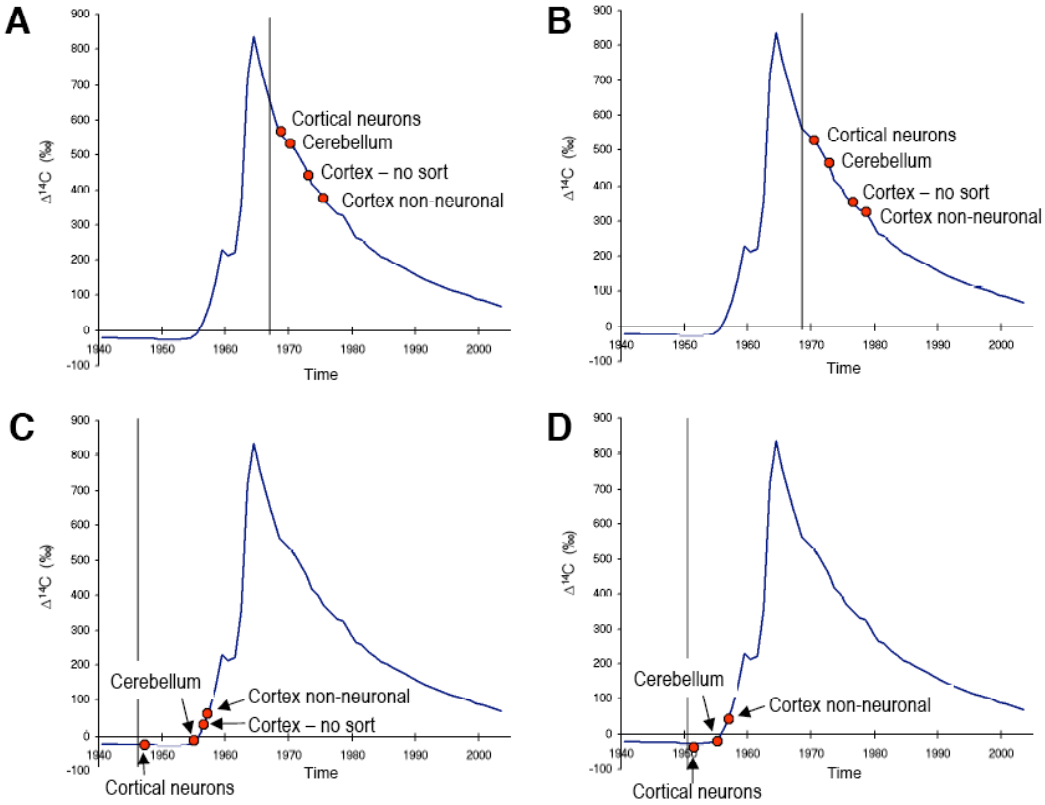
A
B
C
D
Δ14C (‰)
Time
Cortical neurons
Cerebellum
Cortex – no sort
Cortex non-neuronal

Figure 6