

this **redundancy**

Introduction

Sialoglycans have emerged as a critical glyco-immune checkpoint that impairs antitumor response by inhibiting innate and adaptive immunity. We have reported previously that Bi-Sialidase – an engineered human sialidase-Fc fusion – potentiates antitumor immune response by cleaving terminal sialic acids from sialoglycans (desialylating) on tumor cells and immune cells. Furthermore, we have shown that a bifunctional tumor-targeted sialidase, a heterodimeric molecule consisting of one chain of sialidase-Fc and a second chain of a HER2-targeting antibody (trastuzumab), leads to more efficient desialylation of tumor cells than the non-targeted Bi-Sialidase and demonstrates antitumor activity in trastuzumab-resistant and low HER2-expressing tumor models.

To evaluate the impact of targeted desialylation of both tumor cells and immune cells, we designed and characterized a bifunctional PD-L1-targeted sialidase in preclinical models, since PD-L1 is expressed on many types of tumor cells and immune cells. Furthermore, the bifunctional PD-L1targeted sialidase simultaneously inhibits two orthogonal immune checkpoint pathways, immunosuppressive sialoglycans and the PD-1/PD-L1 axis. We generated a humanized anti-human PD-L1 antibody with potency of PD-1/PD-L1 blockade comparable to the existing anti-PD-L1 drugs, atezolizumab and avelumab. Subsequently, we constructed and screened multiple bifunctional PD-L1-targeted sialidases in various configurations and selected a heterodimeric molecule (E-705) as the lead, based on developability and potency.

The PD-L1-Targeted Sialidase (E-705) consists of one chain of sialidase-Fc from the third generation of engineered human sialidase (Neu2) and a second chain of the in-house generated anti-PD-L1 antibody. We further characterized E-705 using various biochemical assays in vitro and tested its antitumor activity in vivo using the transgenic CT26-human PD-L1 mouse tumor model expressing human PD-1 and PD-L1 in replace of the murine counterparts.

Degradation of Immunosuppressive Sialoglycans Using Human Sialidase-Based EAGLE Technology to Treat Cancer



 Impact: Robust anti-tumor response from both innate and adaptive immune cells

Figure 1. Schematic representation of the sialoglycan immune checkpoint axis and the EAGLE therapeutic platform. At the immunological synapse, a dense array of various sialoglycans interact with multiple sialic-acid sensing immune receptors, including Siglecs¹⁻³ (sialic acid-binding Ig-like lectins) and CD28⁴ on immune cells, dampening innate and adaptive immune responses. The interactions between sialoglycans and sialic-acid-sensing receptors are "Velcro"-like with overlapping/promiscuous binding preferences and tremendous redundancy, which poses a challenge for therapeutic intervention of this axis because targeting a single receptor or ligand cannot overcome the redundancy of this biology. The engineered human sialidase-based EAGLE therapeutic platform overcomes this hurdle by removing terminal sialic acids, the common motif of various sialoglycans, to release sialoglycan-mediated immunosuppression.

Impact: Restored Anti-Tumor Immunity

Development of a Bifunctional PD-L1-Targeted Sialidase as a Novel Cancer Immunotherapeutic Approach

Jenny Che, Lihui Xu, Wayne Gatlin, Robert LeBlanc, Lizhi Cao, James Broderick, Li Peng Palleon Pharmaceuticals, Waltham, MA, USA





Figure 2. Schematic representation of the primary MoAs of EAGLE, including 1) desialylation of tumor cells to release tumor-associated sialoglycanmediated immunosuppression of innate and adaptive antitumor immunity, 2) desialylation of T cells to enhance sialoglycan-mediated suppression of T cell function. E-602 is a homodimer of the engineered human sialidase Neu2 (v2.0) genetically fused to a human IgG1 Fc region by an IgG1 hinge. Targeted-Sialidases are bifunctional molecules consisting of the sialidase molety and a tumor-associated antigen (TAA) or an immune cell-targeted (such as PD-1) arm.

Results

Selection of the Bifunctional PD-L1-Targeted Sialidase (E-705) (Lead Identification and Lead Optimization)



E-705 Demonstrated Dual Functions of Cleaving Sialic Acids and Inhibiting PD-1/PD-L1 Interaction



Figure 4. Biochemical and functional characterization of PD-L1-targeted sialidase (E-705). E-705 yielded 20mg/L with 96% purity from a 5-day transient 293F cell expression and a two-step purification of protein A and CHT chromatography. E-705 showed comparable desialylation potency to its parental sialidase-Fc (E-601) toward a fluorescently labeled sialic acid substrate (4-MU-Neu5Ac), confirming that pairing with the anti-PD-L1 arm didn't impact sialidase activity. In addition, E-705 demonstrated binding to PD-L1 and EC50s of inhibiting PD-1/PD-L1 interaction comparable to its parental anti-PD-L1 mAb (h769T-1A) or atezolizumab

Figure 3. The lead identification flowchart of anti-PD-L1 mAb (left) and schematic representation of various PD-L1-targeted sialidase configurations. The lead (E-705) was selected based on expression yield, stability, sialidase activity, and PD-1/PD-L1 inhibition potency.



E-705 Demonstrated Improved Antitumor Activity than PD-L1 Blockade or Sialidase in Transgenic Syngeneic CT26-hPD-L1 Mouse Tumor Model

MC38-hPD-L1 Transgenic Syngeneic Mouse Tumor Model Expressing Human PD-1 and PD-L1



CT26-hPD-L1 Transgenic Syngeneic Mouse Tumor Model Expressing Human PD-1 and PD-L1 Tumor Volume (Mean) Tumor Volume at Day 16



Pharmacodynamics Study of E-705-Mediated Immune Modulation in Tumor Microenvironment



Conclusions

001-1G E-610-1A h769.T-1A E-705

- Degradation of sialoglycans using human sialidase-based EAGLE platform technology can effectively release sialoglycan-mediated immunosuppression of antitumor immune response.
- The PD-L1-Targeted Sialidase (E-705) enabled more efficient desialylation of PD-L1-expressing immune cells and tumor cells and showed improved antitumor activity compared to its parental sialidase or anti-PD-L1 mAb in the CT26-hPD-L1 transgenic syngeneic mouse tumor model.
- The PD-L1-Targeted Sialidase (E-705) offers a novel immunotherapeutic approach of inhibiting two orthogonal checkpoint pathways by cleaving immunosuppressive sialic acids and blocking the PD-1/PD-L1 axis.

References:

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Figure 5. E-705 showed more efficient desialylation of activated DCs with abundant PD-L1 expression than resting DCs with low expression of PD-L1. Monocyte-derived dendritic cells (mDCs) were differentiated from peripheral CD14+ monocytes treated with GM-CSF and IL-4. Activated mDCs were simulated by TLR2/1 agonist Pam3CSK4, a synthetic triacylated lipopeptide. Resting and activated mDCs were treated with E-705, isotype, or silent-sialidase control (E-704), respectively. Activated mDCs showed more than 10-fold higher expression of PD-L1 than that of the resting mDCs. As expected, E-705 demonstrated higher potency (~900-fold) in desialylating activated mDCs (EC50 = 0.02 μ g/ml) than resting mDCs (EC50 = 17.81 μ g/ml).

Figure 6. Efficacy study in MC38-hPD-L1 transgenic syngeneic mouse tumor model expressing human PD-1 replacement of mouse counterparts. (h769.T-1A) showed anti-PD-L1 mAb comparable efficacy to atezolizumab. Furthermore, sialidase (E-610) also demonstrated antitumor activity in this PD-1/PD-L1 biology-focused transgenic mouse tumor model. However, the combination of h769.T-1A and E-610 did not show improved activity versus the single agent, suggesting the MC38 model is not suitable for studying the additive effect of combining desialylation and inhibition of PD1/PD-L1 axis.

Figure 7. Efficacy study in CT26-hPD-L1 transgenic syngeneic mouse tumor model expressing human PD-1 and PD-L1 in replacement of mouse counterparts. E-705 showed improved antitumor activity compared to its parental sialidase (E-610) or anti-PD-L1 mAb (h769.T-1A) alone in the CT26-hPD-L1 transgenic syngeneic mouse tumor model.

Figure 8. FACS analysis of E-705-mediated immune modulation in the tumor microenvironment. Tumors were harvested within 24 hours post the 6th dose of treatment and subjected to immunophenotyping using flow cytometry. A significant decrease of macrophages in the tumor microenvironment was observed from either desialylation (E-610) or PD-L1 blockade. In addition, E-705 and the combination E-610 and h769.T-1A led to slightly more reduced tumor-infiltrating macrophages compared to the corresponding singleagent treatments.