Engineered zinc finger nickases induce homology-directed repair with reduced mutagenic effects

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ABSTRACT

Engineered zinc finger nucleases (ZFNs) induce DNA double-strand breaks at specific recognition sequences and can promote efficient introduction of desired insertions, deletions or substitutions at or near the cut site via homology-directed repair (HDR) with a double- and/or single-stranded donor DNA template. However, mutagenic events caused by error-prone non-homologous end-joining (NHEJ)-mediated repair are introduced with equal or higher frequency at the nuclease cleavage site. Furthermore, unintended mutations can also result from NHEJ-mediated repair of off-target nuclease cleavage sites. Here, we describe a simple and general method for converting engineered ZFNs into zinc finger nickases (ZFNickases) by inactivating the catalytic activity of one monomer in a ZFN dimer. ZFNickases show robust strand-specific nicking activity in vitro. In addition, we demonstrate that ZFNickases can stimulate HDR at their nicking site in human cells, albeit at a lower frequency than by the ZFNs from which they were derived. Finally, we find that ZFNickases appear to induce greatly reduced levels of mutagenic NHEJ at their target nicking site. ZFNickases thus provide a promising means for inducing HDR-mediated gene modifications while reducing unwanted mutagenesis caused by error-prone NHEJ.

INTRODUCTION

Zinc finger nucleases (ZFNs) are chimeras of engineered zinc finger domains fused to the non-specific nuclease domain of the restriction enzyme FokI (1). Dimers of ZFNs generate site-specific DNA double-strand breaks (DSBs) with each ZFN monomer cutting one DNA strand (2). Obligate heterodimeric versions of the FokI nuclease domain have been engineered that minimize homodimeric interactions within a pair (3–6).

ZFNs, as well as engineered homing endonucleases and transcription activator-like effector nucleases (TALENs), can be used to improve the efficiency of homology-directed repair (HDR) in a variety of different organisms and cell types (7–9). Repair of a nuclease-induced DSB mediated by an exogenous ‘donor template’ can be exploited to introduce sequence alterations or insertions...
at or near the site of the break. Although nuclease-induced HDR is highly efficient, repair of a DSB can also occur by the non-homologous end-joining (NHEJ) pathway. NHEJ-mediated repair of nuclease-induced DSBs has been shown to be error-prone, leading to insertion or deletion mutations (indels) at the site of the break (10) or the formation of chromosomal translocations (11). NHEJ and HDR are believed to be competing pathways (12). Thus, although HDR-mediated alterations can be efficiently introduced using engineered nucleases, alleles can also acquire NHEJ-mediated mutations [e.g. (13,14)]. Unwanted alterations at other off-target genomic sites can also be introduced by NHEJ-mediated repair; e.g. two recent reports have shown that ZFNs introduce a greater spectrum of off-target DSBs (and therefore NHEJ-mediated mutations) than previously appreciated (15,16).

Given the potential undesirable consequences of introducing DSBs in living cells, we hypothesized that it might be possible to induce DNA repair with single strand breaks (SSBs or nicks) as a less mutagenic alternative to DSBs. Thousands of SSBs naturally occur per day in human cells, generally without deleterious consequences (17). The concept of harnessing the benign nature of nicks for stimulation of homologous recombination has been previously suggested in the context of theoretical models and recombination induced by RAG proteins (18–21). In addition, homing endonucleases have been demonstrated to stimulate HDR when converted to nickases (22–27). However, conferring novel DNA binding specificities to this class of enzymes without disrupting catalytic activity has proven to be challenging because the domains for DNA recognition and cleavage are not structurally independent (8) as they are for ZFNs and TALENs.

Here, we describe a general method for creating site-specific zinc finger nickases (ZFNickases). To do this, we employed obligate heterodimeric ZFNs (4) and introduced a mutation that had previously been described to inactivate FokI cleavage activity (D450A) (28) into the nuclease inactivating D450A mutation (numbered relative to the native FokI enzyme) (28) was introduced by QuikChange Lightning Site-Directed Mutagenesis (Agilent). The protein lysates were prepared following manufacturer’s instructions for the T7 TnT Quick Coupled Transcription/Translation System (Promega) using 1 μg plasmid template per 50 μl lysate and incubating for 90 min at 30°C.

To generate target sites for in vitro analysis, annealed oligonucleotides with compatible overhangs were cloned into the BsaI restriction sites of pMLM290 and pMLM292 vectors modified to contain 3xFLAG instead of the cytomegalovirus (CMV) promoter (pUC.0). All ZFN nickase alleles can be expressed using the lacZ ORF and also lacks a 5′-truncated EGFP (εGFP) gene in plasmid pLV.LacZεGFP (37). The donor plasmid used for these experiments harbors a 5′-truncated lacZ (εlacZ) gene followed by the corrected EGFP ORF and also lacks a promoter (pUC.0.LacZ-εGFP) (38).

To generate ZFNs and ZFNickases for mammalian expression, zinc finger domains were cloned as XbaI/BamHI fragments into pMLM290 and pMLM292 vectors modified to contain 3xFLAG instead of 1xFLAG epitopes. Previously reported zinc finger domains designed to bind the human CCR5 gene (32,33) were assembled from overlapping oligonucleotides generated by DNAWorks (34) and cloned into the 3xFLAG-pMLM290 and 3xFLAG-pMLM292 vectors. The nuclease inactivating D450A mutation (numbered relative to the native FokI enzyme) (28) was introduced by QuikChange Lightning Site-Directed Mutagenesis (Agilent). The protein lysates were prepared following manufacturer’s instructions for the T7 TnT Quick Coupled Transcription/Translation System (Promega) using 1 μg plasmid template per 50 μl lysate and incubating for 90 min at 30°C.

Chromosomal EGFP repair assay in U2OS cells
For the generation of the reporter cell lines used in the chromosomal enhanced green fluorescent protein (EGFP) repair assay, the cleavage site for the HX735 ZFNs (14) was cloned between the lacZ open reading frame (ORF) and the 5′-truncated EGFP (εGFP) gene in plasmid pLV.LacZεGFP (37). The donor plasmid used for these experiments harbors a 5′-truncated lacZ (εlacZ) gene followed by the corrected EGFP ORF and also lacks a promoter (pUC.0.LacZ-εGFP) (38).

To generate ZFNs and ZFNickases for mammalian expression, zinc finger domains were cloned into a previously described dual expression plasmid in which the cytomegalovirus (CMV) promoter drives expression of two ZFN monomers separated by a self-cleaving T2A
Peptide (6). The D450A mutation was introduced into one or both of the FokI subunits in this vector as needed by subcloning or using the QuikChange Lightning Site-Directed Mutagenesis kit (Agilent).

For the chromosomal EGFP repair assay, U2OS-based reporter cell lines containing the LacZ-HX735-GFP target locus were generated by lentiviral transduction (LV-CMV.LacZ-HX735-GFP) with a viral dose that rendered <1% of cells resistant to geneticin-sulfate (0.4 mg/ml), thus preferentially generating reporter cells with a single copy target locus (37). Reporter cells, cultured in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum (FBS) and 1% penicillin/streptomycin (Invitrogen), were seeded at a density of 50,000 cells/well in 24-well plates. After 24 h, the transfection was performed using X-tremeGENE HP DNA Transfection Reagent (Roche Applied Science) following the manufacturer’s instructions. Transfection cocktail included 150 ng of ZFN or ZFNickase expression plasmids, 600 ng of donor plasmid (pUC.3.LacZ-GFP) and 100 ng of a plasmid encoding for mCherry (39) to identify transfected cells. The extent of gene targeting was assessed after 8 days using flow cytometry (FACSCalibur; BD Biosciences) to determine the percentage of EGFP-positive cells in the fraction of mCherry-positive cells. Experiments were performed at least twice independently in duplicate.

Traffic Light Reporter assay in HEK293 cells

Traffic Light Reporter (TLR) experiments were performed as described by Certo et al. (22). Briefly, oligonucleotides each harboring one or two ZFN or ZFNickase target sites (oligonucleotides ams1228/ams1229 for the VF2468 and VF2471 sites and oligonucleotides ams1230/ams1231 for the CCR5 site) were cloned into the SbfI and SpeI restriction sites of the TLR2.1 (ZFNickase), we developed a qualitative version of an in vitro assay similar to one recently described by Sanders et al. (31) that allowed us to assess the introduction of breaks into either strand of a double-stranded DNA fragment. In this system, a target site for a ZFN is positioned asymmetrically within a DNA fragment that is fluorescently labeled on the 5’-ends of both DNA strands (Figure 1). This DNA is then incubated with different combinations of active and inactive Left/Right monomers that have been co-expressed in vitro using a coupled transcription/translation system (40)."
Testing ZFNickase activities using a human cell-based chromosomal EGFP reporter assay

Having established the activities of ZFNickases in vitro, we next wished to test whether these nickases, like their nuclease counterparts, could induce HDR at their target sites in human cells. To do this, we used a previously described, human cell-based reporter gene assay for monitoring HDR (37). In this assay, a 5'-truncated EGFP reporter gene bearing a ZFN target site of interest is chromosomally integrated using a viral-based vector (Figure 3a). HDR with an appropriate donor construct leads to restoration of an intact EGFP reporter gene. Thus, the percentages of EGFP-positive cells arising after the co-delivery of ZFNs or ZFNickases and the donor plasmid reflect the abilities of ZFNs to stimulate HDR at the target locus.

We tested ZFNs and corresponding ZFNickases targeted to the HX735 site for their abilities to induce HDR in the EGFP reporter assay. ZFNs targeted to the HX735 locus were able to stimulate gene repair, inducing EGFP expression in 0.29% of transfected cells, a statistically significant increase relative to the 0.01% of cells that expressed EGFP upon transfection with a catalytically inactive ZFN (Figure 3b). Interestingly, expression of corresponding HX735 ZFNickases designed to nick one strand or the other restored EGFP expression in 0.14 and 0.05% of cells, although only the former increase in HDR was statistically significant relative to the level observed with the catalytically inactive ZFN. Thus, these results suggest that a ZFNickase can induce HDR in this EGFP reporter gene assay, albeit at a lower level than that observed with its parental ZFN.

Assessment of HDR and NHEJ induced by ZFNs and ZFNickases in human cells

To further test the ability of ZFNickases to induce HDR and to simultaneously assess the rate of NHEJ-mediated mutagenesis at the same target site, we used the recently described ‘TLR’ (22). In this assay, the reporter harbors a nuclease target site (or sites) of interest positioned within
a defective EGFP coding sequence that is followed by an mCherry coding sequence joined out of frame to the EGFP gene via a T2A peptide sequence. HDR with an exogenously provided donor template reconstitutes a functional EGFP coding sequence, turning cells green, whereas NHEJ-induced indels can create frameshifts that place the downstream mCherry protein in-frame, turning cells red (Figure 4a). Thus, with these reporter cells, the extent of nuclease-induced HDR and NHEJ can be monitored simultaneously for a given target site using flow cytometry.

We derived polyclonal HEK293T cell lines harboring the TLR with targets for either the VF2468 and VF2471 ZFNs [a single cell line with both overlapping targets present, just as they occur in the endogenous locus (14)] or the CCR5 ZFNs. For each ZFN pair, we transfected combinations of plasmids encoding active and/or inactive ZFN monomers together with a donor template for correcting the EGFP gene. Flow cytometry was then used to determine HDR and NHEJ rates by quantifying the percentages of EGFP-positive and mCherry-positive cells, respectively (Figure 4b–e). For all three target sites, ZFNs tested showed robust activities, inducing high percentages of EGFP-positive cells (indicative of HDR events) and even higher percentages of mCherry-positive cells (indicative of NHEJ events) in transfected cells (Figure 4b, left column). All but one of the six ZFN Nickases tested for the three target sites induced significantly higher levels of EGFP-positive cells compared with negative controls (Figure 4b, c, d and e). The percentage of EGFP-positive cells for the VF2468 and CCR5 ZFN Nickases are 3- to 10-fold lower than what was observed with their corresponding ZFNs (Figure 4c and e, compare second and third white-colored columns with the first white-colored column), suggesting that HDR is induced by ZFN Nickases but again at a lower rate than is observed with the parental ZFNs. The activities of the VF2471 ZFN Nickases were detectable but quite low despite the high activity of the VF2471 ZFNs (Figure 4d). However, for all three target sites, the ZFN Nickases consistently induce lower percentages of mCherry-positive cells relative to their matched ZFNs, suggesting that fewer mutagenic NHEJ-mediated events are occurring with the nickases compared with the nucleases (Figure 4c, d and e). In addition, the ratio of the percentage of EGFP-positive cells to the percentage of mCherry-positive cells is higher for five of the six ZFN Nickases compared with the parental ZFN (Figure 4f, g and h). We also found, in accordance with previous studies conducted with homing endonucleases and nickases, that increased donor template concentrations were associated with increased nuclease- and nickase-induced HDR frequencies (Supplementary Figure S1 and data not shown) (22,23,27). Interestingly,
**DISCUSSION**

In this report, we describe a general and simple method for converting ZFNs into ZFNickases. Introduction of a previously described D450A mutation into one monomer of a ZFN pair can generate a ZFNickase. This result parallels recent work from Halford and colleagues in which they used a similar approach to convert the wild-type FokI restriction enzyme into a nickase. Our qualitative *in vitro* data demonstrate that each ZFNickase preferentially cuts one DNA strand at a position either identical or within 1 nt of the cut positions of its matched ZFN. Furthermore, the data show that each ZFN monomer cuts the DNA strand to which it makes most of its DNA base contacts, providing direct experimental support for the model of binding and cleavage illustrated in Figure 1. Testing in two different human cell-based reporter systems revealed that ZFNickases can induce HDR-mediated repair, albeit at lower levels than matched ZFNs from which they were derived. Of the eight ZFNickases we tested (two pairs each derived from ZFNs targeted to four different target sites; data presented in Figures 3 and 4), six induced statistically significant levels of HDR. The levels of HDR we observed with the ZFNickases ranged widely, from between 2-fold and >100-fold lower than those observed with the corresponding ZFNs from which they were derived. However, for at least some of the ZFNickases we tested (e.g. HX735 \(-+/+\), VF2468 \(-+/+\) and \(+/+\) and CCR5 \(+/+\) and \(+/+\)), the levels of HDR induced were of sufficiently high frequency (≥0.1%) to be useful for research applications and some potential therapeutic strategies. Our observations that ZFNickases can induce HDR events and that HDR efficiency is positively correlated with the concentration of donor present in cells are consistent with the findings of others using homing endonucleases engineered to induce nicks (22–27). However, to our knowledge, our findings are the first to report that nickases derived from ZFNs can be used to induce HDR events.

Although absolute rates of HDR were lower for ZFNickases than ZFNs in our human cell-based reporter assays, we also observed a consistent reduction in mutagenic NHEJ rates in the TLR assay. This reduction is not entirely surprising given that nicks are typically repaired without causing mutations (17). However, we do not know the origin of the residual NHEJ-mediated events we observed with some of the ZFNickases we tested. Possible explanations include conversion of a nick into a DSB that may occur with replication fork collapse (see below) or weak residual homodimerization of the active ZFNickase monomer that may lead to cleavage at the intended target site. Use of improved second-generation FokI heterodimer variants (3) may reduce activity due to the latter mechanism [we used first-generation FokI heterodimer variants (4) for this study].

Importantly, for five of the six ZFNickases we tested in the TLR assay, the ratio of HDR to NHEJ events was increased compared with the three matched ZFNs from which they were derived. These results demonstrate that ZFNickases can induce HDR events with relatively lower rates of NHEJ-mediated mutations created at the nick site. We do not currently know the mechanism of the ZFNickase-mediated HDR or the improved HDR:NHEJ ratios we observe. One possibility for the improved HDR:NHEJ ratios is that a nick in the path of a DNA replication fork may be converted to a DSB leading to fork collapse, the repair of which would be expected to lead to repair by either NHEJ or HDR. A potential hypothesis for why we observe a preferential shift from NHEJ to HDR with ZFNickases may be the more frequent repair of nick-induced replication fork collapse.
Figure 4. Assessment of ZFNickase-mediated HDR and NHEJ using a human cell-based TLR assay. (a) Schematic of the ‘TLR’ HDR-mediated correction of the EGFP gene with a co-transfected donor template results in EGFP-positive cells. Mutagenic NHEJ events at the nuclease target site result in mCherry-positive cells. (b) Representative flow cytometry plots showing percentages of EGFP-positive and mCherry-positive cells following transfection of TLR cell lines with plasmid encoding the indicated ZFNs and ZFNickases and the donor template. In the experiments shown, cells have been gated for BFP expression (encoded by the plasmid harboring the donor template) to normalize for transfection efficiencies. (c–e) Bar graphs showing mean percentages of EGFP-positive and mCherry-positive cells for experiments performed with the VF2468, VF2471 and CCR5 ZFNs and ZFNickases. Results were derived from three independent experiments with SEM shown. Statistically significant differences in HDR and mutagenic NHEJ rates relative to donor-only control (−/−) are indicated by * (P<0.05) or ** (P<0.01). (f–h) Ratios of percentage of EGFP-positive cells to percentage of mCherry-positive cells for the VF2468, VF2471 and CCR5 ZFNs and ZFNickases using the data from (c–e). Data used to create Figure 4c–h is available in Supplementary Table S3.
by HDR (41), in part due to the availability of repair factors for homologous recombination during DNA replication in S-phase (42). Interestingly, for every target site we tested in our human cell-based assays, one ZFNNickase combination consistently outperformed the other with respect to absolute HDR rates and, for those assayed using the TLR assay, improved HDR:NHEJ ratios. This reproducible difference does not appear to be correlated with whether the nicked strand is transcribed or not, and there were no strand cleavage preferences discernible from the in vitro data. It is possible that strand-dependent differences in HDR activity arise due to different DNA-binding affinities of zinc finger domains in each monomer and how this may affect asymmetric accessibility to the break by cellular repair machinery. Regardless of the precise mechanism, our results suggest that testing both potential ZFNNickases for a given target site is worthwhile to identify the most active nickase possible.

Our work demonstrates that ZFNNickases with predictable strand nicking activities can be easily derived from ZFNs and that these enzymes can be used in cells to induce HDR with improved HDR:NHEJ ratios. It will be of interest in future experiments to test whether ZFNNickase-induced HDR rates can be further increased by using improved FokI heterodimer frameworks and hyperactive FokI variants (3,43). Our observation of reduced mutagenic NHEJ events at the target nicking site suggest that ZFNNickases will also likely induce fewer mutations at potential off-target sites elsewhere in the genome, a prediction that can easily be tested for ZFNs with known off-target sites (15,16). In addition, site-specific nickases may generally be of interest for the study of biological phenomena such as replication fork dynamics. Our results suggest ZFNNickases may provide a means to induce HDR with reduced mutagenesis caused by NHEJ and that additional optimization of this platform should be an important goal for future investigation.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online: Supplementary Tables 1–3 and Supplementary Figure 1.

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