1 Glucose Transporter Expression and Regulation Following a Fast 2 in the Ruby-throated Hummingbird, Archilochus colubris. Raafay S. Ali^{1, 2}, Morag F. Dick², Saad Muhammad^{1, 2}, Dylan Sarver³, G. William Wong³, and 3 Kenneth C. Welch Jr. 1,2 4 ¹ Cell and Systems Biology, University of Toronto, 25 Harbord St, Toronto, ON, Canada M5S 5 6 3G5 7 ² Department of Biological Sciences, University of Toronto Scarborough Campus, 1265 Military 8 Trail, Toronto, ON, Canada, M1C 1A4 ³ Department of Physiology, Johns Hopkins School University School of Medicine, 725 North 9 10 Wolfe Street Physiology 202, Baltimore, MD, United States of America, 21205 11 12 Corresponding author email: kwelch@utsc.utoronto.ca 13 Keywords: hummingbird, glucose transporter, plasma membrane, glucose, fructose 14 Summary statement: Hummingbird ingest nectar rich in glucose and fructose. When fasted, 15 tissue capacity for circulating glucose import declines while remaining elevated for fructose. 16 This may underlie maintenance of high blood glucose and rapid depletion of blood fructose.

Abstract

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Hummingbirds subsist almost exclusively on nectar sugar and face extreme challenges blood sugar regulation. Transmembrane sugar transport is mediated by facilitative glucose transporters (GLUTs) and the capacity for sugar transport is dependent on both the activity of GLUTs and their localisation to the plasma membrane (PM). In this study, we determined the relative protein abundance in whole-tissue (WT) homogenates and PM fractions via immunoblot using custom antibodies for GLUT1, GLUT2, GLUT3, and GLUT5 in flight muscle, heart, and, liver of ruby-throated hummingbirds (Archilochus colubris). GLUTs examined were detected in nearly all tissues tested. Hepatic GLUT1 was minimally present in WT homogenates and absent in PM fractions. GLUT5 was expressed in hummingbird flight muscles at levels comparable to that of their liver, consistent with the hypothesised uniquely high fructose-uptake and oxidation capacity of this tissue. To assess GLUT regulation, we fed ruby-throated hummingbirds 1M sucrose ad libitum for 24 hours followed by either 1 hour of fasting or continued ad libitum feeding until sampling. We measured relative GLUT abundance and concentrations of circulating sugars. Blood fructose concentration in fasted hummingbirds declined from ~5mM to ~0.18mM, while fructose-transporting PM GLUT2 and PM GLUT5 did not change in abundance. Blood glucose concentrations remained elevated in both fed and fasted hummingbirds, at ~30mM, while glucose-transporting PM GLUT1 and PM GLUT3 in the flight muscle and liver, respectively, declined in fasted birds. Our results suggest that glucose uptake capacity is dynamically reduced in response to fasting, allowing for maintenance of elevated blood glucose levels, while fructose uptake capacity remains constitutively elevated promoting depletion of blood total fructose within the first hour of a fast.

39 List of Abbreviations

- **AIC** Akaike Information Criterion
- **AICc** Akaike Information Criterion for small sample sizes
- **ANOVA** Analysis of Variance
- **APS** Ammonium Persulfate
- **cDNA** Complementary Deoxyribonucleic Acid
- **CO**₂ Carbon Dioxide
- **DTT** Dithiothreitol
- f_{exo} Proportion of expired CO₂ fuelled by oxidation of exogenous sugar
- **GAPDH** Glyceraldehyde-3-Phosphate Dehydrogenase
- **GLUT** Glucose Transporter
- **HEK293T** Homo sapiens Embryonic Kidney cell line with Mutant SV40 large T antigen
- **HRP** Horseradish Peroxidase
- 52 LC MRM/MS Liquid Chromatography Multiple Reaction Monitoring Mass
- 53 Spectrometry
- 54 LMM Linear Mixed-effects Model
- **mM** Millimolar
- 56 mRNA Messenger Ribonucleic Acid
- **MW** Molecular Weight
- 58 NCBI National Center for Biotechnology Information
- **NP-40** Nonidet P-40
- **PBST** Phosphate Buffered Saline with Tween 20
- **PM** Plasma Membrane
- **PVDF** Polyvinylidene Fluoride
- **QQ plot** Quantile-quantile plot
- **RIPA** Radioimmunoprecipitation Assay
- **SDS** Sodium Dodecyl Sulfate

- 66 SDS PAGE Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis
- 67 **TEMED** Tetramethylethylenediamine
- 68 **TMIC** The Metabolomics Innovation Centre
- 69 UTSC University of Toronto Scarborough Campus
- 70 WT Whole Tissue

Introduction

Hummingbirds primarily subsist on a diet of floral nectar high in sucrose, glucose, and fructose (del Rio et al., 1992). They are capable of oxidising glucose, fructose, or both, to power their characteristic hovering behaviour (Chen and Welch, 2014). When blood sugar concentrations are elevated, hummingbirds rely exclusively on these exogenous sugars to fuel nearly all the metabolic needs of their active cells (Welch et al., 2018). As such, they exhibit remarkable adaptations that enhance both the capacity for immediate rapid uptake and metabolism and the long-term storage of these sugars (Price et al., 2015; Welch et al., 2018). When possible, circulating sugars are incorporated into hummingbirds' fat stores through denovo lipogenesis by their liver (Suarez et al., 1988). As hummingbirds enter periods of hypoglycaemia, such as sleeping or fasted states, the entirety of their metabolic fuel source switches from circulating sugars to triglycerides derived from these fatty-acid stores (Eberts et al., 2019; Suarez et al., 1990). This switch is rapid, and a transition back to sugar metabolism occurs within a few minutes of sugar ingestion (Suarez and Welch, 2017). Furthermore, the switch from reliance on lipid oxidation to carbohydrate oxidation is nearly complete, such that mixed fuel-use does not occur for very long in hummingbirds with access to sufficient floral nectar (Welch et al., 2018).

Hummingbird digestive physiology facilitates rapid sugar transport across the intestinal lumen and into circulation (Karasov, 2017). A high cardiac output and capillary-to-muscle-fibre ratio ensures high transport capacity of sugars to the site of active cells (Mathieu-Costello et al., 1992; Suarez, 1992). Sugars are then facilitatively imported across the plasma membrane (PM) of active cells (Suarez and Welch, 2011). Here, *in-vitro* studies of hummingbird muscle cells have demonstrated that the phosphorylation capacity of cytosolic kinases for glucose appears sufficient in providing energy for sustained hovering, although this may not be true for fructose (Myrka and Welch, 2018). As both delivery to and phosphorylation of glucose within muscles operate at rates near the theoretical maximum in vertebrates (Suarez et al., 1988; Suarez and Welch, 2017) it is likely that regulation at the site of import itself exerts a great deal of control over the flux through the entirety of the sugar oxidation cascade. Along with delivery and phosphorylation, the sugar import step is a rate-limiting process in the paradigm outlined by Wasserman et al. (2011) and is nearly entirely dependent on the presence and distribution of

active glucose transporters (GLUTs) (Wasserman, 2009). These proteins are a family of transmembrane solute transporters (Mueckler and Thorens, 2013).

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Studies of mammalian GLUTs demonstrate that their expression in the PM is regulated by a variety of intra- and extracellular factors, including blood sugar and insulin concentrations, exercise, and stress (Egert et al., 1999; Guma et al., 1995; Yang and Holman, 1993). The expression and functional distribution and regulation of hummingbird GLUTs, however, remains relatively unknown. Studies on GLUT isoforms of the closest relatively well-examined avian species, the chicken (Gallus gallus domesticus), are fragmented and the distribution of avian GLUT isoforms is not fully understood (Byers et al., 2018; Suarez and Welch, 2011; Sweazea and Braun, 2006). It is known that chicken GLUT1 and GLUT3 share sequence homologies of ~80% and ~70%, respectively, with human GLUTs, but other isoforms such as GLUT2 and GLUT5 only share ~65% and ~64% sequence homology (calculated via NCBI BLAST (Boratyn et al., 2012), summarised in Table S6). It is also clear that they are regulated very differently in each class (Wagstaff and White, 1995; Yamada et al., 1983). Despite this, the literature on mammalian GLUTs provides a useful foundation for understanding the affinities and ligandspecificity of avian, including hummingbird, GLUTs. In mammals, GLUT3, followed by GLUT1, show the highest affinities for glucose; $K_m \approx 1.5$ mM (Thorens and Mueckler, 2010) and $K_m \approx 3\text{-5mM}$ (Zhao and Keating, 2007), respectively. GLUT5 transports fructose ($K_m \approx 11\text{-}$ 12mM; Douard and Ferraris, 2008), and is largely found in mammalian enteric and renal tissue (Douard and Ferraris, 2008), although some presence in hepatic tissue has also been noted (Godoy et al., 2006; Zhao et al., 1993). GLUT2, uniquely, shows affinity for both sugars. While its affinity for glucose and fructose ($K_m \approx 17 \text{mM}$ and $K_m \approx 76 \text{mM}$, respectively; Zhao and Keating, 2007) is relatively low compared to other isoforms, it plays a dominant role in hepatic sugar transport (Wood and Trayhurn, 2003). Importantly, it is only when GLUT isoforms are expressed and active in the PM that transmembrane sugar transport can occur from the blood into the active cell (Guma et al., 1995; Wasserman, 2009; Yamada et al., 1983). In mammals, GLUT4 translocation to the PM by insulin-stimulation following feeding is known to recruit other GLUT isoforms to the PM as well, increasing the sugar import rate into active cells (Guma et al., 1995). Hummingbirds (Welch et al., 2013), much like chickens (Byers et al., 2018), do not express transcript or protein of the insulin-sensitive GLUT4 isoform. Chicken insulin levels do not significantly change with

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dietary status (Simon et al., 2011), and this is presumably also true in hummingbirds. Further, circulating insulin does not significantly increase sugar import in chicken muscles (Chen, 1945), though it may in the liver (Dupont, 2009; Zhang et al., 2013). Lastly, and unlike mammals, hummingbirds have limited intramuscular glycogen stores (Suarez et al., 1990), and therefore rely on newly imported sugars from circulation for carbohydrate oxidation (Welch et al., 2018). Despite missing critical elements of the insulin-GLUT4 pathway, fed hummingbirds utilise circulating sugars, when available, at very high rates to meet their metabolic demands (Suarez and Welch, 2017). Previous studies have confirmed the presence of GLUT1 and GLUT5 transcript in nearly all hummingbird tissue examined (Myrka and Welch, 2018). Immunohistochemistry of hummingbird myocytes using a commercial antibody for GLUT1 have also shown GLUT1 localisation to the PM (Welch et al., 2013), though, the results were not definitive. In this study, using custom antibodies for the different isoforms of hummingbird GLUTs, we sought to identify the tissue-specific protein distribution and to quantify the abundance in the PM, of GLUT1, GLUT2, GLUT3, and GLUT5. We predicted GLUT1 would be detected in hummingbird flight muscle, cardiac, and liver tissue, in accordance with its ubiquitous presence in mammalian tissue (Mueckler and Thorens, 2013), as well as its previous detection in hummingbird myocytes (Welch et al., 2013). As GLUT2 plays a stronger role in enteric (Karasov, 2017) and hepatic (Mueckler and Thorens, 2013) sugar transport, we predicted that its abundance would be limited in muscles and more predominantly found in the liver. In mammals, GLUT3 is observed in close association with GLUT1 (Simpson et al., 2008) and may function as a replacement for GLUT4 in certain muscle developmental stages (Klip et al., 1996). We expected to detect GLUT3 in tissues also expressing GLUT1. We also expected to find GLUT5 in both the liver and muscles, as hummingbird muscles are capable of supporting hovering flight on fructose-only meals (Chen and Welch, 2014). To further characterise the regulatory aspects of hummingbird GLUTs, we compared the abundance of GLUT1, GLUT2, GLUT3, and GLUT5 in the PM of fed and fasted hummingbirds. We also measured levels of circulating glucose and fructose in these birds. Based on previous measurements of hummingbird blood glucose (Beuchat and Chong, 1998), we expected to see high levels of glucose (~40mM) in the fed condition and lower levels in the fasted (~15mM). Previous measurements of hummingbird blood fructose have not been made. However, similar to that of frugivorous bats (Keegan, 1977),

we predicted blood fructose concentrations in fed hummingbirds to be ~5-10mM in fed and ~0mM in fasted hummingbirds. Given the rapid switching between glucose or fructose oxidation and oxidation of lipid stores in foraging versus fasting hummingbirds, we expected a greater abundance of PM GLUT1, PM GLUT3, and PM GLUT5 in flight muscle and liver of fasted hummingbirds. Finally, we expected little difference in between GLUT2 abundance in the PM of tissue from fed and fasted hummingbirds.

Materials and Methods
 170 1.1 Animal Use and Ethics Statement.

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1.1 Animal Use and Ethics Statement. This study was approved and performed adhering to the requirements of the University of Toronto Laboratory Animal Care Committee and the Canadian Council on Animal Care. Twelve adult male ruby-throated hummingbirds (Archilochus colubris) were captured in the early summer at the University of Toronto Scarborough (UTSC) using modified box traps and housed individually in Eurocages (Corners Ltd, Kalamazoo, MI, USA) in the UTSC vivarium. They were provided with perches and fed on a maintenance diet of NEKTON-Nectar-Plus (Keltern, Germany). All hummingbirds were provided with a sucrose solution for 24 hours prior to the experiment. Birds were divided into a fed group (n = 6), which was provided with ad-libitum 1M sucrose solution up to sampling, beginning at 10AM, and a fasted group (n = 6), which was deprived of any food for a 1 hour duration prior to the 10AM sample collection. To minimize interindividual variation in activity level and energy expenditure, birds from both treatment groups were held in small glass jars, perched on wooden dowels, in which the were constrained from flying, for the duration of the 1 hour fast. Respirometry measurements by Chen and Welch (2014) have previously shown that this is sufficient time for the fasted hummingbirds to shift from fuelling metabolism with circulating sugars to fats. Fed hummingbirds will continue to exclusively metabolise sugars. Hummingbirds were then anaesthetised with isofluorane inhalation and euthanized via decapitation. Immediately after decapitation, blood was sampled from the carotid artery using heparinized capillary tubes and spun at 3800 g for 10 minutes at room temperature and the plasma stored at -80 °C. Flight muscle (the pectoralis and supracoracoideus muscles), heart, and liver were extracted and frozen with isopentane cooled with liquid nitrogen. All tissues were stored at -80°C. 1.2 Circulating Sugar and Metabolite Analysis.

- Plasma samples were sent to the Metabolomics Innovation Centre (TMIC) at the University of
- 195 Victoria (Victoria, British Columbia, Canada) to be analyzed via service 45 (absolute
- 196 quantitation of central carbon metabolism metabolites and fructose) found here:
- 197 https://www.metabolomicscentre.ca/service/45. Quantitation of glucose and fructose

- 199 chromatography multiple reaction monitoring/mass spectrometry (LC-MRM/MS) following a
- protocol outlined by Han et al. (2016). Quantitation of central carbon metabolites (organic acids;
- lactate and pyruvate) was done via the protocol outlined by Han et al. (2013).
- 202 1.3 Antibody Design, Production, and Isoform Specificity
- 203 Anti-rabbit polyclonal antibodies for GLUT isoforms were designed in conjunction to minimise
- 204 cross-reactivity using the services of Pacific Immunology (Ramona, CA, USA). Epitope design
- was accomplished using messenger RNA (mRNA) sequences for ruby-throated hummingbird
- 206 GLUT isoforms 1, 2, 3, and 5 that were obtained from the hummingbird liver transcriptome
- 207 (Workman et al., 2018). The concentration of the affinity-purified antibody samples was
- 208 assessed using ELISA by Pacific Immunology (ab-GLUT1 $\approx 1.1 \text{ mg} \cdot \text{ml}^{-1}$, ab-GLUT2 ≈ 5.7
- 209 mg·ml⁻¹, ab-GLUT3 ≈ 2.6 mg·ml⁻¹, ab-GLUT5 ≈ 1.0 mg·ml⁻¹). The final experimental dilutions
- were determined empirically through preliminary experiments and are provided below.
- 211 1.3.1 Generation of mammalian expression plasmids encoding A. colubris GLUT1, GLUT2,
- GLUT3, and GLUT5.

- The cDNA encoding A. colubris GLUT1 (NCBI Accession Number MT472837), GLUT2
- 214 (MT472838), GLUT3 (MT472839), and GLUT5 (MT472840) were synthesized by GenScript
- based on the full-length mRNA sequences derived from our previously published RNA
- sequencing data (Workman et al., 2018). The V5 epitope tag (encoding the peptide
- 217 "GKPIPNPLLGLDST") was inserted at the 3' end of each cDNA immediately after the last
- 218 coding amino acid. All epitope-tagged cDNA sequences were cloned into the EcoRI restriction
- site of the mammalian expression vector, pCDNA3.1 (+) (Invitrogen). All expression plasmids
- were verified by DNA sequencing.
- 221 1.3.2 Specificity immunoblots
- SDS-PAGE was run on cell lysates of HEK293T cells transiently transfected, using
- 223 lipofectamine 2000 (Invitrogen), with hummingbird GLUT1, GLUT2, GLUT3, or GLUT5
- 224 (acGLUT1, GLUT2, GLUT3, or GLUT5) expression vectors; all containing a V5 tag. Cell
- 225 lysates produced using RIPA buffer (50 mM Tris-HCl, pH 7.4; 150 mM NaCl; 1 mM EDTA;
- 226 1%Triton X100; 0.25% deoxycholate) supplemented with protease and a phosphatase inhibitor
- 227 cocktail (MilliporeSigma, Burlington, Massachusetts, USA and Roche, Basel, Switzerland;

respectively). Each lysate was confirmed to express the appropriate recombinant protein at the

expected size using an anti-V5 antibody produced in rabbit (Sigma V8137). Isoform specificity

- was tested via immunoblotting all cell lysates (empty vector control, acGLUT1, GLUT2,
- GLUT3, and GLUT5) with each novel acGLUT antibody and observing GLUT protein signal
- overlap; none was observed. Briefly, each immunoblot lane represents a cell lysate produced
- from an entire well of a 6-well cell-culture dish (Thermo Scientific, Nunc). Lyates were diluted
- with SDS loading dye (final concentration: 50 mM Tris-HCl, pH 7.4, 2% SDS, 6% glycerol, 1%
- 235 2-ME, and 0.01% bromophenol blue) and not boiled. An equal volume of each lysate was added
- to the designated lane on a 12% polyacrylamide gel (Bio-Rad, Hercules, CA, USA) and
- separated by electrophoresis. The BioRad Trans-Blot Turbo semidry system was used to transfer
- protein onto PVDF membranes. Blots were blocked in 5% non-fat milk in Phosphate buffered
- saline with Tween 20 (PBST) and exposed to primary antibodies overnight at 4°C. After
- washing, blots were exposed to HRP-conjugated secondary antibody (Anti-Rabbit IgG, 7074S,
- Cell Signaling Technology, Danvers, MA, USA) for 1 h at room temperature and developed in
- ECL (Amersham ECL Select; GE Healthcare, Chicago, IL, USA). Bands were visualized with
- 243 the MultiImage III FluorChem Q (Alpha Innotech, San Leandro, CA, USA). Primary antibodies
- were diluted 1:1000 in PBST + 0.02% sodium azide. The secondary antibody was diluted
- 1:10,000 in PBST + 0.02% sodium azide.
- 246 1.4 Tissue Sample Preparation.

- 247 Each sample underwent either a plasma membrane fractionation protocol established by
- 248 (Yamamoto et al., 2016) and slightly modified by replacing NP-40 (nonidet P-40) with Triton X-
- 249 100 (Sigma-Aldrich, St. Louis, Missouri) to obtain only PM-proteins, or a
- 250 radioimmunoprecipitation assay buffer (RIPA) homogenisation (part of the same protocol) to
- obtain all proteins contained in a whole-cell. Fractionation used different detergent
- concentrations (0.1%, 1%, 2%) in the homogenisation buffers to solubilise proteins and create
- 253 protein-detergent complexes depending on whether they are in the hydrophilic (cytosolic)
- domain or the hydrophobic (PM) domain.
- 255 1.3.3 Buffer composition.
- 256 Buffer A01 (0.5M DTT, ddH₂O, and 0.1% v/v Triton X-100), A1 (0.5M DTT, ddH₂O, and 1%
- 257 v/v Triton X-100), and 2× RIPA (20mM Tris-HCl, pH 8.0, 300mM NaCl, 2% v/v Triton X-100,

258 1% w/v sodium deoxycholate, 0.2% w/v sodium dodecyl sulfate (SDS), 1mM DTT) were

prepared. All reagents were cooled to 4°C before homogenisation and included Sigma P8340

protease inhibitor cocktail.

- 261 1.3.4 Homogenisation and plasma membrane fractionation.
- 262 20 mg of flight muscle, liver, or heart was cut on a cold aluminum block and immediately placed
- in an ice-bath. The tissue was minced in buffer A01 with scissors and homogenised using a
- VWR handheld pestle homogenizer (BELAF650000000) The homogenate was passed through a
- 265 21G needle three times to liberate nuclear and intracellular proteins. An aliquot of the
- 266 homogenate was left on ice for 60 minutes in 2× RIPA buffer. This whole-tissue RIPA-fraction
- 267 was then centrifuged at 12,000g for 20 minutes at 4°C, allowing proteins to be solubilised. The
- supernatant was collected and stored at -80°C as the whole-tissue (WT) homogenate. The
- remainder of the homogenate was centrifuged at 200g for 1 min at 4°C. The upper phase was set
- aside, and 90µL of buffer AO1 was added to the lower phase which was homogenised for 10s.
- The lower phase was centrifuged at 200g for 1 minute and added to the tube containing the upper
- 272 phase. The combined phases were centrifuged at 750g for 10 minutes. The supernatant consisting
- of non-PM proteins was removed. The remainder of the protein-detergent complexed pellet was
- 274 resuspended with and kept on ice for 60 minutes. After centrifugation at 12000g for 20 minutes,
- and the supernatant containing only PM-associated proteins was collected as the "plasma"
- 276 membrane fraction".
- 277 1.5 SDS-PAGE.
- 278 10% resolving and 4% stacking gels were cast using a 15-well comb and the AA-Hoefer Gel
- 279 Caster Apparatus (10%; 33% 30%-Acrylamide (37.1:1), 33% Separating gel buffer (1.5 M Tris
- 280 Cl, 0.4% SDS), 55% ddH₂O, 0.65% ammonium persulfate (APS), 5.5% TEMED), (4%; 13.4%
- 281 30%-Acrylamide, 9.3% Stacking gel buffer (0.5 M Tris Cl, 0.4% SDS), 33% ddH₂O, 0.06%
- APS, 3.3% TEMED). Samples were incubated in a 1:1 (w/v) ratio of 2× sample buffer (0.2M
- 283 DTT, BioRad Laemmli Sample Buffer #1610737) at room temperature for 20 minutes. The AA-
- Hoefer SE600 Vertical Gel Electrophoresis apparatus was set up with 6L running buffer (10%)
- BioRad 10× Tris/Glycine/SDS #1610732, 90% ddH₂O). The gel was run at 90V for 20 minutes
- and 110V for another 75 minutes with power supplied from an AA-Hoefer PS200HC Power
- 287 Unit.

288 1.4.1 Electroblot and immunoblot

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The SDS-PAGE gel was transferred to 0.45μm pore nitrocellulose (NC) membrane (GE Life

290 Sciences #10600003 Protran Premium 0.45 NC) using the AA-Hoefer TE22 Mighty Small

291 Transfer unit at 110V for 90 minutes with water cooling and immersion in an icebath. The

transfer buffer consisted of 192mM glycine, 24.8mM Tris, 0.00031% SDS, 20% methanol. To

293 normalise, a total-protein stain, SYPRO Ruby Red Blot (BioRad #1703127), was used and

imaged on a Bio-Rad PharosFX Molecular Imager (#1709460) using a 532nm laser and captured

with a 600-630nm band pass filter. The membranes were incubated with primary antibody

overnight at the following dilutions in PBST (phosphate-buffered saline, 0.1% Tween-20) buffer:

297 GLUT1 (1:250), GLUT2 (1:2000), GLUT3 (1:2000), GLUT5 (1:500). Membranes were then

incubated with anti-rabbit horseradish-peroxidase-conjugated secondary antibody (Cell

299 Signalling Technology #7074) at 1:1000 dilution with PBST. Finally, Pierce

300 Electrochemiluminescent Reagent (Pierce 32106) was used to fluoresce conjugates which were

imaged using a BioRad Chemidock XRS+ Gel Imager.

302 1.6 PM fraction purity

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To validate the separation of PM proteins from cytosolic proteins, commercially-available

control antibodies were used that were validated by the manufacturer for cross-reactivity in

305 chickens. Known PM-residing and cytosol-residing proteins targeted and their abundance was

306 used to assess the degree of PM fractionation in flight muscle, liver, and heart samples. The

membranes were incubated at 1:1000 dilution for 90 minutes at room temperature and included

antibodies for 1) E-cadherin (Cell Signalling Tech. 24E10), 2) Na⁺/K⁺ ATPase (Cell Signalling

Tech. 3010), 3) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (Cell Signalling Tech.

310 14C10), and 4) Fatty acid translocase (FAT) (Abgent AP2883c).

311 1.7 Western Blot Band Normalisation.

312 GLUT protein molecular weights were predicted using ExPASy (Gasteiger et al., 2005). Protein

quantitation was done with a Pierce 660nm assay. 5µg of sample protein was loaded into each

well of the polyacrylamide gel, in comparison with wells containing visible protein ladder

315 (Sigma 26616). The antibody staining intensity of each Western blot sample was normalised to

its corresponding total-protein stain intensity using BioRad ImageLab software. Background

317 subtraction was applied to the total protein stain in a lane-wise fashion, while no background

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subtraction was applied to the antibody staining intensity. Fluorescence intensity for the totalprotein stain was measured using 30% of the lane-width as per the recommendation of Gassmann et al. (2009). The antibody stain was measured using a fixed lane-width comprising of the entire lane. Normalised molecular weights were recorded. 1.8 Statistical Analysis. A Student's T-test was performed for the sugar and metabolite concentrations between fed and fasted hummingbirds. We evaluated variation in isoform intensity data for each GLUT by creating linear mixed-effects models (LMMs) in R statistical language (version 3.6.1, rproject.org) using the lme4 package (Bates et al., 2015) for GLUT isoform fluorescence intensity data. We compared relative GLUT 1, 2, 3, and 5 abundance among tissues, and between fed and fasted individuals using a fully factorial design. Assumptions of residual normality were checked through visual inspection of the quantile-quantile (Q-Q) plot, a frequency histogram, and the Shapiro-Wilk Normality Test. When necessary, model parameters were transformed by a chosen function (the details of which are presented in the Results section below) resulting in the greatest homoskedasticity and data was fitted using the following formula: Fluorescence Intensity \sim Treatment \times Tissue + Blot which outperformed more simplified models, as indicated by AICc (Akaike information criterion corrected for small sample sizes), the details of which are presented in Table S5. To account for the contribution of blot-to-blot variation, individual blots were treated as random effects (represented as *Blot* in the formula). Analysis of variance (ANOVA) was performed on the model parameters to determine the significance of any interactions. Post-hoc analysis was performed using the emmeans package (Lenth, 2019) within R software to determine group means and standard error. Pairwise comparison was performed to determine statistical significance of groups using the Tukey HSD method with the contrast function from the emmeans package. All data are presented as mean \pm standard error.

344 Results 345 2.1 Circulating Sugars and Metabolites of Fed and Fasted Hummingbirds 346 Overall, a significant difference was only observed for blood fructose concentrations ($t_{9.9} = -17.2$, 347 p = 0.001) which were higher in fed hummingbirds (5.34 ± 0.2 mM) compared to fasted (0.21 ± 348 0.1 mM). Glucose concentrations in fed hummingbirds (30.04 \pm 2.0 mM) remained similarly 349 elevated in fasted hummingbirds (29.67 \pm 1.5 mM). Lactate concentrations in fed individuals 350 $(4.31 \pm 1.3 \text{ mM})$ were slightly lower than in fasted $(6.35 \pm 0.9 \text{ mM})$ although this was not a 351 significant difference. Likewise, pyruvate concentrations in fed hummingbirds (0.21 ± 0.03 mM) 352 remained elevated in fasted hummingbirds (0.22 ± 0.01 mM). These results are summarised in 353 Figure 1. 354 2.2 Antibody Specificity and GLUT Detection 355 Antibodies showed a high degree of specificity for their isoform in immunoblots of HEK293 cell 356 lysates (Table S3). In hummingbird tissue, GLUT proteins were identified by band molecular 357 weights, and were, with one exception, present in both PM fractions and WT homogenates 358 following PM fractionation (Table S1). GLUT1, GLUT2, GLUT3, and GLUT5 were detected in 359 WT homogenates of flight muscle and heart tissue of ruby-throated hummingbirds, as well as in 360 PM fractions. GLUT1 in liver WT homogenates was minimally detected and was not detected at 361 all in liver PM fractions. GLUT1, GLUT2, and GLUT5 were detected at approximately their 362 expected molecular weights in all tissues. GLUT3 was detected at a size slightly larger than 363 predicted. 364 2.3 Relative GLUT Abundance 365 2.3.1 GLUT1 With regards to the WT homogenates, no significant differences were observed in the relative 366 367 abundance of GLUT1 among tissues ($F_{2,2,5} = 11.58$, p = 0.055) or the interaction of tissue and 368 treatment ($F_{2,13} = 0.262$, p = 0.773). While WT flight muscle, regardless of treatment, had a 369 similar GLUT1 abundance to WT heart, WT flight muscle had a significantly greater abundance 370 compared to WT liver in both fed (flight muscle / liver ratio: 4.75 ± 1.27 , $t_{3.02} = 4.54$, p = 0.040) and fasted (flight muscle / liver ratio: 5.76 ± 1.54 , $t_{3.02} = 4.28$, p = 0.046) treatments. These 371 372 results are summarised in Table 3 and Fig. 2A. The treatment itself, fasting, did have a

- significant effect ($F_{1,13} = 7.99$, p = 0.014) on WT GLUT1 abundance, however, multi-factor
- 374 multiple comparisons using the Tukey HSD method show that only flight muscle WT GLUT1
- abundance was significantly lower in fasted hummingbirds (fasted/fed ratio: 0.73 ± 0.09 ; $t_{13} =$
- 2.63, p = 0.021) (Table 1). While the effect of treatment was not significant as a whole for PM
- GLUT1 ($F_{1,13.02} = 3.74$, p = 0.075; Treatment), we did observe a significant effect of tissue ($F_{1,13.02} = 3.74$, p = 0.075; Treatment), we did observe a significant effect of tissue ($F_{1,13.02} = 3.74$, p = 0.075; Treatment),
- 378 $_{3.78} = 24$, p = 0.009) and the interaction of tissue and treatment ($F_{1, 13.02} = 17.03$, p = 0.012).
- These results are summarised in Table 4 and Fig. 2B. The relative abundance of PM GLUT1
- 380 was >2-fold higher in flight muscle compared to heart within the fed treatment (Fed flight
- 381 muscle / heart ratio: 4.87 ± 1.31 , $t_{4.68} = 5.89$, p = 0.009). Additionally, PM GLUT1 abundance
- was significantly lower in flight muscle of fasted hummingbirds (fasted/fed ratio: 0.61 ± 0.06 , t_{13}
- 383 = 4.66, p = 0.002) (Table 2).
- 384 2.3.2 GLUT2

- 385 Amongst WT homogenates, a significant effect of treatment was observed regarding WT
- 386 GLUT2 relative abundance ($F_{1,11} = 6.22$, p = 0.029). Multiple comparisons revealed that only
- 387 flight muscle had a significantly lower WT GLUT2 abundance in fasted hummingbirds
- (fasted/fed ratio: 0.54 ± 0.08 , $t_{14.5} = 2.63$, p = 0.019), while heart and liver tissue did not show a
- significant difference (Table 1 and Fig. 3A). Regardless of feeding or fasting treatment, no
- 390 significant difference was observed in WT GLUT2 relative abundance among tissues (Table 3).
- No significant difference in relative abundance was noted for tissue or the interaction of tissue
- and treatment for WT GLUT2. Further, no significant difference was observed among tissues,
- treatment, or the interaction of tissue and treatment for PM GLUT2 (Table 2, Table 4, and Fig.
- 394 3B).
- 395 2.3.3 GLUT3
- Fasting significantly affected the relative abundance of WT GLUT3 ($F_{1,11} = 17.08$, p = 0.002).
- 397 Multi-factor multiple comparisons with the Tukey HSD method revealed that both flight muscle
- 398 (fasted/fed ratio: 0.68 ± 0.09 , $t_{24.8} = 2.61$, p = 0.015) and liver (fasted/fed ratio: 0.58 ± 0.09 , $t_{24.8}$
- = 4.58, p = 0.0001) had significantly less WT GLUT3 in fasted humming birds, while no
- significant difference was observed in heart WT homogenates (Table 1 and Fig. 4A). No
- 401 significant difference was observed for relative WT GLUT3 abundance among tissues or the
- interaction of tissue and treatment. Regardless of treatment, WT GLUT3 abundance was similar

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among tissues with the exception of the liver having significantly greater relative WT GLUT3 abundance compared to heart in fed hummingbirds (fed liver / heart ratio: 2.46 ± 0.46 , $t_{3.5} = 5.83$, p = 0.014) (Table 3 and Fig. 4B). In PM fractions, a significant effect of the fasting treatment was observed on the relative PM GLUT3 abundance ($F_{1,16} = 13.13$, p = 0.002). No significant difference was observed among tissues (Table 4), however, the interaction of tissue and treatment was significant ($F_{2,16} = 6.46$, p = 0.009). Through multiple comparisons, it was observed that only liver PM GLUT3 relative abundance was significantly lower in fasted hummingbirds (fasted/fed ratio: 0.58 ± 0.14 , $t_{16} = 4.54$, p = 0.004) (Table 2). 2.3.4 GLUT5 No significant effect of tissue or treatment, or their interaction, were observed for the relative abundance of WT GLUT5. Regardless of treatment WT GLUT5 relative abundance did not differ significantly between tissues (Table 1, Table 3, Fig. 5A). PM GLUT5 did not show any significant effect with tissue, treatment, or their interaction. No significant effect was observed in any tissue with fasting treatment (Table 2, Fig. 5B). Regardless of feeding or fasting, no significant difference was observed in the relative PM GLUT5 abundance among tissues (Table 4).

Tables and Figures

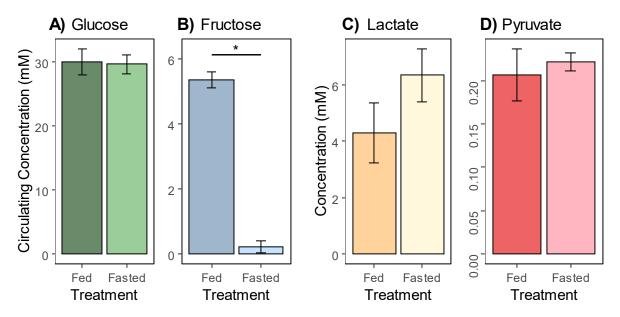
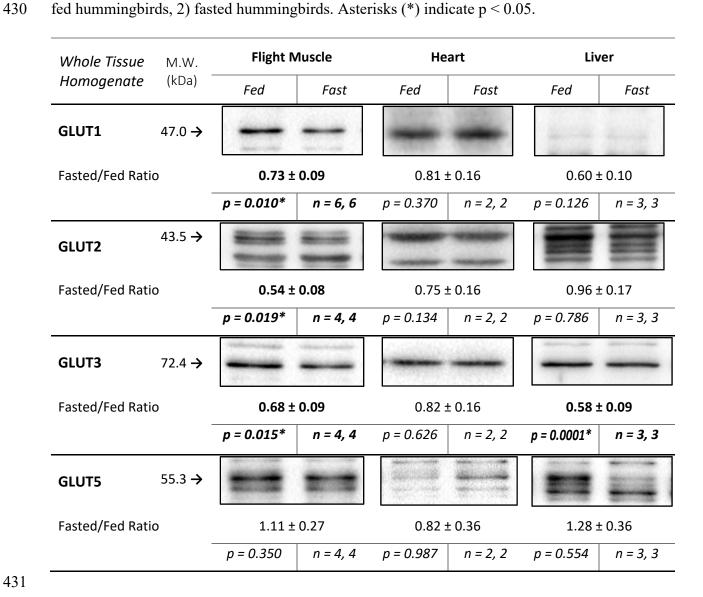


Figure 1: Mean concentrations (mM) \pm standard error of circulating sugars A) Glucose, B) Fructose from plasma samples and metabolites C) Lactate, D) Pyruvate from whole-tissue homogenates of fed (n = 6) and fasted (n = 5). Data is presented as mean concentration in millimoles \pm standard error. Asterisk (*) indicates p = 0.001.

Table 1: Relative WT abundance of GLUT1, GLUT2, GLUT3, and GLUT5 in flight muscle, heart, and liver of fed and fasted hummingbirds. Data and representative immunoblots are presented here for the whole tissue (WT) homogenates of hummingbird tissue. Fasted/fed ratios reflect the relative variation in GLUT protein abundance with fasting treatment. Observed molecular weights (M.W.) are reported. Sample sizes are given for the number of 1) fed hummingbirds, 2) fasted hummingbirds. Asterisks (*) indicate p < 0.05.



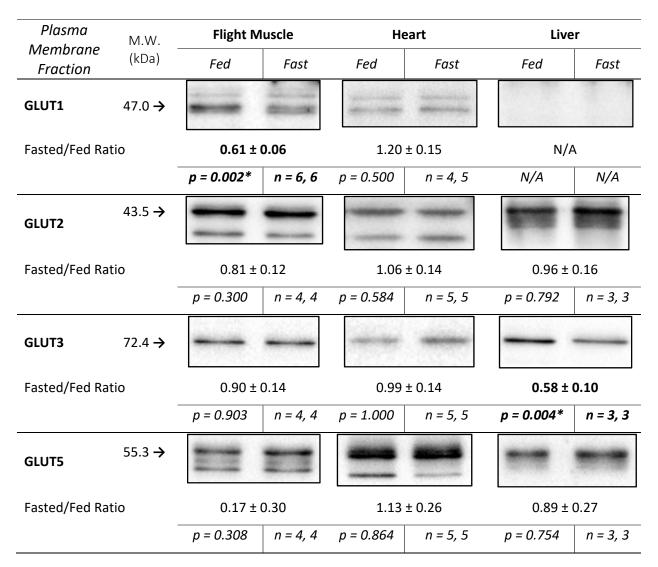
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Table 2: Relative PM abundance of GLUT1, GLUT2, GLUT3, and GLUT5 in flight muscle, heart, and liver of fed and fasted hummingbirds. Data and representative immunoblots are presented here for hummingbird tissue samples that underwent plasma membrane fractionation; only PM-residing GLUTs are presented. Fasted/fed ratios reflect the relative variation in GLUT protein abundance with fasting treatment. Observed molecular weights (M.W.) are reported. Sample sizes are given for the number of 1) fed hummingbirds, 2) fasted hummingbirds. Asterisks (*) indicate p < 0.05.



Whole Tissue	GLUT	Relative	p-value	Sample	Relative	p-value	Sample
Homogenate	Isoform	Fed Ratio		Size	Fasted Ratio		Size
Flight Muscle /	GLUT1	1.95 ± 0.54	0.082	6, 2	1.76 ± 0.49	0.120	6, 2
Heart	GLUT2	0.70 ± 0.35	0.486	4, 2	0.37 ± 0.18	0.399	4, 2
	GLUT3	1.59 ± 0.31	0.175	4, 2	1.32 ± 0.26	0.712	4, 2
	GLUT5	1.82 ± 1.37	0.911	4, 2	2.45 ± 1.97	0.887	4, 2
Flight Muscle /	GLUT1	4.75 ± 1.27	0.040*	6, 3	5.76 ± 1.54	0.046*	6, 3
Liver	GLUT2	0.65 ± 0.32	0.386	4, 3	0.37 ± 0.12	0.068	4, 3
	GLUT3	0.65 ± 0.11	0.086	4, 3	0.75 ± 0.13	0.429	4, 3
	GLUT5	0.59 ± 0.53	0.985	4, 3	0.52 ± 0.46	0.816	4, 3
Heart / Liver	GLUT1	2.44 ± 0.83	0.147	2, 3	3.28 ± 1.11	0.075	2, 3
	GLUT2	0.93 ± 0.52	0.992	2, 3	0.73 ± 0.41	0.699	2, 3
	GLUT3	0.41 ± 0.08	0.014*	2, 3	0.57 ± 0.11	0.185	2, 3
	GLUT5	0.33 ± 0.29	0.697	2, 3	0.21 ± 0.20	0.350	2, 3

Table 4: Relative abundance of GLUT1, GLUT2, GLUT3, and GLUT5 among PM fractions of flight muscle, heart, and liver of fed and fasted hummingbirds. Values represent the relative abundance of GLUT proteins from isolated plasma membrane samples (fractionation efficiency approx. $92.1 \pm 0.5\%$; see Table S2). Asterisks (*) indicate p < 0.05.

Plasma Mem.	GLUT	Relative	p-value	Sample	Relative	p-value	Sample
Fraction	Isoform	Fed Ratio		Size	Fasted Ratio		Size
Flight Muscle /	GLUT1	4.87 ± 1.30	0.009*	6, 4	2.48 ± 0.66	0.075	6, 5
Heart	GLUT2	2.31 ± 2.20	0.782	4, 5	1.77 ± 1.67	0.835	4, 5
	GLUT3	1.68 ± 0.79	0.814	4, 5	1.53 ± 0.71	0.950	4, 5
	GLUT5	1.84 ± 1.18	0.451	4, 5	1.96 ± 1.24	0.318	4, 5
Flight Muscle /	GLUT1	Not detected in liver PM			Not detected in liver PM		
Liver	GLUT2	1.19 ± 1.37	0.954	4, 3	1.00 ± 1.16	0.980	4, 3
	GLUT3	0.48 ± 0.27	0.396	4, 3	0.74 ± 0.42	0.958	4, 3
	GLUT5	0.61 ± 0.47	0.976	4, 3	0.39 ± 0.30	0.747	4, 3
Heart / Liver	GLUT1	Not detected in liver PM			Not detected in liver PM		
	GLUT2	0.51 ± 0.59	0.961	5, 3	0.57 ± 0.65	0.954	5, 3
	GLUT3	0.28 ± 0.16	0.225	5, 3	0.48 ± 0.27	0.730	5, 3
	GLUT5	0.33 ± 0.25	0.643	5, 3	0.20 ± 0.15	0.747	5, 3

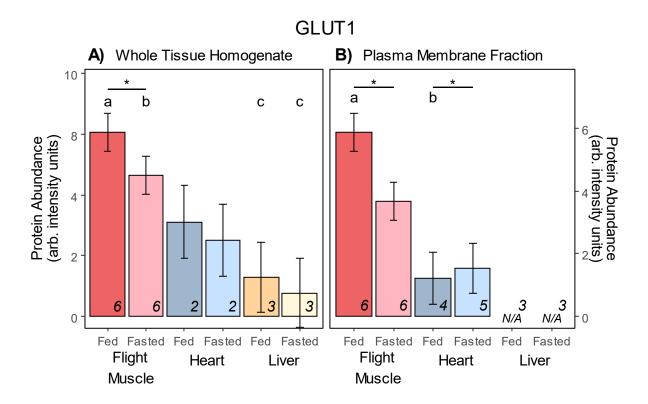


Figure 2. Relative protein abundance of GLUT1 in hummingbird flight muscle, heart, and liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on analyses of normalised immunoblots. *Ad-libitum* fed ("Fed") and 1-hour fasted ("Fasted") hummingbird GLUT1 abundance was measured in A) whole tissue homogenates and B) plasma membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference (p < 0.05) of GLUT1 between fed and fasted conditions within that tissue, summarised in Table 1 and Table 2. Letters (a, b) over tissue groups represent a significant difference (p < 0.05) of GLUT1 between tissue groups in fed or fasted conditions, summarised in Table 3 and Table 4. Sample sizes are superimposed on the bottom-right for each tissue and treatment.

GLUT2

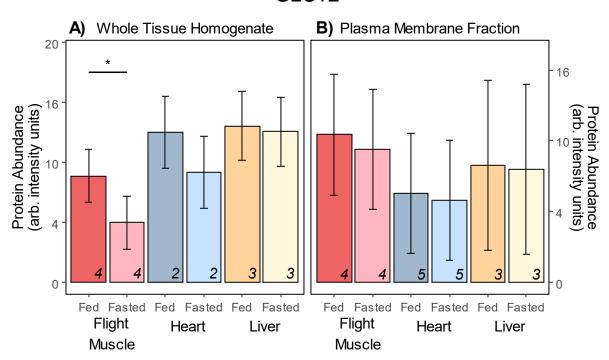


Figure 3. Relative protein abundance of GLUT2 in hummingbird flight muscle, heart, and liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on analyses of normalised immunoblots. *Ad-libitum* fed ("Fed") and 1-hour fasted ("Fasted") hummingbird GLUT2 abundance was measured in A) whole tissue homogenates and B) plasma membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference (p < 0.05) of GLUT2 between fed and fasted conditions within that tissue, summarised in Table 1 and Table 2. Differences in abundance of GLUT2 between tissue groups in fed or fasted conditions, summarised in Table 3 and Table 4. Sample sizes are superimposed on the bottom-right for each tissue and treatment.

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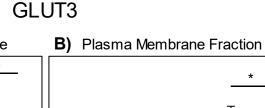
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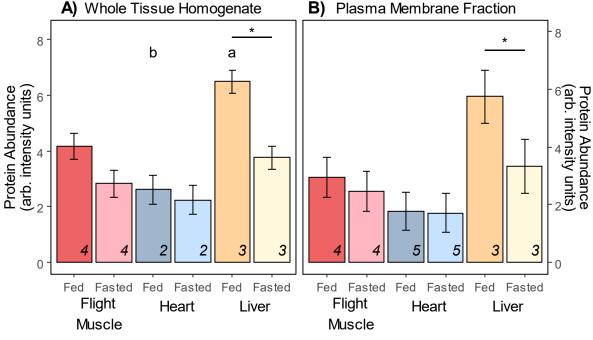


Figure 4. Relative protein abundance of GLUT3 in hummingbird flight muscle, heart, and **liver tissue.** Data represents mean \pm standard error of arbitrary units of intensity based on analyses of normalised immunoblots. *Ad-libitum* fed ("Fed") and 1-hour fasted ("Fasted") hummingbird GLUT3 abundance was measured in A) whole tissue homogenates and B) plasma membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference (p < 0.05) of GLUT3 between fed and fasted conditions within that tissue, summarised in Table 1 and Table 2. Letters (a, b) over tissue groups represent a significant difference (p < 0.05) of GLUT3 between tissue groups in fed or fasted conditions, summarised in Table 3 and Table 4. Sample sizes are superimposed on the bottom-right for each tissue and treatment.

Muscle

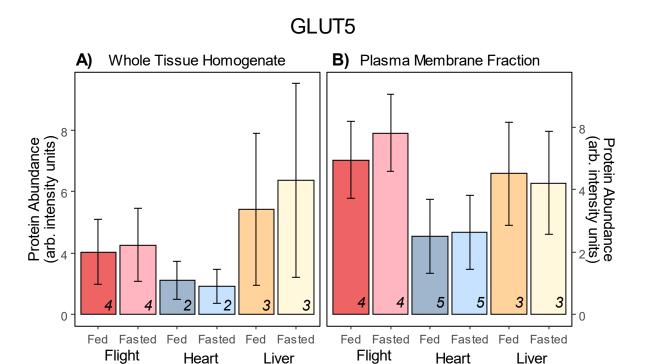


Figure 5. Relative protein abundance of GLUT5 in hummingbird flight muscle, heart, and liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on analyses of normalised immunoblots. *Ad-libitum* fed ("Fed") and 1-hour fasted ("Fasted") hummingbird GLUT5 abundance was measured in A) whole tissue homogenates and B) plasma membrane fraction samples. Differences in GLUT5 abundance between fed and fasted conditions within a given tissue are summarised in Table 1 and Table 2. Differences in overall GLUT5 abundance between tissue groups in fed or fasted conditions, summarised in Table 3 and Table 4. Sample sizes are superimposed on the bottom-right for each tissue and treatment.

Muscle

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Following a 1-hour treatment period, humming birds that were fasted (n = 5) had significantly lower blood fructose concentration compared to those that continued to feed (n = 6) (fed; 5.34 \pm 0.24 mM, fasted; 0.21 ± 0.15 mM, $t_{9.9} = -17.2$, p > 0.001; Figure 1). As this is the first report of blood fructose concentrations in hummingbirds, it is useful to compare our results against available data from other vertebrates that specialise on sugar-rich food sources. In frugivorous bats, such as the Egyptian fruit bat (Rousettus aegyptiacus), blood fructose concentrations are known to rise to ~11mM following a fructose-only meal (Keegan, 1977). Egyptian fruit bats, much like hummingbirds, have been shown to rapidly incorporate fructose into their pool of metabolizable substrates (Keegan, 1977). In the nectarivorous Pallas's long-tongued bat (Glossophaga soricina), the fraction of expired CO₂ supported by labelled carbons (f_{exo}) from a fructose meal takes ~9 minutes to reach 50% (Voigt and Speakman, 2007) while it took rubythroated hummingbirds ~14 minutes (Chen and Welch, 2014). In this study, we also see very low blood fructose concentrations in fasted hummingbirds compared to those that were fed (Figure 1). We further observed a slightly higher lactate concentration in fasted hummingbirds, although not significantly so (Figure 1), suggesting elevated fructolytic pathway activity (Dekker et al., 2010). These results indicate a rapid depletion of circulating fructose levels and may imply the rapid incorporation of exogenous blood fructose into the pool of metabolizable substrates in hummingbirds entering a fast. In contrast, while circulating concentrations of glucose were, as expected, high in fed hummingbirds, they remained elevated in fasted hummingbirds (fed; 30.04 ± 2.03 mM, fasted; 29.67 ± 1.25 mM; Fig. 1). Beuchat and Chong (1998) had previously observed a similar trend in hummingbirds entering a fast; blood glucose concentration remained elevated for the first hour and declined only after ~1.5 hours of fasting. Organs such as the brain are exceptionally demanding of glucose (Tokushima et al., 2005) in gallus gallus chicks and likely other birds as well. Further, lipogenic pathways of the hummingbird liver also shows a preference for glucose over fructose (Dick et al., 2019). Finally, while hummingbirds have the capacity to hover oxidising either glucose-only or fructose-only meals (Chen and Welch, 2014), their flight muscle cells' maximal capacity for monosaccharide phosphorylation is twice as high for glucose compared to fructose in tissue homogenates in vitro (Myrka and Welch, 2018). As hummingbird

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muscles lack extensive glycogen stores (Suarez et al., 1990), processes such as gluconeogenesis in the liver or other tissues may underlie the maintenance of elevated blood glucose. Our observations suggest that glucose uptake capacity is initially downregulated in hummingbirds entering a fast while fructose uptake capacity is unchanged.

Control of glucose and fructose flux is well-described in avian species. Despite the absence of the insulin-GLUT4 system in avian muscle cells (Dupont, 2009), chickens and English sparrows (Passer domesticus) have demonstrated coordinated expression of GLUT isoforms to control sugar transmembrane transport (Sweazea and Braun, 2006; Wagstaff and White, 1995). Less is known about hummingbird GLUT expression and regulation. In this study, we detected a strong immunoblot signal of the protein presence of GLUT 2, 3 and 5 in hummingbird flight muscle, heart, and liver tissue in WT homogenates (Table 1). GLUT2 was observed as a doublet while GLUT3 was detected at a size slightly larger than predicted, both of which may be attributable to variations in glycosylation (Asano et al., 1992; Ohtsubo et al., 2013). GLUT1 protein was detected in hummingbird flight muscle and heart (Table S1). GLUT1 protein in WT liver homogenates of ruby-throated hummingbirds was only minimally visible (Table 1) and was, surprisingly, not detected in PM fractions (Table 2). This result is in contrast to previously reported detection of hepatic mRNA transcript for GLUT1 in both chickens (Byers et al., 2018) and hummingbirds (Welch et al., 2013). However, as GLUT1 is abundant in erythrocytes (Carruthers, 2009), it is possible that the previous mRNA detection, as well as our detection of some hepatic GLUT1 protein, may have resulted from red blood cell contamination. While the presence of transcript does not necessarily mean that the final protein form is being fully transcribed (Vogel and Marcotte, 2012), it is clear that hepatic GLUT1 is not translocated to the plasma membrane. Our findings are similar to others that have failed to detect GLUT1 in the avian liver (Byers et al., 2017; Carver et al., 2001), raising the possibility that the role of hepatic GLUT1 protein may be much more reduced among birds than previously appreciated.

In chickens, GLUT protein expression appears to be dependent on synthesis or degradation of protein (Yamada et al., 1983) rather than the translocation from cytosolic pools that is observed in mammalian cells (Guma et al., 1995). If the same were true in hummingbirds, GLUT abundance of the overall tissue should be tied to the abundance of GLUT protein in the PM. In this study, we noted that flight muscle overall showed the greatest response to fasting, in terms of

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glucose-specific glucose transporter abundance in the PM of these tissues. In this case, reduced

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expression of two high-affinity glucose-specific GLUTs in the PM, GLUT1 ($K_m \approx 3\text{-}5\text{mM}$; Zhao & Keating, 2007) and GLUT3 ($K_m \approx 1.5$ mM; Mueckler & Thorens, 2013), may substantially impact the import of glucose into flight muscle and liver tissues, respectively. As we observed concordant decreases in WT GLUT1 in the flight muscle and WT GLUT3 in the liver, our data suggests that hummingbirds, much like chickens, regulate PM GLUT expression via synthesis or degradation of protein, rather than its translocation. Additionally, a recent study measuring levels of chicken GLUT1 mRNA also noticed a decrease in transcript following fasting (Coudert et al., 2018). We further observed that the fructose-transporting GLUT2 (Fig. 3B) and GLUT5 (Fig. 5B), did not change in PM abundance in any tissues tested following the 1-hour fast (Table 2). GLUT5 abundance did not change in WT homogenates either for any tissues. This suggests that PM GLUT5 and PM GLUT2 remain constitutively expressed in the PM of hummingbirds entering a fast. As expression of PM GLUTs allows for rapid sugar import (Wasserman, 2009), and as the highest affinity for fructose that is exhibited by GLUT5 ($K_m \approx 11\text{-}12\text{mM}$; Douard & Ferraris, 2008), this constitutive expression may underlie the observed reduced blood fructose concentration in fasted hummingbirds. In conclusion, we detected GLUTs 1, 2, 3, and 5 in all tissues, with the exception of GLUT1 in the liver PM. Flight muscle was observed to respond most dynamically to a 1-hour fast, followed by the liver, and finally the heart. We observed a decrease in the PM and WT abundance of glucose-specific GLUT1 in flight muscle and GLUT3 in the liver, which may lead to reduced glucose import capacity and thus maintenance of elevated blood glucose concentrations in fasted hummingbirds. In addition, we observed the constitutive expression of fructose-transporting PM GLUT2 and PM GLUT5 in all tissues, which should permit continued fructose uptake into theses tissue during initial stages of fasting, leading to near-depletion of the circulating pool of fructose. We further observed that the changes in GLUT protein expression occur both intracellularly and in the PM – no decrease of GLUT protein in the PM occurred without a concordant decrease in WT homogenates. These results suggest that hummingbirds, similar to other birds, may rely on mechanisms of GLUT synthesis and degradation, rather than translocation, to regulate extreme fluxes in circulating glucose and fructose concentrations.

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Conflicting Interests

None to declare.

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Supplementary Materials

3.1 Custom antibodies: GLUT1, 2, 3, and 5 detection in PM and WT homogenates

Table S1: GLUTs 1, 2, 3, and 5 observed molecular weights in plasma membrane (PM)

fractions and whole-tissue (WT) homogenates of flight muscle, heart, and liver.

Representative immunoblots are shown for each tissue and fraction.

	Observed _	Flight	Muscle	Н	eart	Liv	er
Mol	ecular Weight	PM	WT	PM	WT	PM	WT
GLUT1 Predicted mW = 53.8 kDa	47.0 kDa →	_	=		=		(A) (B) (A)
GLUT2 Predicted mW = 57.9 kDa	43.5 kDa →	=	=	=	=	-	-
GLUT3 Predicted mW = 53.3 kDa	72.4 kDa →	_	_	-	-	-	.
GLUT5 Predicted mW = 56.9 kDa	55.3 kDa →	-		_	2000 2000 2000 2000 2000 2000 2000 200	***	

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3.2 Plasma Membrane Fractionation Purity

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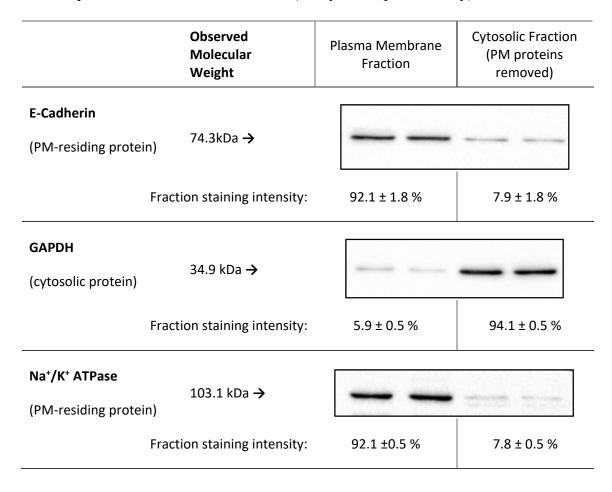
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Table S2: Relative distribution of known cysotolic or PM-residing proteins following PM

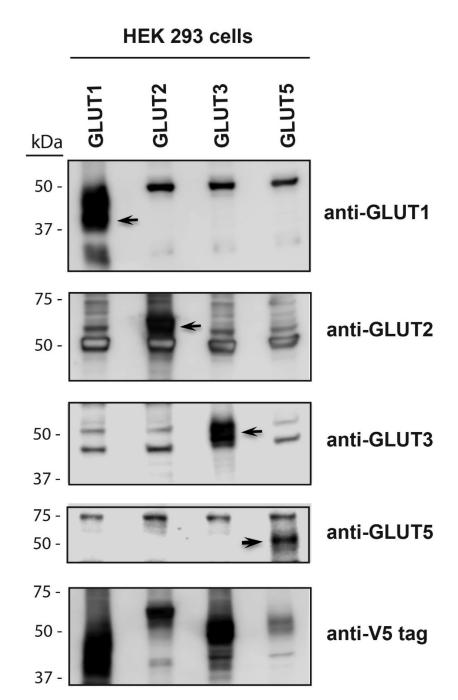
fractionation. Fraction purity indicates the relative abundance of protein in either the PM-only

fraction compared to the without-PM-fraction (i.e. cytosolic proteins only).



3.3 GLUT Amino Acid Sequence and Antibody Epitope

Table S3: Immunoblots on lysates of overexpressed GLUT1, GLUT2, GLUT3, GLUT5 protein. Each immunoblot lane represents a cell lysate produced from an entire well of a 6-well cell-culture dish. Isoform specificity was tested via immunoblotting all cell lysates (empty vector control, acGLUT1, 2, 3, and 5) with each novel GLUT antibody and observing GLUT protein signal overlap.



protein sequences. Highlighted regions indicated epitope targeted during antibody development

to ensure greatest dissimilarity between targeted isoforms

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Protein/Gene	Amino Acid Sequence
GLUT1/SLC2A1	METGSKMTARLMLAVGGAVLGSLQFGYNTGVINAPQKVIEDFYNRTWLYRYEEPITSATLTT
02011/0202/11	LWSLSVAIFSVGGMVGSFSVGLFVNRFGRRNSMLMSNILAFLAAVLMGFSKMALSFEMLIL
	GRFIIGLYSGLTTGFVPMYVGEVSPTALRGALGTFHQLGIVLGILVAQVFGLDLIMGNDSLWP
	LLLGFIFVPALLQCIILPFAPESPRFLLINRNEENKAKSVLKKLRGTTDVSSDLQEMKEESRQMM
	REKKVTIMELFRSPMYRQPILIAIVLQLSQQLSGINAVFYYSTSIFEKSGVEQPVYATIGSGVVN ⁻
	AFTVVSLFVVERAGRRTLHLIGLAGMAGCAVLMTIALTLLDQMPWMSYLSIVAIFGFVAFFEI
	GPGPIPWFIVAELFSQGPRPAAFAVAGLSNWTSNFIVGMGFQYIAQLCGSYVFIIFTVLLILFFI
	FTYFKVPETKGRTFDEIA <mark>SGFRQGGAGQSDKTPDEFHS</mark> LGADSQV
	NCBI Accession Number: MT472837
GLUT2/SLC2A2	MDKKNKMQAEKHLTGTLVLSVFAAVLGFFQYGYSLGVINAPQKVIEAHYGRVLGIAPPDRFP
,	TSASEEDGTVPVTEPWVSTEATLAPEDDPGEDLGTSSHILTMYWSLSVSMFAVGGMVSSFT
	VGWIGDRLGRVKAMLVVNILSIIGNLLMGLAKFGPSHMLIIAGRAVTGLYCGLSSGLVPMYV
	EVSPTALRGALGTLHQLAIVTGILISQVLGLDFLLGNDEMWPLLLGLSGVAALLQFFLLLLCPES
	PRYLYIKLGKVEEAKKSLKRLRGNCDPMKEIAEMEKEKQEAASEKKVSIRQLFTSSKYKQAVIVA
	LMVQISQQFSGINAIFYYSTNIFERAGVDQPVYATIGVGVVNTVFTVISVFLVEKAGRRSLFLA
	GLMGMLISAVAMTVGLALLSKFAWMSYVSMIAIFLFVIFFEVGPGPIPWFIVAELFSQGPRP/
	<u>AIATAGFCNWACNFIVGMCFQ</u> YIADLCGPYVFVIFAALLLIFFLFAYFKVPETKGKSFEEIAAVF
	RRRKLPTKAMTELEDLRGREEA
	NCBI Accession Number: MT47283
GLUT3/SLC2A3	FLQKITTPLVYAVSIAAIGSLQFGYNTGVINAPEKIIQAFFNRTLSERSGEVVSSELLTSLWSLSV
02013/0202/10	IFSVGGMIGSFSVSLFVNRFGRRNSMLLVNILAFAGGVLMALSKLVKAVEMLIVGRFIIGIFCG
	LSTGFVPMYISEVSPTSLRGAFGTLNQLGIVVGILVAQIFGLEAIMGTETLWPLLLGFTVLPAV
	QCVGLLFCPESPRFLLINKVEEEKAQAVLQKLRGTEDVSQDIQEMKEESAKMSQEKKVTVPE
	FRSPSYRQAIIIAIMLQLSQQLSGINAVFYYSTGIFERAGITKPVYATIGAGVVNTVFTVVSLFLV
	ERAGRRTLHLVGLGGMALCTVLMTIALALRDSVEWIKYISIIATFGFVALFEIGPGPIPWFIVAE
	LFSQGPRPAAMAVAGCSNWTSNFLVGLLFPYAEKLLGSYVFLVFLVFLVIFFVFTFFKVPETKG
	rtfedi <mark>srgfegrgdasspspvekve</mark> lnsieaekva
	NCBI Accession Number: MT47283.
GLUT5/SLC2A5	M <mark>KLKGKKHESSDNNDGSK</mark> GMTLTLALVALISAFGASFQYGYNVSVINSPAPFMQEFYNQTY
GLUTS/SLCZAS	YRNGEYMSSEFQTLLWSLTVSMFPLGGLFGSLMVWPLVNNCGRKGTLLINNIFSIVAAVLM
	GTSEIAKTFEVIILSRVIMGIYAGLASNVVPMFLGELSPKNLRGAIGVVPQLFITVGILSAQILGL
	NSILGNAAGWPILLGLTGIPSLLQILLLPLFPESPRYLLIQKGNEEQARQALQRLRGCDDVYDEI
	EEMRREDESEKKEGQFSVLSLFTFRGLRWQLISIIVMMMGQQLSGINAVFYYADRIFQSAGV
	DTNSVQYVTVSIGAINVVMTLLAVFIIESLGRRILLLAGFGLCCLSCAVLTLALNLQNTVTWMS
	YISIVCVIVYIIGHAIGASPIPSVLITEMFLQSSRPAAFMVGGSVHWLSNFTVGLLFLYMEAGLG
	PYSFLIFCAICLATIIYIFIVVPETKNKTFMEINRIMAKRNKVEIQEDKDELKDFHTAPGGQAGKT VSSSSEL
	NCBI Accession Number: MT47284

827 3.4 AIC Scores

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Table S5: Akaike information criterion (AIC) and AIC with corrections for small sample size (AICc) scores presented for each GLUT isoform model. Due to a relatively small sample size, AICc was preferred over AIC. Models with the lowest AICc score were selected for post hoc analysis and are indicated with an asterisk (*). The models tested are as follows:

- 832 1: Fluorescence Intensity ~ Treatment + Blot
- 833 2: Fluorescence Intensity ~ Tissue + Blot
- 834 3: Fluorescence Intensity ~ Treatment + Tissue + Blot
- 4: Fluorescence Intensity \sim Treatment \times Tissue + Blot

GLUT	Model	AIC Score	AICc Score	AIC Score	AICc Score
		WT	WT	PM	PM
GLUT1	1	515	519	31.9	34.4
	2	516	519	23.9	26.4
	3	479	485	25.2	29.2
	4	446	455*	17.4	23.4*
GLUT2	1	604	607	812	814
	2	570	575	773	776
	3	532	540	740	745
	4	462	478*	675	685*
GLUT3	1	270	273	373	375
	2	262	267	356	360
	3	238	246	341	346
	4	208	224*	308	318*
GLUT5	1	297	300	809	811
	2	278	283	770	773
	3	264	272	739	744
	4	234	250*	673	682*

3.5 Mammalian and Avian GLUT Homology

Table S6: Comparison of known avian GLUT isoforms and their homology to humans.

- Data was aggregated from (M. S. Byers et al., 2017; Myrka & Welch, 2018; Sweazea & Braun,
- 840 2006; Kenneth C. Welch et al., 2013) and homology to humans was calculated using NCBI
- 841 BLAST (Boratyn et al., 2012).

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GLUT	Localisation	Feature	Chicken to hummingbird sequence homology	Chicken to human sequence homology	Hummingbird to human sequence homology	Substrates (mammals)
GLUT1	Ubiquitous	Basal glucose transport	98%	80%	88%	Galactose, mannose, glucosamine
GLUT2	Liver, Pancreas, Intestine, Kidney	Insulin dependent	89%	65%	64%	Fructose, Glucose, Galactose
GLUT3	Neurons, Liver, skeletal muscle	Insulin dependent	87%	70%	73%	Glucose
GLUT4	Not found	Absence	N/A	N/A	N/A	Glucose
GLUT5	Intestine, brain, adipocytes, testes, skeletal muscle	Fructose transport	81%	64%	66%	Fructose

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843 **Figure Legends** 844 Figure 1: Mean concentrations (mM) ± standard error of circulating sugars A) Glucose, B) 845 Fructose from plasma samples and metabolites C) Lactate, D) Pyruvate from whole-tissue 846 homogenates of fed (n = 6) and fasted (n = 5). Data is presented as mean concentration in 847 848 Figure 2. Relative protein abundance of GLUT1 in hummingbird flight muscle, heart, and 849 liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on 850 analyses of normalised immunoblots. Ad-libitum fed ("Fed") and 1-hour fasted ("Fasted") 851 hummingbird GLUT1 abundance was measured in A) whole tissue homogenates and B) plasma 852 membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference 853 (p < 0.05) of GLUT1 between fed and fasted conditions within that tissue, summarised in Table 854 1 and Table 2. Letters (a, b) over tissue groups represent a significant difference (p < 0.05) of 855 GLUT1 between tissue groups in fed or fasted conditions, summarised in Table 3 and Table 4. 856 857 Figure 3. Relative protein abundance of GLUT2 in hummingbird flight muscle, heart, and 858 liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on 859 analyses of normalised immunoblots. Ad-libitum fed ("Fed") and 1-hour fasted ("Fasted") 860 hummingbird GLUT2 abundance was measured in A) whole tissue homogenates and B) plasma 861 membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference 862 (p < 0.05) of GLUT2 between fed and fasted conditions within that tissue, summarised in Table 863 1 and Table 2. Differences in abundance of GLUT2 between tissue groups in fed or fasted 864 conditions, summarised in Table 3 and Table 4. Sample sizes are superimposed on the bottom-865 right for each tissue and treatment. 23 866 Figure 4. Relative protein abundance of GLUT3 in hummingbird flight muscle, heart, and 867 liver tissue. Data represents mean \pm standard error of arbitrary units of intensity based on 868 analyses of normalised immunoblots. Ad-libitum fed ("Fed") and 1-hour fasted ("Fasted") 869 hummingbird GLUT3 abundance was measured in A) whole tissue homogenates and B) plasma

membrane fraction samples. An asterisk (*) over a tissue group indicates a significant difference

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homogenates compared pair-wise between flight muscle, heart, and liver of fed and fasted