



Selection of an optimal anti-PD-L1 single domain antibody format for the vectorization into oncolytic vaccinia virus and the generation of bispecific immunomodulators.

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BACKGROUND

Single domain antibodies (sdAbs) isolated after immunization of camelids are particularly attractive formats for their high modularity and small size allowing a better diffusion into tumors. However, the short in vivo half-life of sdAbs, related to the lack of a Fc domain, limits their clinical application. By replicating specifically into tumor cells, the **oncolytic vaccinia virus** (VACV) is an optimal vector to deliver and maintain high intra-tumoral concentrations of therapeutic sdAb. Moreover, sdAb targeting immunological targets, such as **PD-L1**, may synergize the anti-tumoral activity of VACV. Randox & Transgene report the selection and characterization of a sdAb targeting the human PD-L1 and the design of optimal formats, including bispecific anti-PD-L1-TNFSF, for vectorization into VACV.

METHODS

Alpacas were immunized with human PD-L1 protein and sdAb coding sequences were isolated by PCR. Anti-PD-L1 sdAb binders were selected by phage display and sdAb blockers of PD-L1/PD-1 interaction were identified by ELISA. The ability of the selected sdAb to disrupt the PD-L1/PD-1 interaction was verified on transformed and primary cells. To fine-tune an optimal anti-PD-L1, several sdAb formats were designed and vectorized into VACV. The sdAb format exhibiting the best PD-L1/PD-1 blocking activity was selected by the screening of culture supernatants of several VACV-sdAb infected tumor cells. Finally, anti-PD-L1 sdAb-TNFSF fusions were designed to generate a strong TNFRSF agonists active only in a PD-L1 positive environment.

RESULTS

SdAb clone 1A1 exhibited the best PD-L1/PD-1 blocking activity which remained unchanged after extensive humanization (latterly becoming named GS542). GS542 was vectorized in VACV as monomeric, single chain homodimer, and fused to Fc domain or antibody hinge domain to foster dimerization together with full length IgG1 avelumab as anti-PD-L1 benchmark. All constructs were expressed by infected tumor cells. The single chain homodimer displayed the best PD-L1/PD-1 blocking activity, superior to that of avelumab.

Moreover, **GS542-TNFSF fusions** were designed to take advantage of the natural trimerization of TNFSF to increase the avidity for PD-L1 while clustering ligands at the surface of PD-L1+ cells to trans-activate TNFRSF pathways. Evaluation of these GS542-TNFSF fusions showed strong TNFRSF agonist activities **depending** on the presence of **PD-L1+ cells** making these constructs safer agonists.

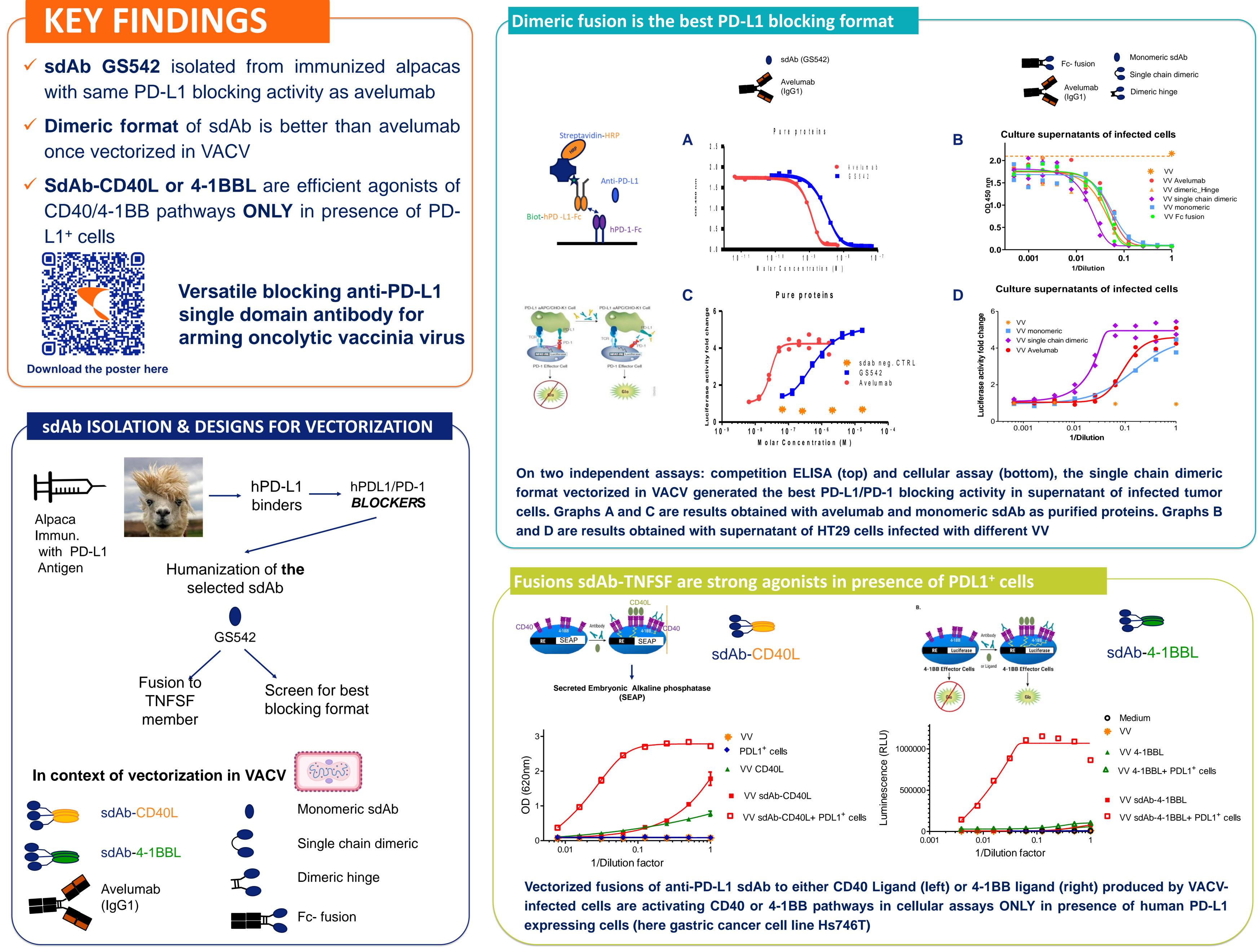
CONCLUSION

An anti-PD-L1 sdAb with a strong blocking activity was selected, humanized and evaluated under different VACV-vectorized formats. The single chain dimeric sdAb expressed by VACV was identified as the best PD-L1/PD-1 blocking format. Furthermore, bispecific anti-PD-L1 sdAb-TNFSF fusions that exhibited strong agonist activities were characterized within a PD-L1+ environment.

- once vectorized in VACV



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