

Characterization of Generalized Modules for Membrane Antigens (GMMA)

vaccine candidates against nontyphoidal *Salmonella*

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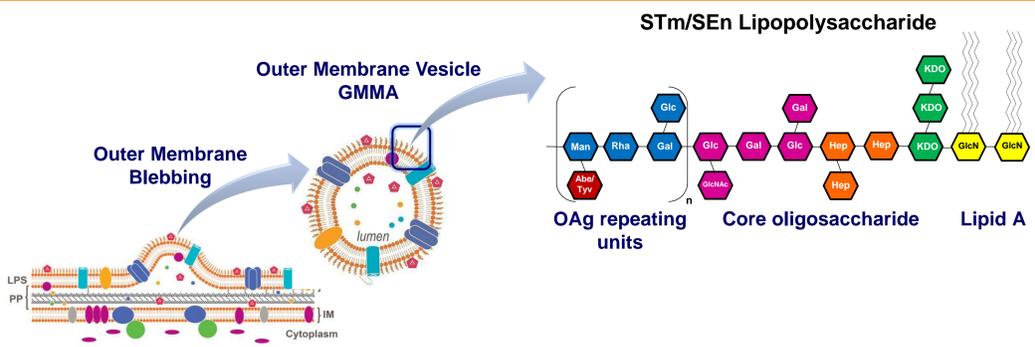
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INTRODUCTION

- Invasive nontyphoidal *Salmonella* disease (iNTS) is a leading cause of bloodstream infections in Africa and no licensed vaccines are currently available. The most common pathogens are *Salmonella* Typhimurium (STm) and *Salmonella* Enteritidis (SEn)¹.
- The O-antigen (OAg) portion of lipopolysaccharide (LPS) is a key antigen for protective immunity and represents a target for the development of effective vaccines against iNTS².
- With the aim to develop a bivalent OAg-based vaccine against STm and SEn, Generalized Modules for Membrane Antigens (GMMA) were proposed as an attractive OAg delivery system³.
- Gram-negative bacteria naturally shed outer membrane vesicles (OMV) which imitate the bacterial surface, maintaining structure, composition, and orientation of outer membrane components, including LPS and OAg⁴.
- Wild type GMMA-producing strains were firstly genetically manipulated to increase GMMA production ($\Delta tolR$) and further mutated to reduce LPS reactivity ($\Delta msbB$, $\Delta htrB$, $\Delta pagP$)⁵.
- Advantages of GMMA vaccines include simplicity and low cost of manufacture, co-delivery of multiple antigens in the context of a membrane and bacterial "danger signals" triggering innate immunity, obtaining a self-adjuncting activity.
- GMMA platform has been applied to different pathogens (*Salmonella*, *Shigella*, *Meningococcus*) for the production of vaccines for low and middle income countries⁶⁻⁷.



- Methods to determine quality, consistency of production and stability of OMV vaccines are of fundamental importance. It is important to characterize the key antigens displayed on OMV surface and presented to the immune system, and also OMV as particles.
- In the context of identification of the most suitable GMMA candidate vaccines against iNTS, we have developed a panel of analytical methods for LPS/OAg and GMMA characterization³.
- Our aim was to evaluate the impact of genetic mutations introduced into GMMA-producing strains on OAg expression, structure and composition, and the resulting impact on GMMA immunogenicity.
- Particle size distribution of GMMA from different mutants was evaluated by comparing three different methods: Dynamic Light Scattering (DLS), Multi-Angle Light Scattering (MALS) coupled with High Performance Liquid Chromatography - Size Exclusion Chromatography (HPLC-SEC), and Nanoparticle Tracking Analysis (NTA)⁸.

- References
- 1. MacLennan CA, et al. *Hum Vaccin Immunother*. 2014. 10(6):1478-1493.
- 2. Tennant SM, et al. *Vaccine*. 2016. 34, 2907-2910.
- 3. De Benedetto G, et al. *Vaccine*. 2017. 35:419-426.
- 4. Berlanda Scorza F, et al. *PLoS ONE*. 2012. 7(6):e35616.
- 5. Rossi O, et al. *Clin Vaccine Immunol*. 2016. 23(4):304-314.
- 6. Gerke C, et al. *PLoS ONE*. 2015. 10(8):e0134478.
- 7. Koeberling O, et al. *Vaccine*. 2014. 32:2688-2695.
- 8. De Benedetto G, et al. <http://dx.doi.org/10.1021/acsomega.7b01173>.
- 9. Micoli F, et al. *Anal Biochem*. 2013. 34:136-145.

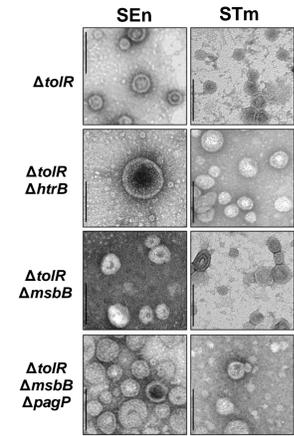
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RESULTS

GMMA analytical characterization

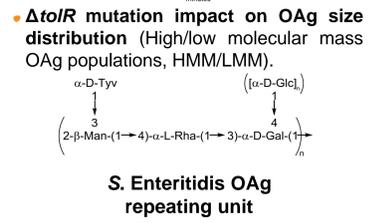
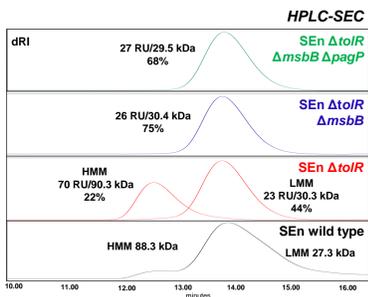
- Analyses were performed directly on STm and SEn GMMA from different mutated strains and on their OAg.
- OAg extracted⁹ from GMMA were compared to OAg produced by corresponding wild type strains.



Analyses on extracted OAg

Test category	Analytical method
OAg size distribution	HPLC-SEC
Relative % of OAg with different chain length	HPLC-SEC/Semicarbazide Phenol sulfuric acid assay
OAg sugar composition, glycosidic linkages and absolute configuration	GLC/GLC-MS HPAEC-PAD
OAg identity	NMR
O-acetylation pattern and level	GLC

OAg size distribution

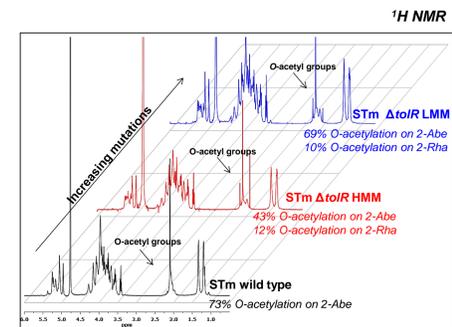


OAg sugar composition

OAg	Tyr	Rha	Man	Gal	Glc
SEn wild type	1.00	1.00	1.00	1.08	0.19
SEn $\Delta tolR$ (HMM OAg)	0.99	1.00	1.04	1.05	0.12
SEn $\Delta tolR$ (LMM OAg)	0.93	1.00	0.99	1.07	0.11
SEn $\Delta tolR$ $\Delta msbB$	0.97	1.00	1.00	1.05	0.09
SEn $\Delta tolR$ $\Delta msbB$ $\Delta pagP$	0.97	1.00	0.99	1.06	0.08

- Similar sugar composition of OAg populations from all GMMA, in agreement with OAg from wild type strain.

OAg identity and O-acetylation degree

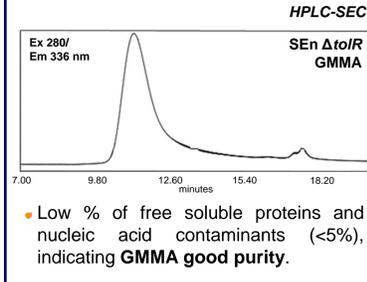


- No major impact of mutations introduced on O-acetylation levels. Additional O-acetyl groups in OAg populations extracted from STm $\Delta tolR$ GMMA (not only on 2-Abe but also on 2-Rha).

Analyses on GMMA

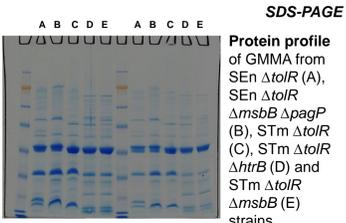
Test category	Analytical method
Purity	HPLC-SEC
Protein content	micro BCA SDS-PAGE
OAg content/identification	HPAEC-PAD
Lipid A content/identification	HPLC-SEC/Semicarbazide MALDI-TOF MS
Particle size distribution/aggregation	DLS HPLC-SEC/MALS NTA

GMMA purity



- Low % of free soluble proteins and nucleic acid contaminants (<5%), indicating GMMA good purity.

GMMA protein content



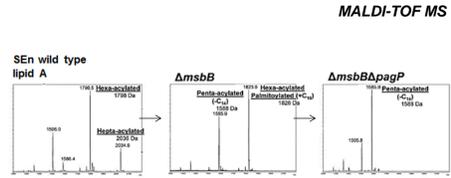
- No major changes in the protein pattern of GMMA produced by lipid A mutated strains, compared to GMMA with no lipid A modification ($\Delta tolR$).

GMMA OAg and lipid A content

GMMA	w/w OAg/GMMA protein ratio	Molar % OAg chains/total LPS	nmol lipid A/mg GMMA protein
SEn $\Delta tolR$	0.6	14	156.6
SEn $\Delta tolR$ $\Delta msbB$	1.7	22	240.1
SEn $\Delta tolR$ $\Delta msbB$ $\Delta pagP$	1.5	12	528.0
STm $\Delta tolR$	0.7	10	172.8
STm $\Delta tolR$ $\Delta msbB$	0.03	<1	108.2
STm $\Delta tolR$ $\Delta htrB$	0.02	0.45	154.8

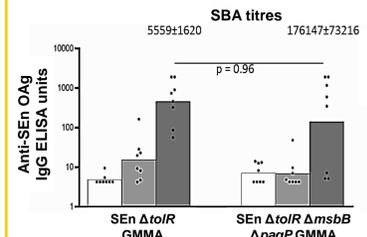
- Impact on OAg production after lipid A detoxification mutations introduced in some strains.
- Large portion of LPS molecules containing just core.

GMMA Lipid A structure



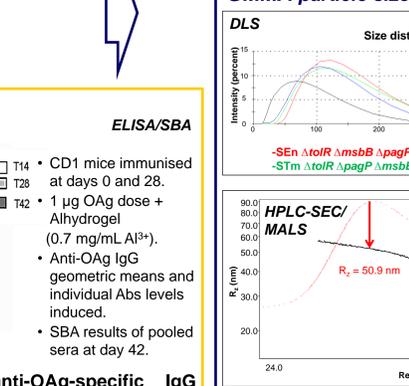
- Combination of $\Delta msbB$ - $\Delta pagP$ mutations as optimal approach to minimize STm and SEn GMMA reactivity, resulting in pure penta-acetylated lipid A.

GMMA immunogenicity



- High levels of serotype-specific anti-OAg-specific IgG functional antibodies induced by all GMMA, with no significant differences despite variations in OAg density and chain length, when tested in mice at the same OAg dose.
- Anti-OAg IgG response booster effect shown by all GMMA.

GMMA particle size distribution



- Strengths and weaknesses shown by each methodology, providing complementary information and allowing a more complete evaluation of GMMA size.
- SEC-MALS and NTA able to better distinguish populations of different size and preferable to DLS for analysis of bimodal samples.
- Real time visualization with simultaneously tracking and counting of individual particles by NTA, but results deeply dependent on the choice of data analysis parameters.
- Higher DLS Z-average diameters compared to MALS size for OAg-positive GMMA. Hydrodynamic diameter increases with the number of OAg chains per particle.

Correlation between GMMA size and their main features

GMMA	OAg presence	Lipid A structure	DLS Z-average (d) nm	HPLC-SEC/MALS 2 x R _z nm	NTA Mode/ Mean (d) nm	OAg chains/GMMA	OAg size (kDa)	ζ-potential (mV)
SEn $\Delta tolR$ $\Delta msbB$ $\Delta pagP$	OAg ⁺	Penta	111.1	76.2	106.0/91.9	2812	30.0	-3.2
STm $\Delta tolR$ $\Delta msbB$ $\Delta pagP$	OAg ⁺	Penta	103.5	72.2	102.5/78.6	2204	34.6	-3.3
STm $\Delta tolR$	OAg ⁺	Hepta/hexa	91.5	73.8	95.8/85.6	768	32.9	-2.7
STm $\Delta tolR$ $\Delta wbaP$	OAg ⁻	Hepta/hexa	57.6	101.8 (Peak 1) 55.4 (Peak 2)	90.1/62.6	/	/	-9.8

CONCLUSIONS

- A comprehensive panel of analytical methods has been assembled for GMMA characterization with particular attention to their surface OAg, which is key target of protective antibody response.
- Such methods are of fundamental importance in the process of vaccine development, to ensure consistency of production and to monitor stability of GMMA over time.
- Mutations introduced in GMMA producing strains to enhance blebbing and reduce LPS toxicity can impact OAg expression levels and structural characteristics. Careful characterization is needed to identify optimal GMMA candidates for inclusion in a vaccine against iNTS.
- Simplicity of manufacturing process, coupled with encouraging immunogenicity data, make the GMMA approach particularly attractive for the development of a vaccine against iNTS.

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