Efficient delivery of Dharmacon™ SMARTpool™ siRNA reagents in difficult-to-transfect cell lines using Lonza™ nucleofector 96-well shuttle system

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Introduction

Dharmacon siRNA-mediated gene knockdown is a powerful tool that has been used to identify gene function and elucidate biological pathways. Successful siRNA experiments involving knockdown of individual genes or collections of gene targets require efficient delivery of highly functional and specific siRNA molecules into appropriate cells.

While lipid-mediated transfection is a common approach for siRNA delivery, many cell types, including suspension cell lines and primary cells, are not compatible with this technology. These limitations prevent analysis of more biologically relevant cell types and confines studies to transformed, adherent cell lines that often exhibit phenotypic and genetic alterations after extended periods of culturing. In addition, several of the lipid delivery reagents can cause cytotoxicity and are capable of inducing a potent interferon response. These unintended phenotypes can significantly affect experimental outcomes and drastically interfere with the understanding of a gene’s function.

The combination of Dharmacon™ SMARTpool™ siRNA reagents with Lonza™ and Nucleofector™ technology overcomes the limitations associated with lipid reagent-mediated transfection. The technology is optimized for transfection of difficult-to-transfect cell types (in particular, primary and non-adherent cell lines) and can be linked to high-throughput applications using the Nucleofector™ 96-well Shuttle System (Lonza).

In this technical note, Dharmacon Molecular Biology Solutions and Lonza™ technologies (Box 1) were applied to Jurkat cells (clone E6-1, ATCC TIB-152) with the aim of performing future siRNA library screens. Jurkat cells are derived from a human acute T-cell leukemia line and are used extensively in the study of T-cell signaling and cancer drug development. As with any suspension cell line, Jurkat cells are difficult to transfect using reagent-mediated delivery (Figure 1).

Figure 1. Lipid-mediated transfection of Jurkat cells is ineffective. Jurkat cells were transfected with 100 nM GAPDH siRNA using various lipid-based reagents, Dharmacon™ DharmaFECT™ 1, 2 and 4 (DF1, DF2, and DF4) and Invitrogen™ Lipofectamine™ 2000 (LF2000). Cell viability was determined 24 hours post-transfection using the Promega® CellTiter-Blue® assay and normalized to untreated cells. GAPDH mRNA levels were analyzed 24 hours post-transfection by the Panomics™ QuantiGene™ branched-DNA assay and normalized to Dharmacon™ siGENOME™ Non-targeting siRNA #1.
**Box 1. Signature Dharmacon molecular biology solutions and Lonza™ technologies**

**Dharmacon—Innovators in RNAi technologies**
- Predesigned, guaranteed siGENOME siRNA products to target every human, mouse, and rat gene in RefSeq database
- Next-generation Dharmacon® ON-TARGETplus™ siRNA reagents reduce off-target effects by up to 90% for highly accurate results
- All siGENOME and ON-TARGETplus siRNA products available as individual siRNA or SMARTpool reagents for maximum experimental flexibility
- Dharmacon siRNA Libraries grouped by pathway or gene ontology for high quality, efficient RNAi screens
- Validated Dharmacon RNAi Control products to ensure experimental reproducibility and silencing specificity

**Lonza™—Leading transfection technology**
- Non-viral Nucleofector® technology for transfection of difficult-to-transfect cell types, such as suspension cell lines and primary cells
- Up to 99% transfection efficiency with siRNA duplexes, even in suspension cells
- Tested for high viability and maintenance of functionality
- Optimized protocols for hundreds of cell lines and primary cells (see lonza.com)
- Proven for siRNA applications with more than 100 publications
- Efficient co-transfection of different substrates such as plasmid DNA and siRNA duplexes, such as for rescue experiments
- Nucleofector® 96-well Shuttle System for high-throughput applications such as siRNA library screening

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**Critical parameters for successful siRNA experiments**
Prior to beginning siRNA experiments using nucleofection, multiple parameters associated with experimental design need to be optimized. In particular: 1). nucleofection conditions (for example, Nucleofector Solution and program), 2). appropriate controls, 3). the most efficacious siRNA concentration and 4). the time point of analysis need to be determined. In addition, identifying the best readout assay for your particular application (for example, mRNA, protein or phenotypic analysis) is critical. Each of these steps are outlined in Figure 2 and described in detail below.

**Optimized programs for siRNA delivery with the nucleofector 96-well shuttle**
Lonza® provides ready-to-use cell-type specific kits and protocols for a large number of primary cells and cell lines. These detailed protocols can be used in conjunction with either the standard Nucleofector® or the Nucleofector™ 96-well Shuttle System and are applicable for delivery of any kind of nucleic acid substrate (DNA vectors, ssRNA, siRNA reagents) without any need for further optimization. The constantly growing list of delivery conditions (currently available for over 500 cell types) is referenced in Lonza’s cell database (bio.lonza.com/6.html).

The 96-well nucleofection protocol for Jurkat clone E6-1 (ATCC® TIB-152®) recommends the 96-CL-120 program and Nucleofector® Solution XX for efficient delivery of siRNAs. We have demonstrated that co-transfection of the ON-TARGETplus SMARTpool siRNA reagent targeting maxGFP™ with pmaxGFP plasmid results in substantial knockdown of maxGFP™ protein (see Box 2). siRNA duplexes have been shown to be delivered at even greater efficiencies than plasmids. The 96-well Shuttle System for high-throughput applications such as siRNA library screening.

Similarly, co-transfection of a functional siRNA with a plasmid expressing a functional version of the target gene that is resistant to the siRNA can be performed with nucleofection to prove specificity of the RNAi phenotype (rescue experiments).
Identification of appropriate experimental controls

To ensure that the conclusions drawn from siRNA experiments are accurate, it is necessary to include the appropriate experimental controls. Our scientists recommend including at least four types of experimental controls in every RNAi experiment: positive and negative control samples, an untreated control sample, and a mock-treated control sample. These controls are described here and should be included in all parametric testing along with the siRNA targeting the gene(s) of interest. We offer a complete portfolio of both positive and negative control siRNAs. Parallel testing of multiple controls under several conditions can be easily performed using the 96-well Shuttle™ System.

Positive control: This should be a validated siRNA pool or individual siRNA targeting a well-characterized housekeeping gene, such as cyclophilin B (also known as PPIB), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), or Lamin. A good positive control reagent targeting a well-expressed but non-essential gene is useful for establishing experimental parameters without affecting cellular viability and can also be used as negative control that is unassociated with any particular pathway under study (for example, it fails to generate a observable phenotype in the assay being employed).

Negative control: Negative siRNA control reagents are bioinformatically designed to have no known target in the cell line of choice. These reagents are important for distinguishing sequence-specific silencing from sequence-independent effects that are associated with the delivery of siRNA into the cell. Such sequence independent effects can include toxicity resulting from transfection in conjunction with nucleic acid delivery or hyper-sensitivity to introduction of double stranded RNA. Investigators are encouraged to test multiple candidates in their own experimental systems to empirically confirm that the negative controls do not result in any observable and unintended off-target effects. Taking this into account, we offer a comprehensive portfolio of multiple negative controls, including the ON-TARGETplus Non-targeting Controls, which have been confirmed by microarray analysis to have little to no off-target signature in HeLa cells.

Box 2. Efficient co-transfection of plasmid and siRNA in Jurkat (clone E6-1, ATCC TIB-152) leads to significant down-regulation of maxGFP protein. Images were taken 24 hours post-nucleofection of either pmaxGFP plasmid alone or plasmid together with the ON-TARGETplus SMARTpool siRNA reagent targeting maxGFP. Cells were stained with the nuclear dye Hoechst.

Visual assessment of nucleofection efficiency with pmaxGFP

Co-transfection of plasmid in conjunction with siRNA allows for a straight forward analysis of siRNA-mediated gene knockdown. Transfection of pmaxGFP alone provides a visual indication of transfection efficiency. Co-transfection of pmaxGFP together with ON-TARGETplus SMARTpool siRNA reagent specifically targeting pmaxGFP provides a rapid and simple assessment of siRNA-mediated knockdown of maxGFP.

Identifying optimal effective siRNA reagent concentrations

When performing siRNA-mediated knockdown experiments it is advisable to conduct a dose-response (concentration) analysis to determine the minimum siRNA concentration necessary for sufficient target knockdown. For nucleofection in the 96-well Shuttle, the optimal siRNA concentration can range from 0.04 – 40 pmol (2 nM up to 2 μM), depending on multiple factors such as the cell type, and the half-life of the mRNA and/or protein of the gene target.

In the context of our optimization studies with Jurkat cells, Figure 3 shows that even the lowest siRNA concentration tested (0.5 pmol, 10 nM) reduces target gene (GAPDH) transcript levels by > 75% with only small effects on cellular viability. Nucleofection of greater amounts of siRNA confirms that maximal silencing is achieved at 5 pmol (250 nM) and that transfection at these or higher siRNA levels has no additional effects on cell viability.

Optimization of read-out assay(s)

Determining optimal analysis time points. As the stability and half-life of various mRNAs and their protein products varies, it is important to empirically determine the best time points for assessing target knockdown. For example, it has been documented that in mammalian cells, mRNA half-life can range from minutes to days while the t½ of protein products can range from less than a few minutes to several days. Taking this into consideration, the experimental design should allow sufficient time for the siRNA to associate with RISC and deplete mRNA/protein concentrations to desired levels.

In general, the recommended time course ranges are 12 to 72 hours (to deplete target mRNA) and 24 to 96 hours to adequately silence target proteins and assess phenotypic outcomes. For GAPDH mRNA levels (half-life, 8 hours) in Jurkats, 24 hours post-nucleofection was the optimal time point for measuring knockdown (data not shown).

Figure 3. Effect of SMARTpool™ siRNA reagent concentration on GAPDH mRNA levels and cell viability in Jurkat cells clone E6-1 (ATCC TIB-152). Cells were nucleofected with various amounts of GAPDH SMARTpool™ siRNA reagent using the 96-well Shuttle with program 96-CL -120. The negative control sample is the Pharmacia siGENOME Non-targeting siRNA Pool. Cell viability was determined 48 hours post-transfection using the Cell Titer-Blue™ assay (Promega) and normalized to untreated cells. GAPDH mRNA levels were analyzed 24 hours post-transfection by the QuantiGene™ branched-DNA assay (Panomics) and normalized to siGENOME Non-targeting siRNA #1.
Selecting appropriate phenotypic read-outs

A variety of detection assays may be used to assess cell viability, mRNA levels, and associated phenotypes during the optimization and implementation of a siRNA experiment. Establishing robust assays for RNAi is important for meaningful results. Moreover, multiparametric measurements through the use of several complementary phenotypic assays are particularly helpful in interpreting biological results and performing hit stratification.

We chose a well-defined and robust assay set for our experimentation using the Nucleofector® 96-well Shuttle System: the CellTiter-Blue Assay (Promega) to indicate cell viability and the Promega® Apo-ONE™ Assay to monitor apoptosis (caspase 3/7 activity). The QuantiGene branched DNA assay (Panomics) was utilized to quantify transcript levels and correlate target knockdown with biological phenotype. Owing to the high-throughput format, the Nucleofector® 96-well Shuttle System facilitates determination of optimal parameters for each of these assays by allowing systematic and parallel testing of several targets and controls under multiple conditions.

To optimize assay conditions, Jurkat cells were nucleofected with a SMARTpool siRNA reagent targeting Polo-like kinase 1 (PLK-1). PLK-1 is a key regulator of mitotic progression in mammalian cells and the knockdown of PLK-1 is known to induce apoptosis in cancer cells. As such, down-regulation of PLK-1 is expected to decrease cell viability and increase caspase 3/7 activity. Initial experiments identified 24 hours post-nucleofection as optimal for measuring PLK-1 mRNA levels and 48 hours for viability and apoptotic measurements (data not shown).

Conclusions

The combination of the highly functional siGENOME siRNA reagents and the Nucleofector® technology provides a unique and powerful method for delivering SMARTpool siRNA reagents and siRNA libraries into cells that have been considered intractable to lipid reagent-based transfection methods. The Nucleofector® 96-well Shuttle System now expands the technology to large-scale screens by expediting assay optimization and enabling high-throughput siRNA transfection in cell lines that previously have been inaccessible.

References


If you have any questions, contact

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