

Expanding CRISPR Genome Editing Strategies in Hematopoietic Stem and **Progenitor Cells for the Treatment of Hematologic Diseases**

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CRISPR/Cas9 Homology Directed Repair Proof of Concept CRISPR/Cpf1 Directed Editing Proof of Concept Introduction FIGURE 1. ddPCR assay for targeted integration measurement Current ex vivo genomic modifications use Study Goal: Evaluate Acidaminococcus BV3L6 (As)Cpf1 at multiple target sites Experimental Method: Thaw and culture CD34⁺ cells → Electroporate with RNP → On-target sequencing lentivirus-mediated gene transfer and Representative Donor Homology Arm (HA) GEP Ca nuclease-directed non-homologous end joining Genome & Cut Site FIGURE 3. Engineered Cpf1 variants FIGURE 4. Cpf1 edits certain target (NHEJ). To expand the types of genomic Targeted Integration expand PAM targeting space sites more efficiently than Cas9 modifications possible, we tested the potential 100 AsCpf1 for homology directed repair (HDR) mediated Variant PAM Expected genor SpCas9 targeted integration and Cfp1-directed edits in FIGURE 2. SpCas9 RNP and AAV6 donor with HBB homology arms cause Editing 20. SpCas9 NGG targeted integration through HDR 1 per 16 human mobilized peripheral blood (mPB) SaCas9 NNGRRT 1 per 64 CD34⁺ cells. Targeted integration may be A ₅₀₋ В SaCas9 KKH NNNRRT 1 per 16 50useful for diseases such as Sickle Cell Disease AsCpf1 WT TTTV 1 per 85 % and B-Thalassemia, and other targets where 25 TYCV/CCCC AsCof1 RR 1 per 42 normal transcriptional regulation is important. 25[.] 25[.] тано 19 25-AsCpf1 RVR TATV 1 per 85 FnCpf1 TTN 1 per 16 Cpf1-directed editing expands the number of 5 11 18 Matched Target Site ID genomic sites accessible for gene therapy % SpCas9 Cpf1 FIGURE 5. PAM variants can FIGURE 6. NLS variants can increase editing at HPFH target site increase editing at target site RNP + + + RNP + + + ---100 ش م AAV6 - NoHA HA - NoHA HA - NoHA HA AAV6 - NoHA HA , Editing atched Site { % Editing (at HPFH site) 52 С D Е 75 % Editir Matched \$ 100 HDR 100-50 D NHEJ % HDR GFP+ colonies) Modification **HDR Experimental Method** 75-Viability 75te 25 Study Goal: Establish baseline HDR at HBB 50-50-50 HisAscothusMS HisAscottunS Hentshishes of Hentsheeptins locus in viable mPB CD34+ cells RURIL HISHISASCHT WT. DR.3 RR.A HisAsCort % 25 25 25 in Experimental Method % AsCpf1 variant-gRNA ID Step Thaw and culture CD34⁺ cells RNP + + + RNP + + + + NoHA HA AAV6 . - NoHA HA AAV6 - NoHA HA - NoHA HA -S. Pyogenes (Sp) Cas9 RNP electroporation + AAV6 transduction A. On-target integration (% HDR) at HBB locus in CD34⁺ cells electroporated with Cas9 RNP ± AAV6 (± homology Conclusions 2 Viability (AO/PI), GFP (flow cytometry) arms or no homology arms, HA or NoHA). Mean ± S.D. of the percentages of on-target integration detected at 5' vector-genome junctions. B. Integrated GFP expression in live CD34⁺ cells 7 days after electroporation, C. On-target - Efficient and reproducible HDR in CD34⁺ cells by Cas9 with minimal impact on cell viability (~80% viability) - Viability and integrated GFP expression On-target integration (ddPCR) integration (% HDR) or indels (% NHEJ) by sequencing. D. Viability in CD34+ cells 48 hours after electroporation. - 30% biallelic and 70% monoallelic targeted integration in Cas9 HDR-modified clones On-target editing (sequencing) E. Percentage of monoallelic (mono) and biallelic (bi) on-target integration (% HDR) by ddPCR analysis of GFP+ - First report of efficient Cpf1 directed editing in CD34+ cells 14 - On-target integration in GFP⁺ GEMMs clones (CFU-GEMMs). For A-D, Mean values ± S.D. from 4 experiments with different CD34+ cell donors are shown. - AsCpf1 edits certain sites more efficiently than SpCas9 in CD34⁺ cells

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