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Proteomic Analysis of Tissue from α1,3-galactosyltransferase Knockout Mice Reveals That a Wide Variety of Proteins and Protein Fragments Change Expression Level

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Abstract

A barrier in a pig-to-man xenotransplantation is that the Galα1-3Galβ1-4GlcNAc-R carbohydrate (α-Gal epitope) expressed on pig endothelial cells reacts with naturally occurring antibodies in the recipient's blood leading to rejection. Deletion of the α1,3-galactosyltransferase gene prevents the synthesis of the α-Gal epitope. Therefore, knockout models of the α1,3-galactosyltransferase gene are widely used to study xenotransplantation. We have performed proteomic studies on liver and pancreas tissues from wild type and α1,3-galactosyltransferase gene knockout mice. The tissues were analyzed by two-dimensional polyacrylamide gel electrophoresis and liquid chromatography - tandem mass spectrometry. The analyses revealed that a wide variety of proteins and protein fragments are differentially expressed suggesting that knockout of the α1,3-galactosyltransferase gene affects the expression of several other genes.

Introduction

The first barrier in a pig-to-man xenotransplantation is that the Galα1-3Galβ1-4GlcNAc-R carbohydrate (α-Gal epitope) expressed on pig endothelial cells will react with naturally occurring xenoreactive circulating antibodies in the recipient's blood leading to hyperacute rejection of the discordant xenograft within a few minutes. Deletion of the α1,3-galactosyltransferase gene will prevent synthesis of the α-Gal epitope and generation of α-Gal transferase knockout animals is therefore an important step for xenotransplantation of vascularised organs [1]. The results from grafting α-Gal transferase knockout organs into non-human primates show that many biological barriers such as human antibodies against pig antigens must be overcome before being a clinical reality [2]. Thus, carbohydrate antigens other than the Gal antigen (i.e. non-Gal antigens) such as blood group AO and related antigens, Tn and Sialyl-Tn antigens and perhaps other saccharides to which humans have preformed antibodies may cause pig xeno-rejection [3,4]. Further, knockout of a gene may eliminate the construction of its specific gene product, but it may also influence the expression of other proteins that may be up- or downregulated [5,6]. The α-Gal epitope is expressed in wild type mice and therefore the α1,3-galactosyltransferase knockout models have been extensively used in xenotransplantation studies. To determine if other proteins are differentially expressed in α1,3-galactosyltransferase knockout mice compared to wild type mice, we performed proteomic analyses of liver and pancreas tissues by using two dimensional polyacrylamide gel electrophoresis (2D-PAGE) and liquid chromatography - tandem mass spectrometry (LC-MS/MS) to identify such protein candidates.

Materials and Methods

C57BL/6 mice, 3-months-old, all male were included in the study. All procedures were conducted under protocols approved by the Danish Animal Care and Ethics Committee.
and conducted in accordance with the Danish Animal Experimentation Act and European Convention for the protection of vertebrate animals used for experimental and other scientific purposes. Half of the mice were α-Gal knockout mice, lacking a functional α1,3-galactosyltransferase gene, C57BL/6/Jimkvl-Tgaltm1Tea. The mice were generated as described by Tearle et al. [7] hereafter termed KO mice. The phenotype was confirmed by development of cataracts at 4–6 weeks of age and by PCR. C57BL/6JomTac mice, hereafter termed wt mice, were used as controls. The mice had free access to food and water and were sacrificed between 10 a.m. and noon. Specimens from the liver and pancreas were frozen in isopentane cooled to -150°C with liquid nitrogen. Some samples were cut on a cryostat in 6µ sections for histochemistry while other were processed for electrophoresis. The lectin to detect the α-Gal epitope in tissue sections was a biotinylated Griffonia simplicifolia isoelectin (GS1-B4: EY Laboratories, San Mateo, CA, USA). The sections were incubated for 24 h at 4°C with 5 μg/ml of the lectin, diluted 1:200 from a stock solution of 1 mg/ml in TBS. The incubation medium contained 20 mM CaCl₂ and MgCl₂. After a 3x5 min rinse in TBS the sections were immersed in Alexa Fluor 488 streptavidin conjugate for 30 min. The sections were mounted with a fluorescence mounting medium with the DNA binding agent 4′,6-diamidino-2-phenylindole (DAPI; Vector Lab, Burlingame CA, USA).

Two-dimensional gel electrophoresis (2D-PAGE)

Liver and pancreas tissue samples were taken from three wt and three KO mice. Tissue samples were dissolved in lysis buffer consisting of 9 M urea, 2% DTT, 2% Triton X-100 and 2% IPG buffer. Horizontal isoelectric focusing was performed using a non-linear pH3-10NL IPG strip, rehydrated for 20 hours at room temperature with a rehydration buffer (8 M urea, 2% CHAPS, 2% IPG-buffer, 0.3% DDT). The first dimension was carried out on a Multiphor II Electrophoresis unit at 500 V for 5 hours and at 3500 V for 14.5 hours. Prior to the second dimension, the IPG strip was equilibrated twice with an equilibration buffer (0.05 M Tris-base, 6 M Urea, 26% glycerol, 1% SDS), and transferred to a polyacrylamide gel. The second dimension separation was run vertically at 50 V for 19 hours [8]. One gel was performed for each tissue sample from one mouse, thus three biological replicates were analysed for each tissue.

Silver staining

Visualisation was achieved by silver staining, suitable for quantitative protein analysis [8,9]. Briefly, gels where fixed overnight in a fixation solution (50% ethanol, 12% acetic acid and 0.0185% formaldehyde), then washed three times for 20 minutes in 35% ethanol, pre-treated for one min in 0.02% Na₂S₂O₃, and rinsed in water 3 times for 2-3 min. Staining of gels with silver nitrate was preformed for 20 minutes, after which they again where rinsed twice with water. Gels where developed using a developer solution (6% Na₂CO₃, 0.0185% formaldehyde, 0.0004% Na₂S₂O₃, 5 H₂O) for approximately 3 min. Development where finally stopped in a stop solution (40% ethanol, 12% acetic acid). The gels where dried in cellophane sheets and sealed in plastic bags.

Image analysis

Silver stained gels where scanned using an ImageQuant LAS-4000 (GE Healthcare) and TIFF images of gels were imported into the PDQuest software analysis program. Two proteomic analyses where done; one with pancreatic tissue and one with hepatic tissue. The 2D-gels where divided in two groups; one representing wt mice and another representing KO mice. Protein spots where automatically defined and adjusted to the background. The quality of each protein spot was critically evaluated in order to ensure that all relevant protein spots were identified. The pixel-intensity of each protein spot was translated to a proportional protein volume, which was normalized to the total density of the gel and given in parts per million. Finally, re-analysis was done manually on all matched spots. Differentially expressed spots were defined as spots that differed at least 2-fold in average relative volume between the groups of wt and KO mice. The results where considered to be significant when p<0.05 using a students t-test. These spots where selected for further identification by LC-MS/MS.

Protein identification

Protein identification by LC-MS/MS was performed essentially as previously described [8]. Briefly, gels containing protein spots selected for identification were re-hydrated in water, the cellophane sheets were peeled off and the protein spots were excised from the gels. Proteins were in-gel digested with trypsin. Gel pieces were first dehydrated in acetonitrile, then dried and the proteins reduced for 1h at 56°C in 10 mM dithiothreitol (DTT) and 100 mM NH₄HCO₃. The solution was exchanged with 55 mM iodoacetamide in 100 mM NH₄HCO₃ for 45 min. Then the gel pieces were washed in 100 mM NH₄HCO₃, dehydrated in acetonitrile, rehydrated in 100 mM NH₄HCO₃, dehydrated in acetonitrile, dried and swelled in digestion buffer (50 mM NH₄HCO₃, 5 mM CaCl₂ and 12.5 ng/µl trypsin Gold (mass spectrometry grade; Promega, Madison, WI, USA). Digestion was performed overnight at 37°C and the peptides were extracted by 1 change of 20 mM NH₄HCO₃, 3 changes of 5% formic acid in 50% acetonitrile. The samples were finally dried and the peptides resuspended in 6 µl of buffer A (water/acetonitrile/formic acid, 97.7/2/0.3, V/V/V). The peptides were separated using an inlet nano LC system composed of a Famos micro autosampler, a Switchos micro column switching module and an Ultimate micro pump from LC Packings (San Francisco, CA) before MS analysis. Of the in-gel digested samples 5 µl was preconcentrated and desalted on a 300 µm inner diameter x 5 mm nano-precolumn (LC Packings) packed with 5 µm C18 PepMap100 material. A 75 µm inner diameter x 15 cm nano-column packed with 3 µm C18 PepMap100 material was used to separate the peptides. Elution from the column was made with a gradient by mixing decreasing volumes of buffer A with increasing volumes of buffer B (water/acetonitrile/formic acid, 9.7/90/0.3, V/V/V). The peptides were eluted into the nano electrospray ion source of the quadrupole time-of-flight (Q-TOF) Premier mass spectrometer (Waters). MS survey scans were acquired using MassLynx 4 SP4 (Waters) from m/z values between 450-1500. The instrument was operated in a data-dependent MS to
MS/MS switching mode. Doubly, triply and quadruply charged peptide ions detected in MS survey scans triggered a switch to MS/MS for obtaining peptide fragmentation spectra with an interval of m/z values between 50-1800. [Glu]-fibrinopeptide B (GFP), 300 fmol/μl, was used as lock mass injected at a flow rate of 300 nl/min. GFP was also used to calibrate the TOF unit. Raw data were processed using ProteinLynx Global Server 2.1 (Waters) with processing parameters: Background Subtract: Normal, Background Threshold: 35%, Background Polynomial: 5, Smoothing Type: Savitzky-Golay, Smoothing Iterations: 2, Smoothing Window: 2 channels, Deisotoping Type: Normal, Deisotoping Threshold: 1%. The processed data were used to search the mouse fraction of the Swiss-Prot database (release 2011_11 or 2013_05) using the on-line version of the Mascot MS/MS Ion Search facility (Matrix Science, Ltd., http://www.matrixscience.com) [10]. Searching was performed with doubly, triply and quadruply charged ions with up to 2 missed cleavages, a peptide tolerance of 20 ppm, one variable modification, Carbamidomethyl-C, and an MS/MS tolerance of 0.05 Da. Spectra of dubious identifications were evaluated manually and omitted if they were of insufficient quality. Contaminating peptides and cross-contaminating peptides from previous samples including keratins, trypsin, BSA and casein were disregarded. At least one 'bold red' peptide with scores giving a less than 5% probability that the observed match was a random event was required in the search for protein hits. All peptides for these hits are reported. If the first search in the mouse fraction of the Swiss-Prot database did not give any hit an additional search in the whole database was performed.

Results

The staining pattern of the tissues used for the present analysis is shown in Figure 1. As expected GS1B4 stains the endothelial cells in the central vein as well as in the sinusoids of the wt liver whereas the α1,3-galactosyltransferase KO liver is unstained. In the pancreas the endothelial cells are unstained while the exocrine cells are stained in the mouse wt pancreas as well as in the KO pancreas. Figure 2 shows representative 2D-gels of wt and KO tissues from mouse liver and pancreas, respectively. Spots whose expression differed by at least 2-fold between the wt and the KO tissues are highlighted.

Liver

In total 22 spots were found to be differentially expressed in α1,3-galactosyltransferase gene KO mice relative to wt mice as shown in Figure 2 panel A. Eight spots were upregulated, marked with green numbers, and 14 spots where downregulated, illustrated by red numbers. All spots were excised and subjected to mass spectrometry identification as summarised in Table 1. Eighteen spots were successfully identified. Of these, 12 were found to contain one protein that accounts for the observed change in expression level. Interestingly, in the vast majority of cases we observed a major deviation of the observed molecular mass by 2D-PAGE with the theoretical molecular mass of the proteins, as illustrated in Figure 3. α-tubulin has a molecular mass around 50 kDa but spot 2514 migrated with a molecular mass below 40 kDa (Figure 3A). A map of the identified peptides showed that spot 2514 contained an N-terminal fragment of tubulin. A change in the concentration of a protein fragment may occur as a result of a change in the synthesis as well as a change in the degradation as it is the case with a full-length protein. Thus, it seems that for some proteins there is a substantial change in protein turnover in the KO liver.

Identified upregulated protein spots included adenosylhomocysteinease fragment (2001), serum albumin (3812), 2-hydroxyacyl-CoA lyase 1 (5813) and isocitrate dehydrogenase [NADP] cytoplasmic fragment (6414). Downregulated spots included heat shock cognate 70 kDa protein 3 fragment (0413), glutathione S-transferase P 1 (2203), betaine-homocysteine S methyltransferase 1 fragment (3209), aldehyd dehydrogenase fragment (3210), myosin-9 fragment (4206), electron transfer flavoprotein subunit α fragment (6102), arginase-1 fragment (7202) and urocanate hydratase (8803). Only one protein of all identified proteins in Table 1 contained a putative N-glycosylation site, namely carboxylesterase 3 (spot 6207).

Pancreas

In total 39 differentially expressed spots were detected by 2D-PAGE analysis (Figure 2, panel B). All spots were excised and resulted in identification of 17 spots as summarised in Table 2. All of these were found to contain a single identification and about a third of them contained fragments of the proteins. Thus, there is also a substantial change in protein turnover for some proteins in the KO pancreas tissue. Of upregulated proteins, the following eight were identified; albumin fragment (2602), tensin-3 fragment (7702), serotransferrin (7808), chymotrypsin-like elastase family member 1 (8305), NADH dehydrogenase [ubiquinone] flavoprotein 1 (8604), ATP synthase subunit alpha, mitochondrial (8615), aconitate hydratase, mitochondrial (8802) and 3-hydroxyacyl-CoA dehydrogenase type 2 (9303). Identified downregulated proteins were 78 kDa-glucose-regulated protein (1811), apolipoprotein A-1 (2315), glutathione S-transferase P1 (3215), 40S ribosomal protein S12 (5005), proteasome subunit β type-3 (5208), serum albumin fragment (5413), myeloperoxidase (5415), GTP-binding protein SAR1a (6202) and serum albumin fragment (6304). Of all identified proteins in Table 2, only four contained putative N-glycosylation sites, i.e., myeloperoxidase, serotransferrin, receptor-type lysinase-protein phosphatase α and chymotrypsin-like elastase family member 1.

Discussion

The α-Gal epitope may be stronger expressed in some organs than in other. As an example incubation with the α-galactose specific lectin GS1B4 stains the endothelial cells in the liver from wt mice [7] while there is no lectin reaction in the
endothelial cells in the wt mouse pancreas [11]. It also seems that heterozygote GalT-KO pigs display a significantly lower activity for α1,3-galactosyltransferase in some organs than in other [12]. In the present analysis, we confirmed presence of the α-Gal epitope on the endothelial cells of the wt liver as well as the absence on the endothelial cells in the pancreas (Figure 1). Liver cells do not stain in wt as well as in KO mice while cells of the exocrine pancreas are stained in wt as well as in KO mice.

Although hyperacute rejection can be prevented in transplantation with organs from α1,3-galactosyltransferase KO, the grafts are lost after some months with signs of thrombotic microangiopathy. This could be due to the action of non-Gal antibodies that aim at proteins or carbohydrates in the transplanted organs from the GalT-KO animal [13]. The presence of non-xenoreactive antigens might also explain why GS1 B4 stains the exocrine pancreatic cells of both mouse strains. GS1 B4 is widely used as a probe for α-D-Galactosyl end groups. It has thus been shown that the isoelectin detects not only the xenoreactive Galα1-3Galβ1-4GlcNAc carbohydrate but also the P blood group antigens P0: Galα1-4Galβ1-4Glcβ- and P1: Galα1-4Galβ1-4GlcNAcβ [14] and galabiose (Galα1-4Gal) which is an epithelial surface cell receptor for Shiga like toxins. GS1 B4 also exhibits broad specificity for blood group B variants and can react with type 1 [Galα1-3(Fucα1-2)Galβ1-3GlcNAc], type 2 [Galα1-3(Fucα1-2)Galβ1-4GlcNAc] and their difucosylated variants [15]. Although the xenoreactive α-Gal epitope seems to be a blood group B epitope that lacks the fucose residue it is important to realize that the two determinants are

Figure 1. GS1B4 staining of wt and α1,3-galactosyltransferase KO mouse tissues. The lectin stains the central vein (v) and the sinusoids are outlined in sections from the wt mouse liver (A) while there is no reaction in sections from the KO mouse liver (B). There is no staining of the blood vessels in pancreas from neither the wt mouse (C) nor from the KO mouse (D). The endocrine cells in islets of Langerhans (IL) are unstained while the exocrine cells in both the wt and the KO mouse show reaction. The green fluorescence reflects lectin staining and blue fluorescence reflects DAPI staining of the nuclei.

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biosynthesized by two distinct α-1,3galactosyltransferases and are thus genetically unrelated [16]. It is therefore a possibility that the staining of exocrine cells in both strains reflects the presence of a glycan with a α-D-Galactosyl end group other than the xenoreactive carbohydrate.

In non-primate mammals anti-Gal antibodies may bind, not only to endothelial cells but also to epithelial cells, mesenchymal cells and extracellular matrix glycoproteins [17]. Terminal Galα1-3Gal is thus present in both glycoprotein- and glycolipid bound forms [18] and Everett et al. [19] measured that on endothelial cells 13 percent of Gal α1-3Gal are present on glycolipid and 87 percent on glycoprotein. In future modifications of immunosuppressive therapy and strategies to induce tolerance, it would be important to reveal if targeted

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**Figure 2. 2D-PAGE images of wt and α1.3-galactosyltransferase KO mouse tissues.** Liver (A) and pancreas (B). Proteins which are at least 2-fold differentially expressed are marked with red (downregulated) and green (upregulated). Identified proteins are listed in Tables 1 and 2.

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### Table 1. Differentially expressed protein spots in mouse α1,3-galactosyltransferase KO liver.

| Spot | Ratio (KO/wt) | wt, Vol. ± SD (ppm) | KO, Vol. ± SD (ppm) | Peptides Identification | Mr (Da) | Mascot Protein Score | Protein name |
|------|--------------|---------------------|---------------------|-------------------------|---------|---------------------|--------------|
| 0413 | 0.31         | 745 ± 251           | 229 ± 98            | FELTGIPAPR              | HSP7C_MOUSE | 70827               | Heat shock cognate 70 kDa protein 3, fragment |
|      |              |                     |                     | SINPDEAVYGAAVQAIALSGDK   |          |                     |              |
| 0511 | 3.31         | 55 ± 20             | 181 ± 48            | ITITNDQNR               | GRP78_MOUSE | 72377               | 78 kDa glucose-regulated protein, fragment |
|      |              |                     |                     | VYGERPLTK               | PDIA1_MOUSE | 57023               | Protein disulfide-isomerase, fragment |
|      |              |                     |                     | VLGANFEEAVAFDEK         |          |                     |              |
| 2001 | 2.35         | 866 ± 232           | 2035 ± 482          | ALDIAEMPIGLMR           | SAHH_MOUSE | 47657               | Adenosylhomocysteinease, fragment |
|      |              |                     |                     | VYEGERPLTK              | PDIA1_MOUSE | 57023               | Protein disulfide-isomerase, fragment |
|      |              |                     |                     | PDIA1_MOUSE             |          |                     |              |
| 2203 | 0.20         | 765 ± 212           | 151 ± 177           | ALDIAEMPIGLMR           | SAHH_MOUSE | 372377              | Adenosylhomocysteinease, fragment |
|      |              |                     |                     | VYEGERPLTK              | PDIA1_MOUSE | 57023               | Protein disulfide-isomerase, fragment |
|      |              |                     |                     | PDIA1_MOUSE             |          |                     |              |
| 2514 | 2.73         | 344 ± 56            | 937 ± 365           | QLFHEPLLITQGK           | TBA1A_MOUSE | 50104               | Tubulin α-1A/1B/1C chain, fragment |
|      |              |                     |                     | AVFDLEPTVIDEVR          | TBA1B_MOUSE | 23594               |                |
|      |              |                     |                     | NLDIERPTYTNLNR          | TBA1C_MOUSE | 164514              |                |
|      |              |                     |                     | LGEYGFQNAILVR           |          |                     |              |
| 3113 | 0.31         | 1526 ± 441          | 471 ± 228           | TAHIVLEDGTK             | CPSM_MOUSE | 164514              | Carbamoyl-phosphate synthase [ammonia], mitochondrial, fragment |
|      |              |                     |                     | EKVDDLFLGK              | ETFB_MOUSE | 27606               | Electron transfer flavoprotein subunit β, fragment |
|      |              |                     |                     | GSHVEPQKAKAESLGPOVAR    |          |                     |              |
| 3209 | 0.14         | 704 ± 198           | 97 ± 59             | VNEAACDIAR              | BHMT1_MOUSE | 44992               | Betaine–homocysteine S methyltransferase 1, fragment |
| 3210 | 0.26         | 481 ± 99            | 126 ± 123           | VAEOQTLTALYVANIJK       | ALDH2_MOUSE | 56502               | Aldehyde dehydrogenase, mitochondrial, fragment |
|      |              |                     |                     | KYTEATEK                | ALBU_MOUSE | 68648               | Serum albumin, fragment |
|      |              |                     |                     | LCTVHHRK                |          |                     |              |
| 5813 | 0.37         | 594 ± 118           | 218 ± 173           | NLPIYSEEEMEK            | MYH9_MOUSE | 226233              | Myosin-9, fragment |
| 6102 | 0.31         | 1613 ± 517          | 500 ± 285           | LLYDLADQLHAAGASR        | ETFA_MOUSE | 34988               | Electron transfer flavoprotein subunit α, mitochondrial, fragment |
| 6207 | 0.34         | 910 ± 258           | 310 ± 94            | IGASTQAAQR              | CES3_MOUSE | 61749               | Carboxylesterase 3, fragment |
| 6311 | 6.34         | 390 ± 494           | 2475 ± 1042         | TIILYDTNLDPVSAK         | HKH_MOUSE | 32370               | Ketohexokinase |
|      |              |                     |                     | LALLTITGTAEMTKK         | NQO2_MOUSE | 26231               | Riboflavin:uridine diphosphate oxidoreductase [quinone] |
|      |              |                     |                     | TAHIVLEDGTK             | CPSM_MOUSE | 164514              | Carbamoyl-phosphate synthase [ammonia], mitochondrial, fragment |
|      |              |                     |                     | EKVDDLFLGK              | ETFB_MOUSE | 27606               | Electron transfer flavoprotein subunit β, fragment |
|      |              |                     |                     | GSHVEPQKAKAESLGPOVAR    |          |                     |              |
| 6414 | 4.46         | 244 ± 68            | 1089 ± 498          | HAYGDOYR                | IDHC_MOUSE | 46644               | Isoctamyl dehydrogenase [NADP] cytoplasmic, fragment |
|      |              |                     |                     | LDNNTLEFLSFAK           |          |                     |              |
disruption of the α1,3-galactosyltransferase gene also affects
the expression of other proteins in the genetically modified
animals. Some evidence for this hypothesis is reported in the
literature: The content of sialic acid is altered in the GalT-KO
organisms and Park et al. [12] noticed an increase of Neu5Gc
content in heart, lung, liver and kidney from heterozygote GalT-
KO pigs. Diswall et al. [13] found increased levels of uncapped
LacNac precursor and fucosylated H type 2 determinants in

Table 1 (continued).

| Spot | Ratio | wt. Vol. ± SD (ppm) | KO, Vol. ± SD (ppm) | Peptides | Identification | Mascot Protein Score | Protein name |
|------|-------|---------------------|--------------------|----------|---------------|---------------------|--------------|
| 6901 | 2.92  | 41 ± 11             | 119 ± 34           | N.I.     |               |                     |              |
| 7104 | 0.28  | 1343 ± 337          | 375 ± 344          | DHGDLAFVDVPNDOSSQVK / IDPSAPLDK | ARG1_MOUSE / 34786 / 71 | Arginase-1, fragment |
| 7202 | 0.13  | 1033 ± 405          | 132 ± 121          | VMEETFSYLLGR | ARGI_MOUSE | 34786 | 66 | Arginase-1, fragment |
| 8201 | 0.26  | 1671 ± 109          | 431 ± 378          | N.I.     |               |                     |              |
| 8803 | 0.46  | 498 ± 40            | 228 ± 150          | VAIAVAINQAIASGK | HUTU_MOUSE | 74543 | 82 | Urocanate hydratase |

Searches were performed in the Swiss-Prot mouse database.
* N.I.: not identified.
doi: 10.1371/journal.pone.0080600.t001

Figure 3. Spot No. 2514 is a fragment of α-tubulin. A) Spot 2514 migrates with a molecular mass below 40 kDa. The identified peptides from the spot are distributed in the N-terminal of α-tubulin and spot 2514 thus corresponds to a fragment of α-tubulin, since α-tubulin possesses a molecular mass around 50 kDa.
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Figure 3.


| Spot | Ratio (KO/ wt, Vol ± SD) (ppm) | KO, Vol ± SD (ppm) | Peptides | Mascot Identification | Mr (Da) | Protein Score | Protein name |
|------|-------------------------------|-------------------|----------|-----------------------|---------|---------------|--------------|
| 0204 | 0.18 1527 ± 41                | 282 ± 217         | N.I.*    |                       |         |               |              |
| 0406 | 0.28 216 ± 61                 | 60 ± 48           | N.I.     |                       |         |               |              |
| 1811 | 0.15 926 ± 261                | 138 ± 70          | ITITNDQNR| GRP78_MOUSE 72377     | 72377   | 244           | 78 kDa glucose-regulated protein |
|      |                               |                   |          |                       |         |               |              |
| 0406 | 0.28 216 ± 61                 | 60 ± 48           | N.I.     |                       |         |               |              |
| 1811 | 0.15 926 ± 261                | 138 ± 70          | ITITNDQNR| GRP78_MOUSE 72377     | 72377   | 244           | 78 kDa glucose-regulated protein |
|      |                               |                   |          |                       |         |               |              |
| 2303 | 0.14 420 ± 199                | 59 ± 67           | N.I.     |                       |         |               |              |
| 2313 | 3.12 1032 ± 198               | 3221 ± 1189       | N.I.     |                       |         |               |              |
| 2315 | 0.16 1030 ± 353               | 282 ± 217         | N.I.     |                       |         |               |              |
| 2602 | 4.88 242 ± 140                | 1182 ± 504        | LVLYLGLDNAGK| RS12_BOVIN 14505     | 14505   | 97            | 40S ribosomal protein S12 |
| 3215 | 0.33 531 ± 80                 | 72 ± 48           | N.I.     |                       |         |               |              |
| 5005**| 0.20 1120 ± 485               | 228 ± 88          | LVEALCAEHQNLK| RS12_BOVIN 14505     | 14505   | 97            | 40S ribosomal protein S12 |
| 5101 | 0.18 493 ± 168                | 89 ± 45           | N.I.     |                       |         |               |              |
| 5205 | 0.14 531 ± 80                 | 72 ± 48           | N.I.     |                       |         |               |              |
| 5208 | 0.32 791 ± 277                | 254 ± 57          | FQPYYTEPVIAGLDPK| PSB3_MOUSE 22949    | 22949   | 43            | Proteasome subunit β type-3 |
| 5409 | 0.10 742 ± 293                | 74 ± 112          | N.I.     |                       |         |               |              |
| 5413 | 0.23 448 ± 103                | 104 ± 64          | LSQTPNADFAEITK| ALBU_MOUSE 68648     | 68648   | 48            | Serum albumin, fragment |
| 5415 | 0.12 1319 ± 488               | 160 ± 64          | TITGHCMNR| PERM_MOUSE 81130      | 81130   | 25            | Myeloperoxidase, fragment |
| 6002 | 0.27 1336 ± 400               | 359 ± 167         | N.I.     |                       |         |               |              |
| 6022**| 0.25 1960 ± 152               | 495 ± 158         | LVFLGLDNAGK| SAR1A_BOVIN 22395     | 22395   | 66            | GTP-binding protein SAR1a |
| 6203 | 0.31 527 ± 163                | 164 ± 20          | N.I.     |                       |         |               |              |
| 6304 | 0.19 1797 ± 817               | 341 ± 115         | KYEATELEK| ALBU_MOUSE 68648      | 68648   | 344           | Serum albumin, fragment |
| 6311 | 0.25 774 ± 205                | 193 ± 160         | N.I.     |                       |         |               |              |
| 6501 | 0.18 1558 ± 347               | 273 ± 185         | N.I.     |                       |         |               |              |
| 6701 | 7.43 622 ± 776                | 4621 ± 1848       | N.I.     |                       |         |               |              |
| 7702 | 4.88 198 ± 207                | 969 ± 366         | FPDYGKIELVFSATPEK| TENS3_MOUSE 155491  | 155491  | 36            | Tensin-3, fragment |
| 7805 | 3.23 109 ± 45                 | 351 ± 22          | N.I.     |                       |         |               |              |
| 7808 | 3.25 181 ± 185                | 586 ± 139         | GTDFQNLQLEGK| TRFE_MOUSE 76674      | 76674   | 55            | Serotransferrin |
| 7821 | 3.15 227 ± 32                 | 717 ± 131         | LYGHNAYTAR|                       |         |               |              |

Protein Expression in α-Gal Transferase KO Mice

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GalT-KO pig tissues. It is also reported that xenotransplantation may result in formation of antibodies directed towards a series of stress response and inflammation related proteins [20]. To evaluate whether knockout of the α1,3-galactosyltransferase gene affects the expression of other proteins, we used a proteomic approach to analyze two different organs, liver and pancreas from wt as well as KO mice. These organs vary with respect to the expression of the α-Gal epitope, as it is present on the endothelial cells in the liver while absent on the endothelial cells in the pancreas. Indeed, we found several proteins as well as fragments in both organs with changed expression levels. Thus, it seems that protein turnover for some proteins is greatly influenced in the KO mice. The reason for these changes is unknown at present. Only few of the identified proteins contain N-glycosylation sites so it is unlikely that the presence or absence of the α-Gal epitope per se do play any role in the expression changes seen of proteins as well as their fragments.

### Conclusion

We have analysed two different tissues of α1,3-galactosyltransferase KO mice and revealed that deletion of this gene that directly affects the expression of the α-Gal epitope affects a number of proteins with a wide variety of functions. Thus, it seems that protein turnover, i.e., synthesis and/or degradation, for some proteins is greatly influenced in tissues of the KO mice.

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### Author Contributions

Conceived and designed the experiments: LTU ML SK BH. Performed the experiments: LTU ML SK BH. Analyzed the data: LTU ML SK HV BH. Contributed reagents/materials/analysis tools: SK HV BH. Wrote the manuscript: LTU SK HV BH.

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