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Creation of an Open-Access, Mutation-Defined Fibroblast Resource for Neurological Disease Research

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Abstract

Our understanding of the molecular mechanisms of many neurological disorders has been greatly enhanced by the discovery of mutations in genes linked to familial forms of these diseases. These have facilitated the generation of cell and animal models that can be used to understand the underlying molecular pathology. Recently, there has been a surge of interest in the use of patient-derived cells, due to the development of induced pluripotent stem cells and their subsequent differentiation into neurons and glia. Access to patient cell lines carrying the relevant mutations is a limiting factor for many centres wishing to pursue this research. We have therefore generated an open-access collection of fibroblast lines from patients carrying mutations linked to neurological disease. These cell lines have been deposited in the National Institute for Neurological Disorders and Stroke (NINDS) Repository at the Coriell Institute for Medical Research and can be requested by any research group for use in in vitro disease modelling. There are currently 71 mutation-defined cell lines available for request from a wide range of neurological disorders and this collection will be continually expanded. This represents a significant resource that will advance the use of patient cells as disease models by the scientific community.
Introduction

Neurodegenerative diseases, including Alzheimer’s disease (AD), Parkinson’s disease (PD), frontotemporal dementia, amyotrophic lateral sclerosis (ALS), Huntington’s disease (HD), ataxias and dystonias are a major socioeconomic problem, and understanding the biological basis of neuronal death in these disorders is a major challenge for basic research. Many of the loci responsible for early-onset, familial forms of these disorders have been identified. Mutations in APP, PS1 and PS2 are associated with AD [1–4], SCA1, LRRK2, PRK2, PSEN1 and GBA [5–9] are associated with PD; SOD1, TARDBP and FUS mutations lead to familial ALS [10–12]; frontotemporal dementia and parkinsonism linked to chromosome-17 is associated with MAPT (FTDP-17T) and PGRN mutations (FTDP-17U/GRN) [13–15]; and CAG expansion of the HTT gene causes HD [16].

Using this genetic information as a basis for developing cell and animal models has greatly enhanced our understanding of the biological mechanisms underlying neuronal degeneration in these disorders. However, current cell models of neurological disease are limited by two major drawbacks: non-physiological protein expression levels and/or a non-neuronal cell type [17–19]. Patient-derived cells such as fibroblasts have been used as models in several studies looking at the basis of neurological disorders, including AD [20]. Recently, human somatic cells, such as fibroblasts, were reprogrammed to pluripotency by the exogenous expression of the transcription factors OCT4, SOX2, KLF4 and NANOG, LIN28 and MYC [20–22]. These induced pluripotent stem cells (iPSC) can be subsequently differentiated into neurons and glia, therefore by generating iPSC from patients carrying disease-linked mutations physiological expression of mutated genes in the cell type specifically affected in disease can be achieved. This technology has already been used to successfully model a range of neurological diseases including AD, PD, ALS and Ataxia [23–27].

Despite the fact that many of these diseases are adult onset, several groups have used iPSCs to model aspects of disease pathology. Perhaps the most notable of these is AD, where cells derived from patients with mutations in several genes have successfully recapitulated common pathology. Neurons generated from patients carrying point mutations in PSEN1, APP duplications and trisomy 21 (and thus an extra copy of the APP gene) each faithfully recapitulate features of AD pathology including increased Aβ production and elevated tau phosphorylation [26,28,29]. The presence of overlapping phenotypes in multiple patients with the same mutation, as well as mutations in different genes linked to the same disease, provides increased confidence that iPSC can be used to reveal disease phenotypes. Importantly, gamma secretase inhibitors prevented increased Aβ production in these cells, demonstrating the suitability of iPSC-neurons as a platform for drug screening [26,29].

Further, iPSC have provided evidence for the importance of correct cellular context in disease models. Spinocerebellar ataxia type 3 is caused by an expansion of a polyglutamine coding repeat in the ATXN3 gene. iPSC-neurons generated from SCA3 patients recapitulate the pathological hallmark of SCA3 patients: accumulation of detergent-insoluble aggregates of full length and cleaved Ataxin 3 [25]. This phenotype was specific to neurons, and furthermore was dependent on the presence of functional ion channels, demonstrating the ability of iPSC to uncover disease mechanisms by allowing the study of mutations in the context of functional human neurons.

The use of iPSC as disease models is reviewed comprehensively by Cherry et al [30]. There is now compelling evidence of the power of patient-derived iPSC to model disease pathology, offer insight into disease mechanisms and act as a platform for drug screening. However, it has also become apparent that there is extensive intra- and inter-patient variability [23, 25], and it is necessary to use both multiple iPSC lines per patient and multiple patients per gene in order to reliably assign disease phenotypes.

Although the sporadic forms of AD, PD and ALS are common, the familial forms caused by defined mutations are relatively rare, and for many research groups interested in these and other rarer neurological diseases, the limiting factor in the use of iPSC is access to patient fibroblasts with the disease-causing mutations of interest. For HD, where all affected individuals have the same type of mutation, an expanded CAG trinucleotide repeat, it is desirable to have access to subjects with a range of expansion size, which is the primary determinant of the rate of pathogenesis. Furthermore, recent reports have demonstrated the necessity of using multiple patient lines with mutations in the same gene, in order to ensure that observed cellular phenotypes are caused by the genetic lesion of interest and not patient variability [25,26]. With this in mind, our goal was to generate a resource of fibroblast cell lines with mutations that are linked to neurological disease. There are currently 67 mutation-defined fibroblast lines available to request from the Coriell repository, and more lines currently undergoing expansion and quality control. These include cell lines with multiple different mutations in each specific gene as well as cell lines from multiple patients carrying the same mutation. Further lines will be collected and deposited as patients are identified in...
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<td>R1346X</td>
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Disease, gene, mutation and mode of inheritance for fibroblast cell lines. The current status of each line (available, submitted but not yet in catalogue) is indicated. Where the status is left blank, this indicates fibroblast lines have been generated but are awaiting submission to the NINDS repository. All variants are heterozygous unless otherwise stated. References indicate where families have been described in the literature. D = autosomal dominant, R = autosomal recessive. 

[doi:10.1371/journal.pone.0043099.t001]
Fibroblast cultures were generated from 3–6 mm skin punch biopsies taken under local anaesthetic following informed consent. Biopsies were dissected into ~1 mm pieces and cultured in 5 cm² petri dishes in DMEM, 10% FBS, 1% L-Glutamine until fibroblasts were seen to grow out from the explants. When fibroblasts reached confluency, they were detached from culture dishes using Tryple® (Invitrogen) and transferred to larger culture vessels for further expansion. Cells are frozen at the lowest passage possible while still obtaining an adequate number of total cells for distribution (typically 2–4 passages or approximately 2×10⁶ total cells; cells are distributed at 5×10⁵ cells per ampoule). The passage number of the cells on distribution depends on demand for a particular cell line, however 40–60 ampoules of cells are generally derived per biopsy, whilst keeping the passage number between 2–4. Cells will be distributed at the lowest available passage, which is indicated for each sample listed in the Repository online catalogue.

Quality control of fibroblast cultures

Fibroblast cultures are tested for Mycoplasma contamination prior to frozen storage, and after recovery from liquid nitrogen prior to distribution. The gender of cell lines is verified by PCR with a Y chromosome-specific primer pair. Replicate cultures or matched cultures of differing cell types from the same individual are analyzed by PCR using microsatellite and Y chromosome-specific primer pairs to assure cell culture identity.

Immunocytochemistry

Fibroblasts were fixed in 4% paraformaldehyde for 30 min at room temperature then blocked and permeabilised in blocking buffer (10% FBS, 0.1% Triton X-100 in phosphate buffered saline) for 30 min at room temperature. Cells were incubated with rabbit polyclonal anti-FSP1 (1:100, Abcam) and mouse monoclonal anti-human fibroblasts clone TE-7 (1:100, Millipore) diluted in blocking buffer overnight at 4°C. Cells were then incubated with Alexa Fluor 488 and 568 antibodies (1:500) for 1 h at room temperature and nuclei were stained using DAPI. Images were acquired using a Zeiss LSM 710 confocal microscope.

Western blotting

Cells were washed in PBS and then lysed on ice for 30 minutes in lysis buffer (50 mM Tris-HCl, 150 mM NaCl, 1% v/v Tween-20, 0.2% NP40, 10%v/v Glycerol) containing Complete protease inhibitor cocktail (Roche). Lysates were centrifuged for 10 min at 11,000 g_{av}, 4°C and protein concentrations were estimated using the BioRad DC Protein Assay Kit. Equal amounts of protein were electrophoresed on NuPAGE 4–12% Bis-Tris Gels (Invitrogen) and transferred onto nitrocellulose membranes (Whatman). Membranes were probed with primary antibodies to FSP-1 (rabbit polyclonal, 1:500, Abcam) and β-actin (mouse monoclonal, 1:5000, Sigma Aldrich) overnight at 4°C. Membranes were then incubated with appropriate secondary antibodies (Alexa Fluor 680 anti-mouse IgG, Invitrogen and IRDye 800 anti-rabbit IgG, Rockland Immunochemicals, both 1:5000) for 1 h at RT before visualisation using an Odyssey Infrared imaging system (LI-COR Biosciences).

Population doubling levels

Population doubling level (PDL) is a measurement of the total number of times the cells within the population have doubled since their primary isolation. PDLs were calculated using the following equation:

\[
PDL = 3.32\log\left(\frac{\text{total viable cells at harvest}}{\text{total viable cells at seed}}\right)
\]

The total viable cells at seed was determined at the first seeding following proliferation of cells from the skin explant, or from the frozen ampoule for fibroblast cultures generated outside of Coriell. The total number of viable cells at harvest was determined immediately prior to cryopreservation.
Results

Collection of fibroblast cell lines

We have generated a collection of fibroblast cell lines from patients with mutations that are linked to neurodegenerative disorders, including AD, PD, ALS, FTD, HD, dystonias and ataxias. Also included in the collection are idiopathic sporadic Parkinson’s disease fibroblast lines and normal control fibroblast lines, including family members of mutation carriers. These have been deposited in the National Institute for Neurological Disorders and Stroke (NINDS) Repository at the Coriell Institute for Medical Research (Camden, NJ) and the lines carrying known mutations are detailed in Table 1. Access to these cell lines is open to the scientific community and they are available to all researchers for use in basic research. This collection will be continually expanded and will be a valuable resource for research into basic disease mechanisms of neurological disorders. An up to date list of lines available upon request from the NINDS Repository can be found at: http://ccr.coriell.org/sections/collections/NINDS/FibroSubcollList.aspx?SsId=10&PgId=681.

Fibroblast cell lines are deposited along with a clinical data elements (CDE) form that outlines the clinical background of the patient from whom the cells are derived. This protects the identity of the patient (see below) while providing the end-user with confidence in the clinical diagnosis. CDE’s for PD, ALS, and HD have been developed with input from researchers in the field. For AD and other dementia cell lines, there is currently no CDE; however, information (e.g., sex, year of birth, and MMSE score at the time of biopsy) is included.

![Fibroblast morphology and marker expression remain consistent during prolonged culture](image)

Figure 2. Fibroblast morphology and marker expression remain consistent during prolonged culture. Fibroblast lines were immunostained with antibodies FSP1 and TE7 at multiple consecutive passages (A). Passage numbers are indicated above the panels. Morphology, FSP1 and TE7 staining did not change during five consecutive subculturings (n = 6, representative images from line NM34737, carrying the PSEN1 M146I mutation are shown). FSP1 levels were also detected by western blotting of fibroblast cell lysates (B). FSP1 was detected as a single band at 12 kDa in all fibroblast lines examined (top panel, n = 6). β-actin was used as a loading control (bottom panel). No variation in FSP1 levels was observed between passages or between cell lines. doi:10.1371/journal.pone.0043099.g002

![Fibroblast morphology and marker expression remain consistent during prolonged culture](image)
Table S1. A full list of PDLs for individual cell lines in provided in Table S1.

Figure 3. Population doubling levels of fibroblast cell lines. Population doubling levels were calculated for each of the cell lines available in the NINDS repository at the time of cryopreservation. Individual points of the graph correspond to the PDL of individual fibroblast lines, the horizontal line represents the mean PDL for each disease category. PDLS ranged between 2–8 with a mean PDL of ~5 for both control and disease cell lines.

Discussion

The search for the genetic basis of disease has provided the impetus for the generation of animal and cell models that recapitulate key disease features and allow better understanding of the underlying biological mechanisms leading to cell death. A major challenge to understanding the basis of neurological disorders is our ability to model disease causing mutations at physiological levels, in a relevant cell type. The recent development of iPSCs, which can subsequently be differentiated into neurons and glial cells, is redefining the way we approach in vitro modelling of neurological disorders. We have developed a collection of primary fibroblast lines from patients carrying mutations that are associated with neurological disorders that can be accessed by all bona fide research groups.

Although others have developed collections of disease-specific iPSCs [32], we focussed on developing fibroblast cell lines. The cell lines in our collection express high levels of the fibroblast markers FSP1 and TE-7, and are cryopreserved at low population doubling levels for distribution. However, although fibroblasts are the most common cell type in cultures established from dermal outgrowths, these cultures actually represent a heterogeneous cell population including endothelial cells, pericytes and several types of stem/progenitor cells [62]. This cellular diversity could influence the ability of each individual fibroblast line to give rise to iPSC.

The molecular mechanisms underlying the reprogramming of fibroblasts to iPSC are poorly understood and there has been much debate as to whether the process is stochastic (all cells within a given population have the potential to be reprogrammed) or elite (only a subset of cells with particular properties can be reprogrammed). In a recent study, Wakeo and colleagues determined that iPSC were exclusively generated from a subpopulation of cells positive for both the stem cell marker SSEA3 and the mesenchymal marker CD105 [63]. These cells, termed muse cells (multilineage-differentiating stress enduring cells), express the pluripotency markers Oct3/4, Nanog and Sox2 and represent approximately 2% of cells present in fibroblast cultures.

This work provides support for the elite model of reprogramming and suggests the efficiency of reprogramming from each of the fibroblast cultures within this collection may depend on the proportion of Muse cells present, which was not examined in this study. However, even in a pure Muse cell population the efficiency of reprogramming remains low (0.03%), and it therefore seems likely that there is some stochastic influence on reprogramming. This notion is supported by multiple reports describing the addition of extra reprogramming factors and small molecules that...
increase the efficiency of reprogramming (reviewed in [64]). Thus, the elite vs stochastic debate remains open, but it is important for research groups requesting cells described in this manuscript to be aware of the implications of fibroblast culture diversity. By making fibroblast lines available, the end-users retain the flexibility to repurpose them by their method of choice.

This collection contains cell lines with mutations in a wide range of genes as well as multiple different mutations in each gene. In many cases, cell lines from several patients with the same mutation are available which will control for patient variability and allow robust phenotypes to be defined. The rarity of familial forms of neurodegenerative diseases means this represents a valuable resource which we anticipate will be widely used by the scientific community, advancing the use of patient cells for in vitro disease modelling.

Supporting Information

Table S1 Population doubling levels for fibroblast lines in the NINDS repository. NINDS reference number, disease, mutation and population doubling level for each cell line currently available from the NINDS repository.

(DOCX)

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