Beam Therapeutics Presents Updated Data from Novel Base Editing Programs for Sickle Cell Disease at ASH 2020

December 5, 2020

BEAM-101 Data Highlight Precision of Base Editor with No Off-Target Editing Observed; Will Support Planned IND Submission in the Second Half of 2021

In Vivo Data from Makassar Base Editing Program Demonstrate Long-term Engraftment and Editing Retention at 16 Weeks

CAMBRIDGE, Mass., Dec. 05, 2020 (GLOBE NEWSWIRE) -- Beam Therapeutics Inc. (Nasdaq: BEAM), a biotechnology company developing precision genetic medicines through base editing, today announced that updated data from the company's complementary base editing approaches to treat hemoglobinopathies are being presented during poster sessions at the 62nd American Society of Hematology Annual Meeting and Exposition (ASH 2020). The meeting is being held virtually December 5-8, 2020.

"Base editing is ideally suited to precisely edit the genetic mutations that cause disease without disrupting any other part of the genome," said Giuseppe Ciaramella, Ph.D., president and chief scientific officer of Beam. "The new data for BEAM-101 highlight the precise targeting of our base editor with no off-target editing observed and will support our planned Investigational New Drug application submission in the second half of 2021. In addition, the *in vivo* proof of concept data presented from an early version of our Makassar base editor demonstrate robust engraftment after 16 weeks. Our final editor from this program, BEAM-102, has achieved even higher levels of editing of the sickle mutation. In aggregate, today's data support the opportunity for our base editors to offer potentially disease-modifying treatments for people with sickle cell disease, which affects nearly 100,000 Americans and millions worldwide."

Title: *Adenine Base Editing of Gamma Globin Gene Promoters Shows No Detectable Off-Target RNA or DNA Editing*
Session: 801. Gene Editing, Therapy and Transfer: Poster I
Date: Saturday, December 5, 2020
Publication Number: 1545
Data Summary:

- BEAM-101 reproduces single base changes seen in individuals with hereditary persistence of fetal hemoglobin, or HPFH. Individuals with sickle cell disease (SCD) or beta-thalassemia, who also have HPFH, typically experience a milder form of the disease or may be asymptomatic.
- Using adenine base editors (ABEs), BEAM-101 recreates HPFH by installing base edits in the gamma globin gene promoters, HBG1 and HBG2, that disrupt repressor binding and lead to increased expression of gamma globin. Two theoretical types of off-target events that are possible as a consequence of these edits are guide-dependent and guide-independent deamination.
- To determine the potential for guide-dependent off-target editing, Beam evaluated BEAM-101 in a homology-dependent biochemical assay. In the findings presented today, no guide-dependent off-target effects were observed in CD34+ hematopoietic stem and progenitor cells (HSPCs) edited at a supra-saturating dose of BEAM-101.
- Beam assessed guide-independent off-target effects using single-clone whole genome sequencing (scWGS), which revealed that no significant fold change of guide-independent A-to-G DNA mutations occurred in edited cells compared to unedited controls.
- Further, whole transcriptome sequencing and somatic variant calling showed no guide-independent RNA deamination in CD34+ HSPCs edited at a supra-saturating dose of BEAM-101.
- Together, the findings support precision editing with BEAM-101 with a very low risk for potential off-target toxicities.

Title: *Adenine Base Editing of the Sickle Allele in CD34+ Hematopoietic Stem and Progenitor Cells Eliminates Hemoglobin S*
Session: 801. Gene Editing, Therapy and Transfer: Poster I
Date: Saturday, December 5, 2020
Publication Number: 1543
Data Summary:

- Beam's Makassar base editing program aims to treat SCD by directly editing the causative HbS point mutation to recreate a naturally occurring normal human hemoglobin variant, HbG-Makassar. The Makassar variant has been reported to have the same function as the wild-type variant and does not cause SCD.
- In today's presentation, Beam showed new long-term *in vivo* data generated using an early version of the Makassar base editor, which yielded approximately 50% conversion of the sickle allele to a Makassar allele.
- At 16 weeks post-transplant of CD34+ cells containing the sickle trait, Beam observed equivalent human chimerism between unedited and edited cells and evidence of multi-lineage reconstitution in mouse models.

- Levels of editing were sustained after long-term hematopoietic engraftment. Further, editing of the sickle allele led to the expression of the Makassar globin protein *in vivo*.
- Additional data presented by Beam showed that the final optimized editor used in BEAM-102 has achieved greater than 90% bi- and mono-allelic Makassar editing in SCD CD34+ HSPCs *in vitro*. Beam expects that these improvements will lead to even greater editing levels and higher Makassar globin conversion in future *in vivo* studies.

About Beam Therapeutics
Beam Therapeutics (Nasdaq: BEAM) is a biotechnology company developing precision genetic medicines through the use of base editing. Beam's proprietary base editors create precise, predictable and efficient single base changes, at targeted genomic sequences, without making double-stranded breaks in the DNA. This enables a wide range of potential therapeutic editing strategies that Beam is using to advance a diversified portfolio of base editing programs. Beam is a values-driven organization committed to its people, cutting-edge science, and a vision of providing life-long cures to patients suffering from serious diseases. For more information, visit www.beamtx.com.

Forward-Looking Statements
This press release contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995. Investors are cautioned not to place undue reliance on these forward-looking statements, including, but not limited to, statements related to: our plans for scientific publications; our expected timing for filing an investigational new drug application; and the therapeutic applications and potential of our technology, including our ability to develop precision genetic medicines for patients through base editing. Each forward-looking statement is subject to risks and uncertainties that could cause actual results to differ materially from those expressed or implied in such statement, including, without limitation, risks and uncertainties related to: our ability to develop, obtain regulatory approval for, and potentially commercialize our product candidates, which may take longer or cost more than planned; our ability to raise additional funding, which may not be available; our ability to obtain, maintain and enforce patent and other intellectual property protection for our product candidates; the potential impact of the COVID-19 pandemic; that preclinical testing of our product candidates and preliminary or interim data from preclinical and clinical trials may not be predictive of the results or success of ongoing or later clinical trials; that enrollment of our clinical trials may take longer than expected; that our product candidates may experience manufacturing or supply interruptions or failures; risks related to competitive products; and the other risks and uncertainties identified under the heading "Risk Factors" in our Annual Report on Form 10-K for the year ended December 31, 2019, our Quarterly Report on Form 10-Q for the quarters ended March 31, 2020, June 30, 2020, and September 30, 2020, and in any subsequent filings with the Securities and Exchange Commission. These forward-looking statements (except as otherwise noted) speak only as of the date of this press release. Factors or events that could cause our actual results to differ may emerge from time to time, and it is not possible for us to predict all of them. We undertake no obligation to update any forward-looking statement, whether as a result of new information, future developments or otherwise, except as may be required by applicable law.

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