This is the published version of a paper published in *Data in Brief*.

Citation for the original published paper (version of record):

Proteome profiling of secreted and membrane vesicle associated proteins of an invasive
and a commensal Staphylococcus haemolyticus isolate
*Data in Brief*, 22: 914-919
https://doi.org/10.1016/j.dib.2018.11.147

Access to the published version may require subscription.

N.B. When citing this work, cite the original published paper.

Permanent link to this version:
http://urn.kb.se/resolve?urn=urn:nbn:se:umu:diva-162514
Proteome profiling of secreted and membrane vesicle associated proteins of an invasive and a commensal Staphylococcus haemolyticus isolate

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Article info
Article history:
Received 21 November 2018
Accepted 24 November 2018
Available online 11 January 2019

Abstract
Bacterial membrane vesicles (MVs) mediate bacterial virulence by enabling secretion and long distance delivery of bacterial effector molecules. Staphylococcus haemolyticus has now been demonstrated to produce membrane vesicles (MVs). The protein content of S. haemolyticus MVs was identified by Mass spectrometry and compared to proteins identified in the total secretome. This information is presented in this data article. Further background and interpretation of the data can be found in the article: Comparative exoproteome profiling of an invasive and a commensal S. haemolyticus isolate (Cavanagh et al., in press). Data are available via Proteome Xchange with identifier PXD010389.

DOI of original article: https://doi.org/10.1016/j.jprot.2018.11.013
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1. Data

*Staphylococcus haemolyticus* is a skin commensal now emerging as an opportunistic pathogen, apart from being multiresistant to several antimicrobial agents, little is known about its virulence factors [2]. Bacterial membrane vesicles (MVs) are mediators of bacterial virulence, and has recently been found in gram positive bacteria [3]. It has been shown that *S. haemolyticus* produces MVs, and that the protein cargo is strain specific [1]. The data presented in this article provide information on the proteins identified in the MV cargo and in the total secretome of a clinical and a commensal *S. haemolyticus* strain. Unique and common proteins found in MVs and the total Secretome of both strains are presented. Proteins found to be enriched in the MV cargo as compared to the total Secretome are presented for both strains.

2. Experimental design, materials and methods

Membrane vesicles (MVS) were isolated from a commensal *S. haemolyticus* strain (57-1), and a clinical *S. haemolyticus* strain (51-08), according to the methods described in [1,4]. Briefly, proteins secreted into the bacterial growth medium was harvested after the culture was centrifuged and filtered through a 0.22 μm polyethersulfone membrane (Millipore express plus, Merck Millipore,
Burlington, USA). MVs were isolated by ultra centrifugation and purified using an Optiprep gradient, presence of proteins in the different OptiPrep fractions were visualized by SDS PAGE Comassie Blue staining, Fig. 1.

Proteins in the MV samples and the total secretome were precipitated and digested in solution, prior to protein identification by Mass spectrometry using a Thermo Scientific Q-Exactive mass spectrometer.

The raw data were processed in the MaxQuant software v1.6.0.16 using label-free intensity based absolute quantification (iBAQ) according to the method published in [1]. The raw data are deposited in the Proteome Xchange with identifier PXD010389.

A quantitative comparison of proteins secreted by the two bacterial strains was performed using the relative iBAQ values (riBAQ) in Perseus programme v1.5.6.0 [5]. Proteins with minimum two peptides identified was used. All contaminants were first filtered out and the relative iBAQ values for each sample were log10 transformed. Missing values were replaced from normal distribution using width $= 0.3$ and downshift $= 1.8$ settings.

Differentially secreted proteins in the MV cargo and in the total secretome of strains 57-1 and 51-08, were then visualized using Volcano plot with FDR $< 0.05$ and artificial within group variance $s_0 = 0.3$, Figs. 2 and 3. For qualitative comparisons, only proteins present in at least two replicates in each group were considered further. The riBAQ values for proteins identified in the total secretome and in the MV cargo of the commensal and the clinical strain respectively is presented in Tables S1 and S2.

Functional annotation and grouping of proteins into orthologous groups were performed using EggNOG version 4.5.1 [6], while the cellular localisation of each protein was predicted using the PSORTb subcellular localisation tool version 3.0.2 [7]. The presence of potential signal sequences in each peptide was identified using SignalP v4.1 [8,9]. Secretome P v2.0 was used to predict non-classical protein secretion [10].

Proteins uniquely found in the MV cargo of the commensal and clinical strain are presented in Tables S3 and S4 respectively, while common proteins found in the MV cargo in both strains are presented in Table S5.

It has previously been shown that MVs are enriched in virulence factors [11]. An enrichment analysis was performed comparing the MV cargo to the total secretome. If proteins were detected with a threshold detection rate of FDR 0.05 in the MV sample as compared to in the TS, these proteins were defined as enriched.

Fig. 1. Presence of proteins in the different fractions after OptiPrep were visualized by SDS PAGE Comassie Blue staining.
Proteins enriched in the MVs compared to the total secretome of the commensal strain and the clinical strain are shown as red squares in the volcano plots in Figs. 2 and 3. Enriched proteins are listed in Tables S6 and S7.

Proteins uniquely found in the total secretome of the commensal and clinical strain are presented in Tables S8 and S9 respectively, while common proteins found in the total secretome of both strains are presented in Table S10.

Acknowledgements

The study was supported by grants from the Northern Norway Regional Health Authority, grant number HNF1344-17. The publication charges for this article have been funded by a grant from the publication fund of UiT The Arctic University of Norway. The funding source had no involvement in project design, data collection, analysis, interpretation and publication.
Fig. 3. Volcano plot used to visualize the differentially secreted proteins in the MVs and in the total secretome of strain 57-1. Enriched proteins are depicted as red filled squares.

Transparency document. Supporting information

Transparency document associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.11.147.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.11.147.
References


