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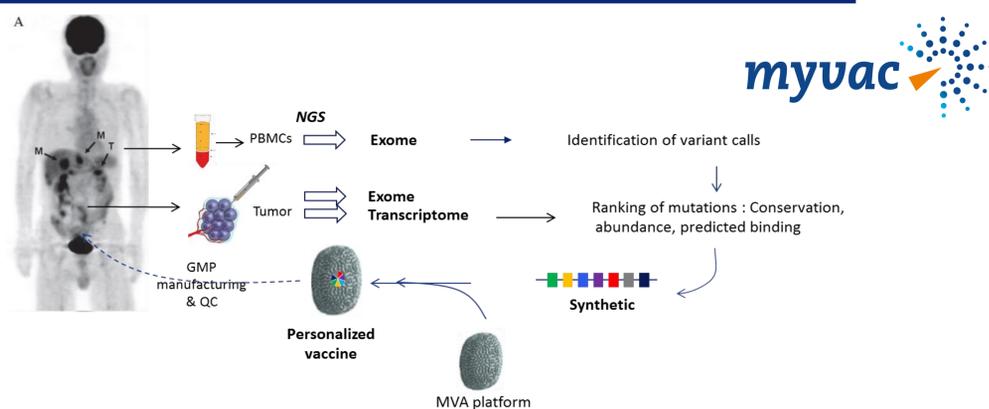
BACKGROUND

Anarchic cellular proliferation and deficient DNA repair mechanisms result in accumulation of mutations in cancer cells potentially leading to expression of tumor specific neoantigens (TSNA). Given their *ad hoc* onset in the tumor, TSNA are not subject to central tolerance and may constitute ideal targets for therapeutic cancer vaccines. However, clinical implementation of TSNA directed vaccination requires a potent immunizing vaccine formulation allowing the reproducible generation of a bespoke vaccine for every patient within acceptable time and cost. Herein, we propose a workflow to meet both requirements using a modified vaccinia Ankara (MVA) based vaccine referred to as MyVAC™. Technical feasibility was shown, and immunogenicity of the vaccine was demonstrated using an exemplar patient with Non Small Cell Lung Cancer.

METHOD

Blood and tumor tissue sample from a patient with lung adenocarcinoma were sequenced and compared to reference genome to identify tumor specific variants. Consequently, identified mutations were assembled as a polypeptidic sequence in a recombinant MVA. The said viral vaccine was used to immunize human HLA-transgenic mice (HHD), and CD4 and CD8 cellular responses against the target neoantigens were assessed by ELISPOT. Response obtained in the HHD murine model were compared to spontaneous responses observed in the patient.

IDENTIFICATION OF PATIENT SPECIFIC MUTATIONS



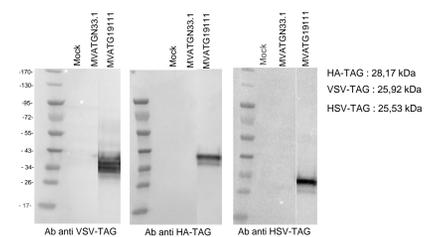
Exome sequence was aligned to the reference genome using Speedseq/BWA; somatic variants were identified with SpeedSeq somatic and annotated with SnpEff. Variants were filtered (SQLite database) using the following filters: normal and tumour sequencing depth \geq 10, genotype quality score of ≥ 20 (99% confidence), normal genotype is homozygous reference, tumour genotype is not homozygous reference. This yielded 2,218 variants that were further filtered using the following criteria: variant occurs in coding region, at least one observation of the variant in RNAseq with no observations in the normal transcriptome. **Twenty-three variants were identified of which 22 were missense variants and one frame shift variant through deletion. The mutations were observed in 18 different genes.**

GENERATION OF PATIENT SPECIFIC VACCINE

- A viral based vaccine was generated to targeted 18 mutations identified in the patient**
- Eighteen mutated sequences coding identified above were selected and assembled into three fusion cassettes:
 - peptides spaced by 5-aa linkers (GSGSG, SGSGS, GSTSG or SGTGS) in 3 expression cassettes containing a signal peptide
 - 3 mutated fragments encoded 29mer peptides, 1 was 20mer, 1 was 30mer, 1 was 31mer and 1 was 76mer
 - Mutated fragment were separated by a linker sequence
 - The three expression cassettes were cloned into the Transgene MVA vector, each cassette containing a TAG sequence for control of transgene expression. This MVA vector is referred to as TG19111.
 - The corresponding control vector, empty of the mutated fragment was also made and is referred to as MVATGN33.1.

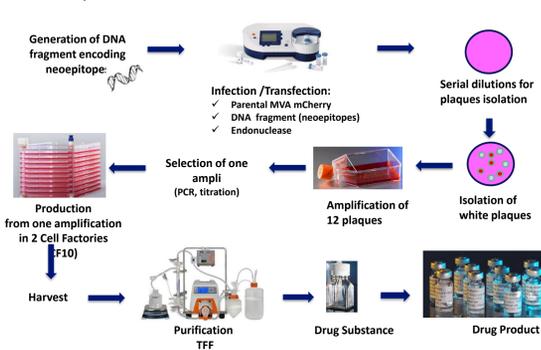
In vitro expression of neopeptide fusions

CEF were infected at MOI 0.2 by either MVA (MVATGN33.1: negative control), MVATG19111. Western-blot performed 24 h later using anti-TAG antibodies



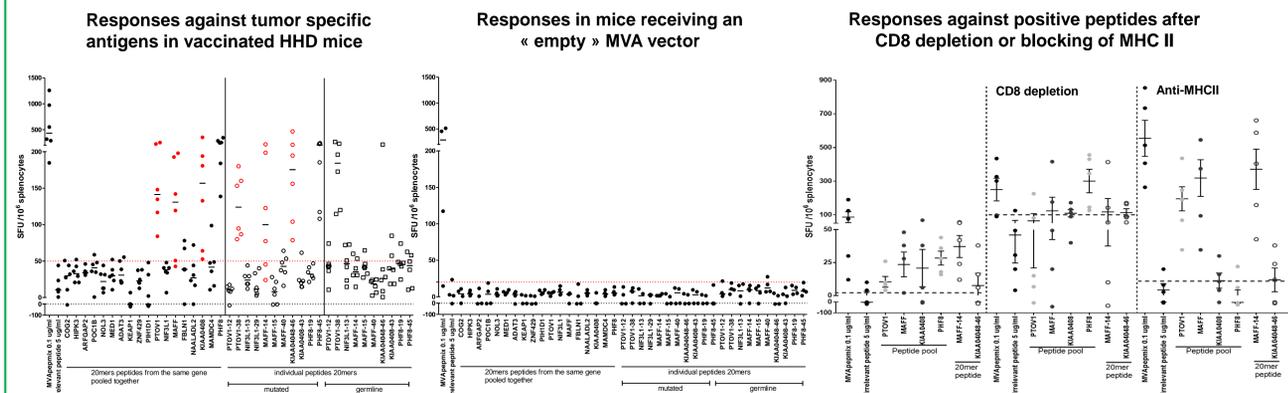
GMP-manufacturing of customized MVA product

- 1 batch per patient: around 150 clinical doses at 10^8 pfu/dose
- <10-weeks process for the generation of clinical lots of viral vaccine
- Fully integrated GMP-compliant aseptic process
- In house GMP facility for modular manufacturing of multiple lots to be certified by Q4 2018



IMMUNOGENICITY OF VACCINE IN HHD TRANSGENIC MICE (HUMAN HLA-A2)

HDD mice were immunized by I.V route at D1 and D7 with 10^7 pfu of MVATG19111 or MVATGN33.1. Immunogenicity was evaluated in splenocytes at D14, by ELISPOT using overlapping 20mer peptides. For highly immunogenic peptides, ELISPOT was repeated in presence of anti-class II MHC or of anti-CD8 depleting beads. Additionally, we performed prediction of immunogenicity using BIMAS and SYFPEITHI algorithms against all tested mutations, predicted immunogens are highlighted in red.



- T cells responses were detected for 4 mutations, and sporadic responses for 3 other mutations
- Responses were restricted to mutated proteins and no cross reaction was detected against non mutated protein
- Both CD4 and CD8 responses were detected in response to MVA vaccination
- 3 out of 4 immunogenic peptides could have been predicted from sequencing data using *in silico* prediction

IMMUNOGENICITY OF MUTATIONS IN PATIENT

Pre-existing immunity to the non-synonymous mutations identified by NGS was studied by IFN γ ELISPOT in patient PBMCs. Positive responses are highlighted in yellow

Gene_Name	Peptide ID	Peptide Sequence
COG2	A003_m6_1	EIAGS S EAAALTDVLEDAPE
	A003_m15_26	PVYFQIRPREIAGS S EAAAL
	A003_m15_27	QTSQSAFCSVVKLKL A EPSSC
HIPK3	A003_m6_2	VKRLK A EPSSCVFQERNYPR
	A003_m15_27	QTSQSAFCSVVKLKL A EPSSC
	A003_m15_29	WDTFLMLWNPFA K AYRYV
ARFGAP2	A003_m5_3	MAAE R NKTEIQTLEFRRAV
	A003_m6_4	FKPHA K AYRYVGHKDVVTSV
	A003_m10_28	MLWNFKPHA K AYRYVGHKDV
NOL3	A003_m15_29	WDTFLMLWNPFA K AYRYV
	A003_m6_5	NAQER L SETIDRERKRLVET
	A003_m15_30	GWDRAPTMGNAQER L SETID
MED1	A003_m8_31	MGNAQER L SETIDRERKRLV
	A003_m6_6	LPPKK Q HQTEDEDFORELFS
	A003_m15_32	KTKKKSSRLPPEK Q HQTE
ADAT3	A003_m6_7	DGLPY V CTGYDLYVTRPCA
	A003_m15_33	AVRKLDADEDEGLPY V CTGYD
	A003_m6_8	VGVAV P NPAGS R LSRTVP
KEAP1	A003_m15_34	TRMTSGRSGGVAV P NPAG
	A003_a11_20	VPVEALLFLGQK S PMGSI I
	A003_a11_21	GQK S PMGSI I VFPVQ P GLK
ZNF429	A003_a11_22	EKTA L QI THLPQ R EARMPCC
	A003_a11_23	LKE K TALQI THLPQ R EARMP
	A003_a11_24	I I VFPVQ P GLK E KTA L QI TH
PIH1D1	A003_a11_25	AGS R LTSRTVP V EALLFLQ Q
	A003_m6_9	EMVDETPDGVSLLEPRLECS
	A003_m6_10	EMVDETPVVC S HEAEDFWPE
PTOV1	A003_m15_35	KEPCMKRHEM V DETPDGV S
	A003_m15_36	KEPCMKRHEM V DETPVVC S
	A003_m6_11	NPEWR I MKNRPFMGISQ Q N
NIF3L1	A003_m15_37	LEDKYNLQ L PEWR I MKNR P
	A003_m6_12	PIG S PLPGLTIGLAVSEHR
	A003_m15_38	GARVFGALG P TG S LPGL T L
MAFF	A003_m6_13	ERL V LALENRVG I YSP H TA
	A003_m15_39	KRITWNTW K ERL V LA L EN R
	A003_m6_14	ALM G LLVRELNRHLR G LSAE
FBLN1	A003_m4_15	M G LLVRELNRHLR G LSAE V
	A003_m15_40	ENT P HL S DEALM G LLVREL N
	A003_m6_16	CEY S LVGYCGQGV F QAC V
KIAA0408	A003_m15_41	RAAQ Q Q S CEY S LVGY Q C
	A003_m15_42	QYLD N DLQAT L DLEW D EM
	A003_m14_46	AL R RT H NY T IS L Q S EAL M
MAMDC4	A003_m15_43	PAL R RT H NY T IS L Q S EAL M
	A003_m6_18	GT T DF Q PEAG G WEDAS V GR
	A003_m15_44	AG G ED E Q A C T T D F Q PEAG
PHF8	A003_m6_19	CV G VE Q KAAD I D L Y H CP N C
	A003_m15_45	MC Q W F H G SC V GV E Q E KAAD

- Spontaneous preimmunity was observed in PBMC against:
 - mutated POC18
 - mutated KEAP1
 - mutated NIF3L1
 - mutated MAFF
 - mutated KIAA0408
- Responses were restricted to mutated proteins and no cross reaction was detected against non mutated protein

CORRELATION OF HUMAN AND MURINE RESPONSES

Correlation of preimmunity in the patient and vaccine-induced immunity in HHD mice.

Mutated gene	Spontaneous responses in PBMCs	Responses in HHD mice after vaccination
MAFF	+	+
KIAA0408	+	+
PTOV1	-	+
PHF8	-	+
POC1B	+	-
KEAP1	+	-
NIF3L1	+	-

- Immunity against mutations in the MAFF and KIAA0408 genes was observed in both settings
- Mutations in PTOV1 and PHF8 elicited responses after vaccination, in HDD were not detected in patient
- Responses to mutations in POC1B, KEAP1 and NIF3L1 were detected in the patient but not after vaccination in the HDD model. This discordance may be due to difference in antigen processing between the two species.

CONCLUSIONS

- A polypeptide vaccines based on the MVA platform is able to induce clinically relevant immune responses in HHD mice. After administration in HDD mice, both CD4 and CD8 T cells responses were detected. These responses could be predicted by an *in silico* approach, highlighting the need for a built-in antigen selection system in the process.
- An accelerated process for the generation of MyVAC product, and for its aseptic manufacturing was successfully developed.
- Clinical translation will be initiated in 2019

