



Brown Undergraduate Research Journal

Brown Research Club

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About the Brown Undergraduate Research Journal

First published in Spring 2019, the Brown Undergraduate Research Journal (BURJ) was developed by the Brown Research Club (BRC) in order to provide a unique platform for the showcasing of research completed by undergraduates and recent Brown University graduates. This work may have been completed in a University laboratory in collaboration with a faculty member, independently with the use of archival materials, or during the summer through a research internship.

One of the central aims of the BURJ is to be inclusive of all topic areas; you will notice that our current issue features submissions ranging in focus from cell biology to Slavic studies. Ultimately, our goal is to empower students at Brown to hone and demonstrate their academic writing skills, regardless of concentration or career trajectory. This ambitious goal could not have been achieved without the invaluable contributions of our incredibly talented BRC Journals team, which was responsible for the editing and compilation of this journal:

Editing

Kat Clum '22

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Graphic Design and Assembly

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We hope that you enjoy the second issue of the BURJ and thank you for supporting Brown's undergraduate research community!

Allen Green '21, Rahma Ibrahim '22, and Evan Mizerak '22

BRC Co-Presidents

Science During the COVID-19 Pandemic

Over the past year, the COVID-19 pandemic has touched nearly every aspect of our academic, professional, and personal lives, and the research operations of Brown University undergraduates have been no exception. This section highlights perspectives from the authors of some of the work in this issue of the BURJ, lending insight as to how the pandemic influenced the course of their projects and the creative ways in which they adapted to these obstacles.

Many students were able to accomplish the impressive work documented herein despite conducting research remotely and accessing resources online through various databases:

- *Olwyn Kells* conducted her research entirely remotely, funded by a Brown University Collaborative SPRINT Research Award
- *Alex Philips* conducted his research during class but executed data analysis remotely after transitioning to remote learning
- *Gerilyn Maselli* completed a remote internship at the US Naval War College. Despite working remotely, she collaborated with experts at the institution over Zoom and managed to leverage resources including the National Security Archives and West Point's Counter-Terrorism Center to finish her research.

Other students whose work was initially intended to take place in a clinical setting demonstrated remarkable adaptability while innovating ways to continue their efforts remotely.

- *Suraj Zaveri* initially planned to meet patients in person to collect and analyze data, but instead shifted to calling patients over the phone and setting up many Zoom calls.
- *Kahini Mehta* was originally conducting research at Butler Hospital but had her research cut short due to the pandemic, and fortunately went on to contact a professor with a tabled paper she was interested in working on remotely.
- *Surya Khatri* described learning invaluable lessons about patient-physician relationships in the time of COVID. He outlined the difficulties of conducting a case study contingent upon patient interaction and access to clinical laboratories, particularly during a time of great confusion for both medical professionals and patients alike.

Table of Contents

Biomedical Sciences

- *Diversity in Modern Human Populations: An Analysis of Genetic Variation in TRIM5*..... 7
Kriti Devkota, David Peede, and Emilia Huerta- Sánchez
- *Altered lipid metabolism implicates the fatty acid synthase fasn-1 in autophagy pathway in Caenorhabditis elegans*.....13
Zinab Eisa, Jenny Lee, Melinda Li, and Christine Lu
- *PDGF-BB Concentration is Suppressed During Treatment of Gorham-Stout Disease with Sirolimus and Zoledronic Acid*.....19
Surya Khatri
- *Novel Application of a Redox-probing Technique for the Non-invasive Quantification of Oxidative Stress in Perspiration*.....21
Evrin Ozcan

Public Health

- *Cognitive-Behavioral Interventions Targeting Substance Use and Co-Occurring Mental Health Disorders: A Meta-Analysis*.....23
Kahini Mehta
- *Effect of Medicaid Expansion on Medicaid Acceptance by RI Physicians Using All Payer Claims Database (APCD) Data*.....25
Alexander Phillips
- *Universal Health Coverage and the Global Impact of COVID-19*.....31
Gauri Gadkari, Kento Suzuki, Riki Fameli, Rinchen Dolma, Youkie Shiozawa
- *Three month assessment of post-traumatic stress disorder, depression, and functional recovery in patients hospitalized early in the COVID-19 pandemic in the New Orleans region*.....37
Kevin Conrad, Hope Bernier, Suraj Zaveri, Rea Cleland, Morgan Winchell, Marianne Maumus

Humanities and Social Sciences

- *Humanitarian Consequences of the bin Laden Manhunt*.....44
Gerilyn Maselli
- *Westernizing Fashions: The Nationalization of Gender Identity in Early Modern Russia*.....49
Olwyn Kells
- *United States Baseball's Exploitation of Latin America and its Athletes*.....53
Ingrid Ren
- *A Ramseyan Resolution of Ontological Commitment in First-Order Paraphrases of Beauty Judgments*.....54
Ben Zimmerman

Diversity in Modern Human Populations: An Analysis of Genetic Variation in *TRIM5*

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Field: Biology, Computational Biology

Abstract

Simian immunodeficiency virus (SIV), the evolutionary precursor to human immunodeficiency virus (HIV), has been circulating for thousands of years and contributes to the morbidity and mortality of thousands around the world [1]. The replication of retroviruses (e.g. SIV) is inhibited upon entry into the host cell by *TRIM5*, a crucial innate immune system signaling protein [2]. In this study, we examined patterns of genetic variation in the *TRIM5* gene for 53 contemporary human populations from the Human Genome Diversity Project [3] to elucidate the evolutionary history of *TRIM5* based on known patterns of genetic diversity arising from human demographic events. We utilized computational tools in Python and R to calculate nucleotide diversity and heterozygosity. Results show increased genetic diversity in *TRIM5* compared to the rest of chromosome 11 and increased heterozygosity in five non-African populations compared to the African average. These findings provide a basis for further analysis of natural selection and archaic introgression that can provide insight into the host-microbe interactions in HIV infection.

Methods

The individual genomes from the Human Genome Diversity Project (HGDP) were obtained from the International Genome Sample Resource (IGSR) and merged in *BCFTools* [4] to provide population-level variant call format (VCF) files. The VCF files for each population were then filtered to

only include biallelic single nucleotide polymorphisms (SNPs) and sites with less than 10% missing genotype information. Each filtered VCF file was then subsetted into two files per population, one just containing sites for the *TRIM5* region and the other containing sites for chromosome 11 excluding the *TRIM5* region. To analyze the genetic diversity of the populations, heterozygosity and π were calculated using the python package *scikit-allele* [5]. Heterozygosity provided the average proportion of heterozygous individuals in a region for each population. Within population nucleotide diversity, commonly referred to as π , is the average number of nucleotide differences between genotypes drawn from the same population [6]. We expect nucleotide diversity and heterozygosity to decrease with distance from African due to the effects of isolation and smaller gene pools as human migration extends out of Africa [7,8]. Therefore, African populations were used as a threshold of high genetic diversity for both π and heterozygosity. In R Studio, t-tests were performed for each population on the mean heterozygosity for *TRIM5* with respect to the rest of chromosome 11 and with respect to African populations. T-tests were also performed for each super population on the mean π for *TRIM5* with respect to the rest of chromosome 11 and with respect to the African super population. The t-tests determined the significance of the calculated heterozygosity and π values to compare the diversity within different regions of the same population and across populations. Results were summarized and visualized in R using the *ggplot2* package [9].

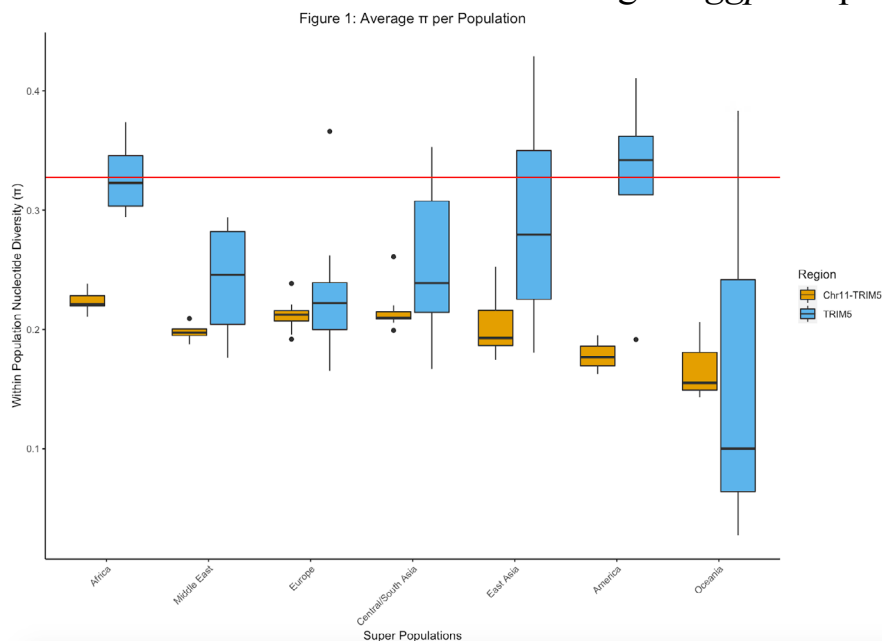


Figure 1: This plot shows π values for the *TRIM5* region in blue and the rest of chromosome 11 in yellow for each super population. The red line represents the average *TRIM5* π value for the African super population.

Table 1: *TRIM5* Pi and Het Values by Population

Super Populations	Populations	<i>TRIM5</i> Pi	<i>TRIM5</i> Het
Africa	San	0.32737574+++	0.429487179+++
Africa	Mbuti	0.32737574+++	0.405982906+++
Africa	Biaka	0.32737574+++	0.342405421++
Africa	Bantu	0.32737574+++	0.367071525++
Africa	Yoruba	0.32737574+++	0.512903384****+
Africa	Mandenka	0.32737574+++	0.403307359+++
Middle East	Mozabite	0.240430516	0.359343373+++
Middle East	Bedouin	0.240430516	0.195537018
Middle East	Palestinian	0.240430516	0.24056287
Middle East	Druze	0.240430516	0.354997419+
Europe	Basque	0.231841915	0.471372106*+++
Europe	Sardinian	0.23184192	0.233227299
Europe	BergamotItalian	0.23184192	0.18544137
Europe	Tuscan	0.23184192	0.261029412
Europe	French	0.23184192	0.255625327
Europe	Orcadian	0.23184192	0.322585034+
Europe	Russian	0.23184192	0.186
Europe	Adygei	0.23184192	0.256944444
Central/South Asia	Kalash	0.255954228+	0.413636364+++
Central/South Asia	Balochi	0.255954228+	0.34135773+++
Central/South Asia	Brahui	0.255954228+	0.225876153
Central/South Asia	Makrani	0.255954228+	0.278003623
Central/South Asia	Pathan	0.255954228+	0.216421461
Central/South Asia	Sindhi	0.255954228+	0.166666667
Central/South Asia	Burusho	0.255954228+	0.295823452
Central/South Asia	Hazara	0.255954228+	0.24431449
Central/South Asia	Uyгур	0.255954228+	0.372222222
East Asia	Lahu	0.291037695+++	0.428571429
East Asia	Cambodian	0.291037695+++	0.425925926+++
East Asia	Dai	0.291037695+++	0.585858586*+++
East Asia	She	0.291037695+++	0.604292929*+++
East Asia	Miao	0.291037695+++	0.437254902+++
East Asia	Tujia	0.291037695+++	0.363636364+
East Asia	Han	0.291037695+++	0.343456745+
East Asia	Yi	0.291037695+++	0.261029412
East Asia	Naxi	0.291037695+++	0.385416667+
East Asia	Japanese	0.291037695+++	0.253261359
East Asia	Tu	0.291037695+++	0.252136752
East Asia	Hezhen	0.291037695+++	0.174603175
East Asia	Daur	0.291037695+++	0.222222222
East Asia	NorthernHan	0.291037695+++	0.431899642+
East Asia	Mongolian	0.291037695+++	0.316239316
East Asia	Xibo	0.291037695+++	0.216931217
East Asia	Oroquen	0.291037695+++	0.206349206
East Asia	Yakut	0.291037695+++	0.238039216
America	Maya	0.323817165++	0.56218254*+++
America	Pima	0.323817165++	0.413333333+++
America	Colombian	0.323817165++	0.183673469
America	Karitiana	0.323817165++	0.44040404+++
America	Surui	0.323817165++	0.395491803+++
Oceania	PapaunHighlands	0.170314862	0.126262626
Oceania	PapaunSepik	0.170314862	0.019736842
Oceania	Bougainville	0.170314862	0.508377897*+++

Results

Within Population Nucleotide Diversity (π)

Nucleotide diversity was calculated for each super population. When analyzing nucleotide diversity, the Central/South Asian, East Asian, and American super populations showed significantly elevated values for π in *TRIM5* compared to the rest of chromosome 11. Though the rest of chromosome 11 had a larger sample size (i.e. greater number of base pairs), *TRIM5* still had a significantly elevated π value. There was no evidence for significantly elevated π values in *TRIM5* for any of the super populations when compared to the average African π value (Fig. 1). These results provide evidence that within population nucleotide diversity is greater in the *TRIM5* region than in the rest of chromosome 11 and confirms the expected trend of

Table 1: Mean π and heterozygosity values of the *TRIM5* region for each population are given in this table. T-tests were performed to determine whether the values for *TRIM5* were significantly higher than the average values for the African populations after adjusting for multiple comparisons. ‘***’ p-value < 0.001, ‘**’ p-value < 0.01, and ‘*’ p-value < 0.1. T-tests were also performed to determine whether the values for *TRIM5* were significantly higher than values for the rest of chromosome 11 after adjusting for multiple comparisons. ‘+++’ p-value < 0.001, ‘++’ p-value < 0.01, and ‘+’ p-value < 0.1.

Figure 2: Average Proportion of Heterozygous Individuals per Population

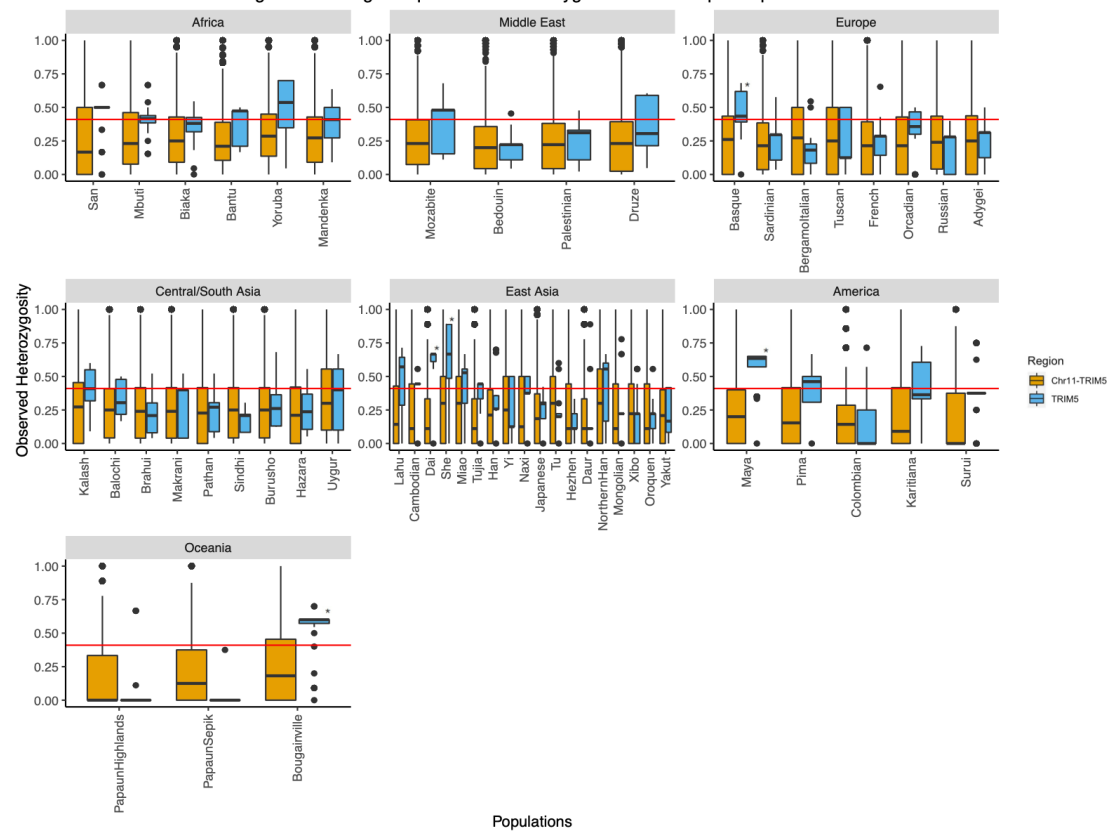


Figure 2: Each panel shows the average proportion of heterozygous individuals for the *TRIM5* region in blue and the rest of chromosome 11 in yellow for each super population. The red line represents the average heterozygosity in the *TRIM5* region for the African populations. Populations with values significantly greater than the African average are indicated with stars (*).

decreased nucleotide diversity with increased distance from Africa.

Heterozygosity

Many populations — including those with significantly elevated heterozygosity for *TRIM5* — showed significantly higher heterozygosity in *TRIM5* than in the rest of chromosome 11 (Table 1). Along with relatively small standard deviations among the *TRIM5* sample, this confirmed that sample size did not skew the determination of significance. The Basque, Dai, She, Mayan, and Bougainville populations had significantly higher heterozygosity than the African average for *TRIM5* (Fig. 2). These results provide evidence that the proportion of heterozygous individuals is greater in the *TRIM5* region than in the rest of chromosome 11 and greater in some populations than in Africans.

Discussion

TRIM5 is essential to the host immune response for the recognition and degradation of HIV. It has been previously shown that *TRIM5* exhibits signatures of natural selection [10]. However, there has been little research done in examining genetic variation in *TRIM5* and other genes associated with HIV. Therefore, this work seeks to provide this information in addition to general insights on the evolutionary history of *TRIM5* that could provide a basis for further research on host-microbe interactions in HIV infection. The majority of populations showed a significantly greater proportion of heterozygous individuals within the *TRIM5* region as opposed to the rest of chromosome 11. Super populations also show significantly elevated π values for *TRIM5* compared to the rest of chromosome 11. It was expected that chromosome 11 would have approximately the same variation throughout. However, the results from both tests provide strong evidence that *TRIM5* has greater variation than the rest of chromosome 11.

Five populations — Basque, Dai, She, Maya, and Bougainville — showed significantly elevated heterozygosity values than the African average. These populations have a greater proportion of heterozygous individuals in the *TRIM5* region than the average of African populations, but they do not have a significantly greater π value than the African super population. Testing significance for individual populations was not possible due to the nature of computing π . Overall, this suggests that there is a higher proportion of heterozygous individuals in *TRIM5* in these populations than in the African populations, but we cannot make claims about differences in nucleotide diversity due to the limitations of this study.

Our results suggest that genetic variation in *TRIM5* differs from what we would expect from known human demographic events and neutral evolution. These differences are likely due to environmental pressures, archaic introgression, natural selection, or a more complex scenario that includes all three evolutionary pressures. Further research should be done to confirm the exact underpinnings of this variation.

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Altered lipid metabolism implicates the fatty acid synthase *fasn-1* in autophagy pathway in *Caenorhabditis elegans*

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Field: Molecular Biology, Cell Biology, and Biochemistry (MCB)

Introduction

Despite the vast amount of information regarding autophagy, lipids, and the interface between these two metabolic players, the specific mechanism by which autophagy regulates aging is unknown. Thus, we investigated the interactions between *fasn-1*— a key modulator of fatty acid synthesis— and the many pivotal roles for autophagic genes such as *lgg-1* in lipid regulation provides more insight on the consequences of faulty macroautophagic activity in defective autophagy. With immunostaining, RNA interference, and other methods of quantification of protein expression, nucleotides, and lipids, we found that *fasn-1* knockout worms exhibit less fatty acid synthesis and less lipophagy, but also an unknown compensation mechanism for autophagic processes. Because *fasn-1* catalyzes the de novo synthesis of fatty acids and has been implicated in lipid accumulation, we would expect less fatty acid synthesis, and thus less free fatty acids, meaning a decrease in lipid accumulation and autophagy in *fasn-1* RNAi worms. Alternatively, to maintain homeostasis, either one of the two mechanisms can occur: an increase in other fat regulatory genes, 6 or an increase or no change in expression of LGG-1 (an ortholog of the protein *Atg8* which associates with the autophagosomal membrane in order to maintain autophagy despite the reduced de novo synthesis of fatty acids. Due to the many orthologs in common with the human genome, this association between *fasn-1* and LGG-1 in *C. Elegans* has promising implications on autophagy- related aging mechanisms and common diseases caused by defects in lipid metabolism.

Autophagy is a degradative cellular process that plays an essential role in maintaining normal physiological function.¹ However, with aging, autophagic activity decreases, resulting in the accumulation of various damaged and futile macromolecules including amino acids, nucleotides and lipids⁶, encouraging age-related diseases such as cancer and neurodegeneration.⁷ Lipid catabolism, termed lipophagy, is a process through which lipids are degraded into free fatty acids by autophagy.² Cytosolic neutral lipases have been the conduit for lipolysis occurrence in most lipid catabolism studies.¹³ *Caenorhabditis elegans* is known to have at least three of these lipases, which are necessary for breaking down triglycerides into free fatty acids, ultimately for energy.¹⁴ Lipase activity increases with an increase in the expression of nutrient-sensitive transcriptional factors, inducing *de novo* biosynthesis of autophagosomes and lysosomes.⁵ Accordingly, this not only enhances their fusion, but also increases the degradation of substrates.⁵ Synthesis of *de novo* fatty acids is achieved through cyclic activities of fatty acid synthase (FAS), a multi-enzyme protein containing six catalytic activities encoded by *fasn-1*.¹⁵

Methods

Fatty acid synthase, encoded for by *fasn-1* is a primary actor in the synthesis of lipids through the synthesis of fatty acids.²⁴ We utilized *Caenorhabditis elegans* as a model organism to investigate the interactions between *fasn-1* and the most prominent autophagic marker, LGG-1³ via a GFP::mCherry:LGG-1 probe. We expected inhibition of *fasn-1* to result in less lipid accumulation, less lipolysis, and therefore less autophagy. With RNA interference, immunostaining, and other methods to quantify protein expression, we found that *fasn-1* RNAi resulted in less transcriptional capacity for various autophagic genes, including *lgg-1* despite fluorescence microscopy illustrating an increase in GFP fluorescence and interestingly, a decrease in RFP fluorescence. Additionally, through lipid metabolism quantification assays, we found a significant decrease in the capacity for lipase activity, despite similar triglyceride levels in control and *fasn-1* RNAi treated animals.

Results and Discussion

From our results, the GFP signal in *fasn-1* treated worms is greater than in

control animals, indicating more LGG-1 protein in *fasn-1* RNAi treated animals. However, when taken with the results from the qPCR, this data seems to conflict as not only do *lgg-1* gene expression levels go down with *fasn-1* treatment, but so do expressions for other autophagy genes. Taken together, these results indicate that *fasn-1* knockdown caused either an increase in autophagosome formation, resulting in more GFP signal or less degradation of LGG-1 protein, also contributing to greater GFP signal. In both cases however, an increase in the number of autophagosomes -either as a result of greater autophagosome accumulation or less LGG-1 degradation- does not reflect an induction of autophagy and instead points to inefficient or blocked autophagy.³¹

The composition of cellular membranes are supplied in part by fatty acids, particularly PUFAs or polyunsaturated fatty acids.³² Knocking down *fasn-1* will result in decreased fatty acid synthesis including PUFAs, which play a critical role in membrane formation, an essential component of autophagic degradation.³² As a result, less membrane formation will be able to occur which will not only decrease or block autophagic flux, but also the LGG-1 protein that may be engulfed in the autophagosome membrane. Another explanation in accordance with this model is that *fasn-1* knockdown actually decreases autophagosome formation, as there isn't enough fatty acids being synthesized *de novo* to produce the phospholipids that make up the autophagosomes. Thus, determining if increased GFP signal is from increased induction of autophagy, increases in autophagic flux, decreased turnover of LGG-1, or is a result of an autophagic block requires further experimentation. Especially useful would be the observation of autophagosomal turnover in both presence and absence of lysosomal degradation, achieved through RNAi knockdown of lysosomal genes such as *cup-5* in *C. elegans*.¹⁰

In *de novo* fatty acid synthesis, acetyl CoA carboxylase and fatty acid synthase solely comprise the enzymatic activities required for the production of palmitic acid.³³ Subsequently, palmitic acid is then incorporated into either TAGs or phospholipids.¹⁵ This helps explain why TAG concentration remained the same for both samples, suggesting that the quantity of palmitic acid produced by *fasn-1* in treated animals is being incorporated into TAGs rather than phospholipids. Furthermore, *C. elegans* storage lipids, or lipid droplets, are comprised of TAGs enclosed by a monolayer of phospholipids.^{34, 35}

Assuming that for treated animals synthesized palmitic acid is incorporated more so into TAG stores than in phospholipids^{14, 15}, the observation that there is less lipid accumulation in treated animals is consistent. Though the same concentration of TAGs is present, there is less lipid droplet accumulation because there is not enough phospholipid synthesis to form the monolayer enclosing TAGs in the lipid droplet. Accordingly, it can be further explicated that less lipid accumulation translates into less lipophagy, as suggested by the decrease in lipase activity we observed.

Taken together, these results suggest that *fasn-1* plays a role in autophagic processes such as lipophagy and lipid metabolism, however more research is required to further characterize its specific roles in these pathways. Increased understanding of the interface between lipid metabolism and autophagy might lead to better understanding of how aging-related common diseases caused by defects in lipid metabolism are caused, and even further, may be treated.⁴

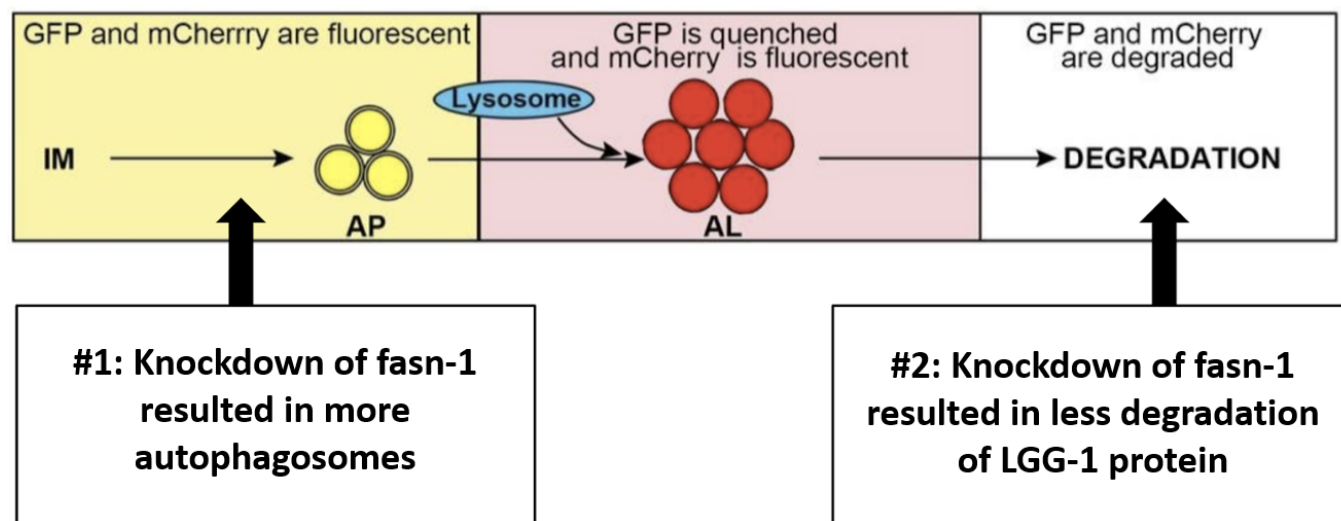


Figure: Two interpretations based on fluorescence imaging data for how *fasn-1* knockdown affected autophagic flux

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PDGF-BB Concentration is Suppressed During Treatment of Gorham-Stout Disease with Sirolimus and Zoledronic Acid

Author: Surya Khatri

PI: Dr. Janet Crane (Department of Pediatrics Center for Musculoskeletal Research, Department of Orthopaedic Surgery, The Johns Hopkins University)

Field: Biology, Chemistry, Mathematics

Objectives

Gorham-Stout Disease (GSD), often referred to as vanishing bone disease, is a rare skeletal condition characterized by immense osteolysis and bone resorption. The etiology of GSD is unknown but manifests with osteoclast bone resorption that is replaced by fibrous and vascular tissue. We have previously published that osteoclast lineage cells secrete platelet derived growth factor with two B subunits (PDGF-BB) that stimulate blood vessel formation. The objective of this study was to investigate if the PDGF-BB concentration is altered in the peripheral blood of a patient with GSD.

Methods

A sixteen-year-old Caucasian male presented with a large right pleural effusion. Extensive medical workup revealed partial bone resorption of his right 1st-3rd ribs, right clavicle, and right transverse process of first thoracic vertebrae. The pleural fluid was consistent with transudate and felt to be reactive. Biopsy of the right first rib revealed a vascular malformation with cells positive for lymphatic endothelium, consistent with the diagnosis of GSD. He was immediately started on sirolimus and referred for co-treatment with a bisphosphonate. After the correction of vitamin D deficiency, he was started on zoledronic acid 0.025 mg/kg (1.4 mg) IV every 4 weeks. Two

weeks after his second dose, the patient had a recurrence of large right pleural effusion. He was given an additional zoledronic acid 0.02 mg/kg (1 mg) as laboratory testing revealed a rebound of Serum was collected prior to the first and before the sixth monthly zoledronic acid infusion. PDGF-BB was measured by an enzyme-linked immunosorbent assay kit.

Results

The concentration of PDGF-BB was lower in the patient with GSD relative to a healthy child control (270 pg/ml). The PDGF-BB concentration in the patient with GSD on sirolimus alone was 90 pg/ml and was 130 pg/ml when on both sirolimus and zoledronic acid.

Conclusions

Although there is massive osteoclast-mediated osteolysis observed in GSD, the serum PDGF-BB concentration was not elevated, but rather suppressed in this patient with GSD relative to a healthy control. We are unable to rule out excessive PDGF-BB in the pathophysiology of GSD as serum was not able to be collected prior to treatment with sirolimus. Further studies are underway to determine if sirolimus and/or zoledronic acid can suppress PDGF-BB synthesis as well as additional studies to evaluate other potential angiogenic biomarkers to improve the diagnosis and monitoring of GSD.

Novel Application of a Redox-probing Technique for the Non-invasive Quantification of Oxidative Stress in Perspiration

Author: Evrim Ozcan

PI: Professor Payne (Fischell Department of Bioengineering, University of Maryland College Park)

Field: Biology, Chemistry, Bioelectronics

Abstract

Oxidative stress has been linked to many diseases and increases during exhaustive exercise. Yet, no measurement characterizes the holistic nature of oxidative stress non-invasively. The project presented quantifies oxidative stress in human sweat, a non-invasive easily-attainable biological fluid. By implementing a redox-probing method, the multi-faceted profile of oxidative stress is measured, an improved approach over current evaluations of singular molecular species. The analysis detects significant variations between control and sweat samples ($p \leq 0.0213$). These differences suggest that antioxidants in sweat are generated by the body to counteract the oxidatively stressed environment during exercise. Additionally, the jagged nature (increase, decrease, increase) in output metrics for the 9 and 7-hour samples, compared to the steady, steady, decrease of the 4-hour sample, suggests oxidative stress dependence on workout duration and sleep hours. This dependence on sleep is further suggested by the average electrical signal attenuation from 1.37 to 1.7 as sleep decreased from 9 to 4 hours. Expanding the study to a larger sample size would allow additional exploration of the relationship between sleep and oxidative stress levels during exercise. The research presented takes a key-step forward in providing a rapid and simple measurement of oxidative stress for both clinical and athletic fields.

Public Health

Cognitive-Behavioral Interventions Targeting Substance Use and Co-Occurring Mental Health Disorders: A Meta-Analysis

Author: Kahini Mehta

PI: Professor Molly Magill, (Department of Public Health, Brown University)

Field: Biology, Psychology

Integrated cognitive behavioral interventions (CBI) refer to programs that coordinate treatments for the behavioral and cognitive symptoms of co-occurring disorders. This meta-analysis reviewed 15 clinical trials (18 study sites/arms), examining the efficacy of an integrated cognitive behavioral intervention (CBI) delivered to individuals with an alcohol or other drug use disorder and a co-occurring mental health disorder (AOD/MHD). Outcomes were alcohol or other drug use and mental health symptoms at posttreatment through follow-up.

The inverse-variance weighted effect size was calculated for each study and pooled under random effects assumptions.

Integrated CBI showed a small effect size for AOD ($g = 0.188$, $p = 0.061$; $I^2 = 86\%$, $\tau^2 = 0.126$, $k = 18$) and MHD ($g = 0.169$, $p = 0.024$; $I^2 = 58\%$, $\tau^2 = 0.052$, $k = 18$) outcomes, although only MHD outcomes were statistically significant. Analysis by subgroup suggested that effect magnitude varied by type of contrast condition (integrated CBI + usual care versus usual care only; integrated CBI vs. a single-disorder intervention), follow-up time point (posttreatment versus 3 to 6 months), and primary AOD/MHD diagnosis, although these sub-groups often contained significant residual heterogeneity. In a series of mixed effects, meta-regression models, demographic factors were non-significant predictors of between-study heterogeneity. For AOD outcomes, greater effects were observed in higher quality studies, but study quality was not related to effect size variability for

MHD outcomes.

The current meta-analysis shows a small and variable effect for integrated CBI with the most promising effect sizes observed for integrated CBI compared to a single disorder intervention (typically an AOD-only intervention) for follow-up outcomes, and for interventions targeting alcohol use and/or post-traumatic stress disorder. Given the clinical and methodological variability within the sample, results should be considered a preliminary, but important step forward in our understanding of treatment for co-occurring AOD/MHD.

Effect of Medicaid Expansion on Medicaid Acceptance by RI Physicians Using All Payer Claims Database (APCD) Data

Author: Alexander Philips

PI: Emily Oster (Department of Economics, Brown University) and Ira Wilson (Department of Health Services, Policy, and Practice, Brown University)

Field: Public Health

Background and Literature

Medicaid is a public health insurance program in the United States providing health care coverage to low-income families and people with disabilities. In states which expanded Medicaid alongside the rollout of the Affordable Care Act (ACA) in January 2014, coverage was extended to all individuals up to 138% of the Federal Poverty Line. Medicaid is the largest means-tested program in the United States representing 16 percent of total national health expenditure¹ and is the nation's major source of long-term care financing.² In Rhode Island, 24% of the state population is covered by Medicaid.³ Widespread Medicaid acceptance by physicians is an essential factor in promoting access to healthcare for a state's low-income and disabled populations.

Literature has suggested that providers may choose not to accept Medicaid due to high administrative burden,⁴ payment uncertainty,⁵ high rates of broken appointments,⁶ and low reimbursement rates compared to Medicare or commercial insurance which vary considerably by state.^{7,8} Physician acceptance of Medicaid has been shown to vary considerably by specialty.⁹ Furthermore, Medicaid patients may not make up a large proportion of a physician's patient population, so physicians may not forego much income by refusing to accept Medicaid.

In addition to expanding Medicaid, the ACA attempted to mitigate phy-

sician disincentives for accepting Medicaid by increasing reimbursement rates for select primary care services during 2013 and 2014; the federal government paid for the full costs of this increase, raising fees for all primary care physicians (PCPs).¹⁰ Alongside federal fee increases, RI increased reimbursement rates for managed care organizations and nursing facilities during this time.¹¹ Evidence on expansion and accompanying incentives on physician appointment availability is mixed.^{12,13} Evidence on changes to state-specific physician acceptance are limited by using Medicaid fee-for-service (FFS) data alone (and excluding managed care data),¹⁴ using self-reported data from physicians,¹⁵ or being national in scope.¹⁶

Objectives and Methods

This paper examines how Rhode Island's Medicaid expansion on January 1, 2014 affected its acceptance among RI physicians and varied by physician specialty. The motivation of this paper was derived from two ideas in this policy space: (1) health care providers may choose whether or not to treat Medicaid patients in non-emergency settings and (2) there is variation in how Medicaid expansion was implemented in different states. Understanding the effect of Medicaid expansion on physician acceptance in the state specific context of RI is important in ensuring physician buy-in to the success of a social program taking up a large portion of the RI state budget and serving the state's low-income and disabled population.

The primary outcome of interest studied in this paper is Medicaid acceptance by RI physicians over time, measured as the proportion of physicians who make a Medicaid FFS or Medicaid Managed Care claim in a given month. This outcome was first studied at the intensive margin to see if new physicians accepted Medicaid after expansion, and then at the extensive margin to see if aggregate Medicaid acceptance changed after expansion. A secondary outcome of interest was the number of Medicaid patients seen per physician per month. This outcome was quantified to detect if physicians who were already accepting Medicaid before expansion saw more Medicaid patients per month after expansion. An event study design was used to quantify effects in these two outcomes of interest before and after Medicaid expansion in RI. A tertiary outcome of interest was variation in physician acceptance and Medicaid patients per month across PCPs/specialists and across pediatric/non-pediatric PCPs.

The sources of data for this study are the RI All-Payer Claims Database (APCD) and the Center for Medicare and Medicaid Services (CMS) Provider Taxonomy. APCDs include information collected from private and public payers including medical claims, pharmacy claims, dental claims, and provider information.¹⁷ Medicaid acceptance can uniquely be studied using the APCD since it has complete data on all medical claims from all payers and all physicians in the state. The CMS Provider Taxonomy can be linked to APCD provider data to allow for more specific information on physician specialty.

Results

The data suggests that RI Medicaid expansion led to new physicians accepting Medicaid and increases the aggregate proportion of physicians accepting Medicaid by about 0.028. Additionally, physicians accepting Medicaid pre-expansion see an average of about 9 more Medicaid patients per month post-expansion. Figures show that PCPs and specialists saw a sharper increase in Medicaid acceptance after expansion. Difference in differences regressions show that Medicaid acceptance post-expansion among PCPs was driven by non-pediatric PCPs. The results regarding proportion increase in Medicaid acceptance are also robust to physicians entering/exiting practice in RI during the Medicaid expansion period.

Discussion

Medicaid expansion in RI impacted physician behavior in two forms: new physicians accepting Medicaid who were not accepting Medicaid before expansion, and physicians who were accepting Medicaid before expansion seeing more Medicaid patients per month.

The increase in Medicaid acceptance could be a function of many things including concurrent increases in reimbursement rates for primary care services, changes in physician attitudes, and expanding Medicaid Managed Care provider networks. Future work should involve looking closer at these state-specific mechanisms of physician acceptance of Medicaid. Studying the behavior and incentives of non-pediatric PCPs, who are most likely driving the increase in Medicaid acceptance among PCPs, is of particular interest. Furthermore, physicians may not be the sole decision makers in whether they accept Medicaid; the managed care networks,¹⁸ group practices, or accountable care organizations (ACOs) they are a part of may be the drivers of deci-

sions regarding Medicaid acceptance.

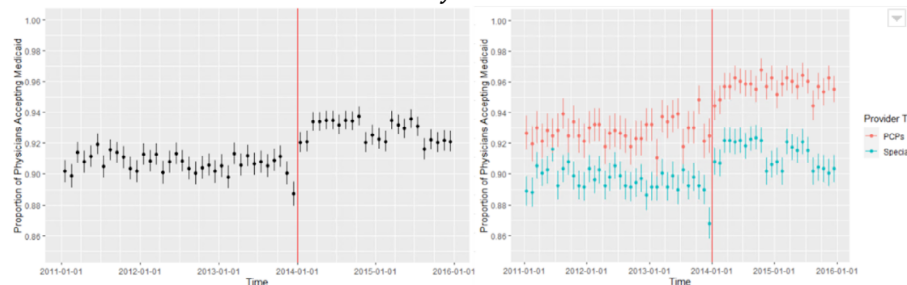
This paper serves as a first step in further study of provider acceptance of Medicaid in a state-specific context. This paper also demonstrates that data in state APCDs can be successfully leveraged for subsequent analyses. Finally, it brings attention to important questions being asked in this policy space: How well have state-specific conditions and incentives affected physician acceptance of Medicaid? How does Medicaid acceptance vary by specialty and is this of concern? The answers to these questions will play an important role in informing the broader debate on how we can deliver efficient and equitable health care in the United States.

Table 1: Mean Acceptance and Patients Seen in Year Before and Year After Medicaid Expansion Among Subsets of Physicians												
	Proportion Accepting Medicaid					Medicaid Patients Seen Per Month						
	N	Yr 2013	Yr 2014	Diff	t-stat	Sig.	N	Yr 2013	Yr 2014	Diff	t-stat	Sig.
All Physicians	1649	0.9052	0.9304	0.0252	9.12	< 0.001	1062	34.48	46.93	12.45	19.77	< 0.001
All PCPs	560	0.9304	0.9576	0.0272	6.47	< 0.001	385	45.91	57.43	11.52	8.8	< 0.001
All Specialists	1089	0.8923	0.9164	0.0241	6.63	< 0.001	677	27.98	40.96	12.98	20.63	< 0.001
Non-Pediatric PCPs	440	0.9123	0.9466	0.0343	6.89	< 0.001	273	29.15	42.22	13.07	8.55	< 0.001
Pediatric PCPs	120	0.9965	0.9979	0.0014	0.71	0.48	112	86.75	94.51	7.76	0.78	0.004

Table Notes: These are crude mean estimates which are formalized in subsequent regressions. PCPs is an abbreviation for primary care providers.

Table Notes: These are crude mean estimates which are formalized in subsequent regressions. PCPs is an abbreviation for primary care providers.

Figure 1- Medicaid Acceptance by Physicians over Time
All Physicians:



Primary Care Physicians (PCPs):

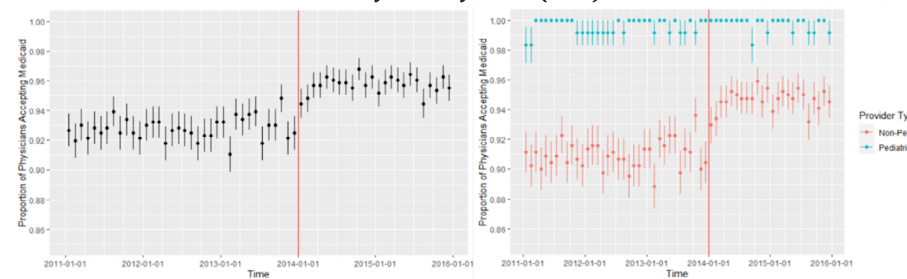


Figure Notes: Physicians are defined as accepting Medicaid in a month if they make at least one claim in the Medicaid FFS or Medicaid Managed Care line of business in that month. The vertical red line occurs at January 1, 2014, the time when Medicaid expansion took effect in RI.

Figure 2- Medicaid Patients Seen Per Month by Physicians over Time: Aggregated (left) and by Provider Type (right)

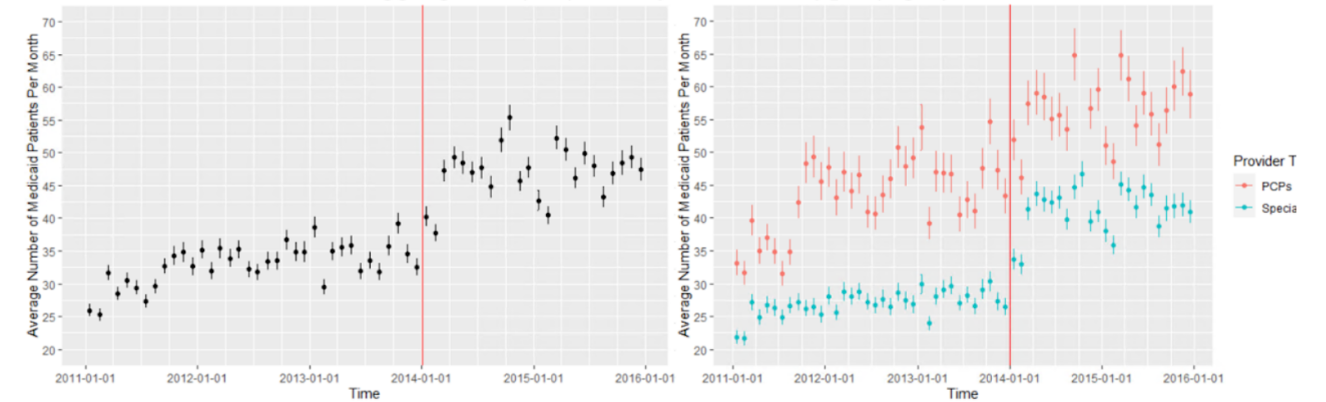


Figure Notes: The number of patients a physician sees per month was determined by counting the number of unique patient IDs found in a physician's medical claims during each month. The vertical red line occurs at January 1, 2014, the time when Medicaid expansion took effect in RI.

Table 2: OLS Regressions Across All Physicians

	Medicaid Acceptance				Medicaid Patients Seen Per Month			
	0.028 (0.0035)	0.028 (0.0034)	0.028 (0.0031)	0.028 (0.0022)	8.86 (0.725)	8.86 (0.715)	8.86 (0.594)	8.86 (0.294)
ACA ^a								
Primary Care ^b		0.037 (0.0017)				1.62 (0.437)		
Physician Specialty FE	No	No	Yes	No	No	No	Yes	No
Physician FE	No	No	No	Yes	No	No	No	Yes

Table Notes: Linear month time trends and robust standard errors were used in all regressions. Standard errors are reported in parentheses.

^a Indicator variable (1 if after Medicaid expansion, 0 if pre expansion)

^b Indicator variable (1 if physician is a PCP, 0 if not)

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Universal Health Coverage and the Global Impact of COVID-19

Authors: Gauri Gadkari, Kento Suzuki, Riki Fameli, Rinchen Dolma, Youkie Shiozawa
Field: Public Health

Abstract

Since the beginning of the COVID-19 pandemic, we have witnessed enormous disparities in the severity of its global impact. A significant factor that may influence the outcome of the disease is accessibility to sufficient health care. The main objective of this study is to determine the effects of universal health coverage (UHC) status on COVID-19 outcomes within a given country. A mixed methods approach of quantitative and qualitative analysis was used. The four quantitative outcomes explored were: cumulative case counts per 100,000; case fatality rates; testing per 1,000; and recovery rates. A total of 29 countries worldwide were investigated, including 17 UHC countries and 12 non-UHC countries. For each country, data on all six outcomes, as well as qualitative data of specific health policies, were recorded to examine the effects of a country’s UHC status on the outcomes of the pandemic in the population. Our preliminary analysis shows that UHC status may not protect against mortality in a pandemic, as countries with a case fatality rate (CFR) greater than 5% were countries with UHC. We noticed, however, that many Asian countries with UHC reported lower CFRs than their European counterparts. Additionally, our study shows that UHC countries had higher recovery rates than non-UHC nations. As the pandemic continues, follow-up analyses must be conducted in the near future to analyze the effects of UHC and access to healthcare.

Background

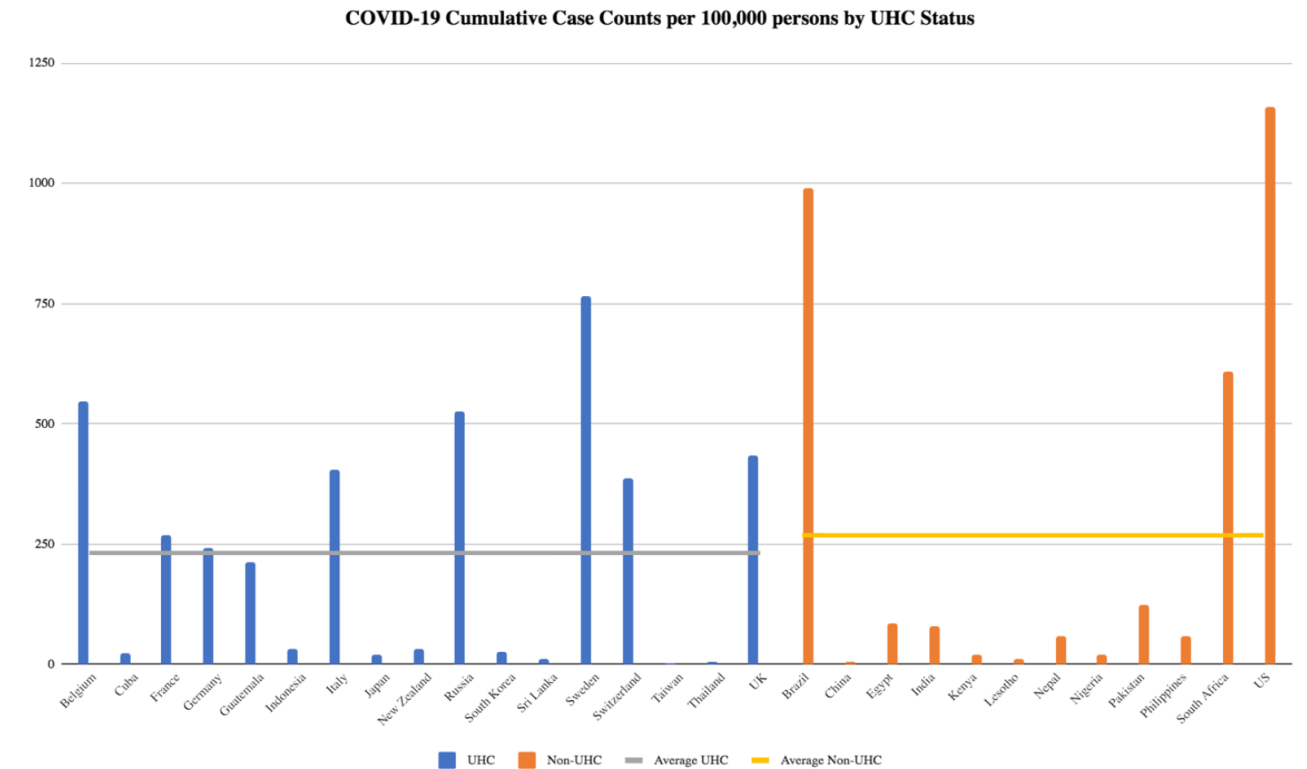
The impact that COVID-19 is causing in different parts of the world is disparate, and access to health care plays a crucial role in determining the severity of the spread of infectious diseases on a national scale [1]. One of the many measures to assess health care access in a country is its universal health coverage (UHC) status. The World Health Organization defines UHC as providing access to essential and quality healthcare services to all people without suffering financial hardships [2]. UHC is a central target of the 2030 Sustainable Development Goals (SDG), and is considered a critical component of sustainable development and poverty reduction, as well as a key element to reducing social inequities. Given the recent rise in demand for UHC across the globe, it is important to probe the extent of its role in mitigating deleterious outcomes from the pandemic.

Methods

We used a mixed methods approach to understand the differences between countries' response to the COVID-19 virus. *Quantitative approach:* The key measures were case counts per 100,000 persons, case fatality rate (CFR), recovery rate, and COVID-19 testing per 1,000 persons. For the purpose of being in the same time frame across measures that were changing daily, quantitative data collection ended on July 18th, 2020 to make the values comparable. Simple descriptive analysis was used to compare countries across these measures to get a preliminary understanding of COVID-19 responses. Microsoft Excel was utilized to standardize the data and produce the statistical graphics. *Qualitative approach:* A qualitative content analysis method was used to gain an in-depth understanding of how each country's socio-political background influenced the type and effectiveness of steps taken. The content search was conducted in the months of May - July 2020, using Google Scholar and PubMed with the search terms: "COVID-19" and the name of the individual countries. The qualitative data for this project was compiled from newspapers, television, journal articles and social media.

Results

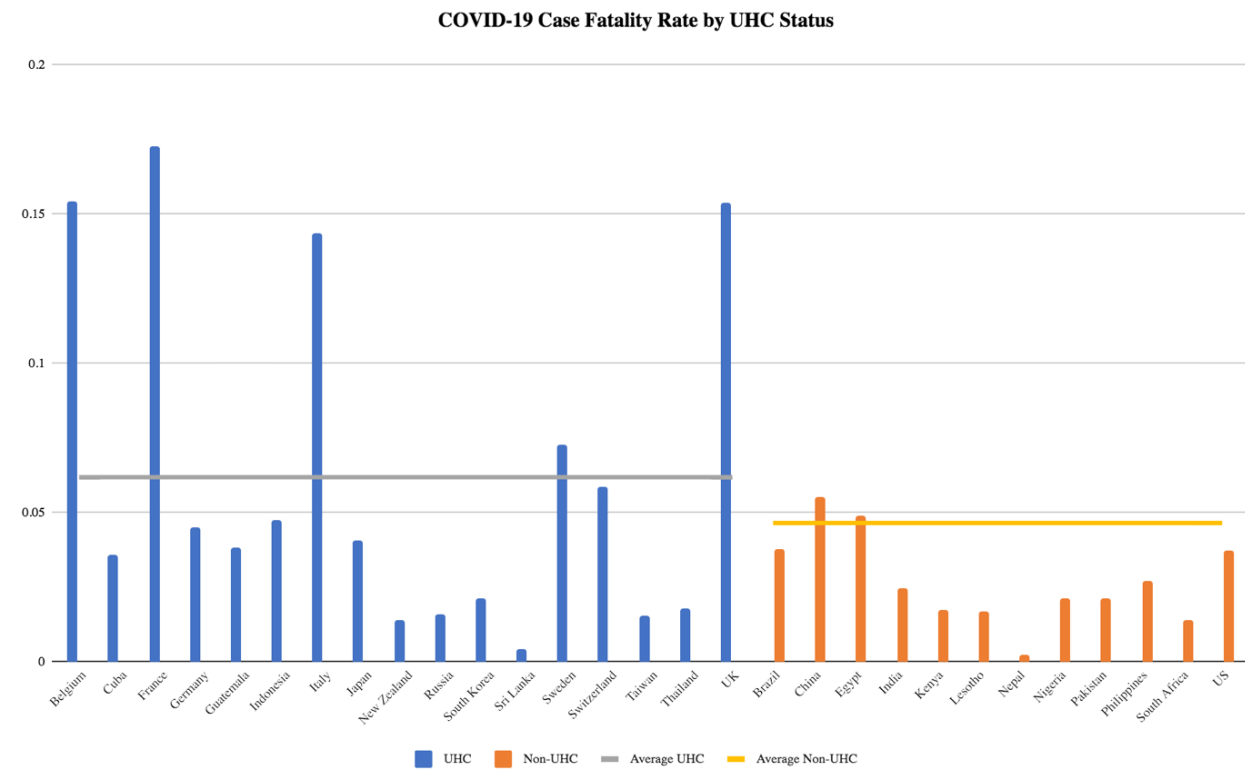
I. COVID-19 Cumulative Case Counts per 100,000 persons



On the date the data was collected (July 18, 2020), the U.S. and Brazil — both countries without a UHC system — reported the highest number of cumulative cases per 100,000 persons. The majority of the countries reporting greater than 200 cases per 100,000 persons have a UHC system. In contrast, many of the non-UHC countries reported case counts lower than that.

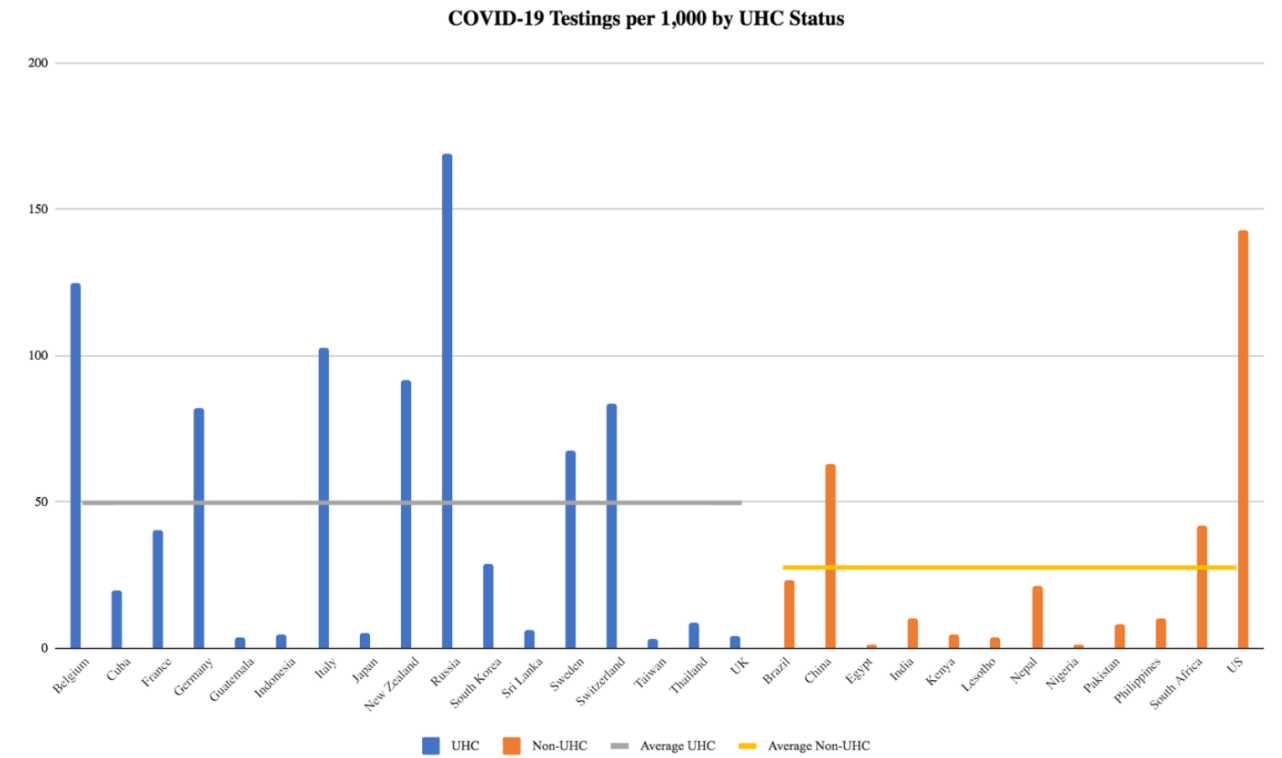
Since recognition of cases is highly dependent on testing capacity and the number of tests conducted by each country, these findings likely reflect potential biases. Some researchers claim that Brazil may have 12 times more cases of the novel coronavirus than are being officially reported by the government [5]. The country did not possess the manufacturing power to produce the large number of tests needed, and found it difficult to compete with other, wealthier countries in purchasing tests from China. Laboratories were also unequipped to process so many tests [4].

II. Case Fatality Rates



European countries with a UHC system including Italy, Belgium, the United Kingdom, and France were observed to have CFR > 5%. The majority of non-UHC countries reported less than 5% CFR. There is concern however over the validity of the information provided by some of the countries. Researchers argue that there is a vast underestimate of the true death toll from the pandemic in many nations across Latin America and the Caribbean, where in some countries over 80% of excess deaths remain unaccounted for [3].

III. COVID-19 Testings per 1,000 people



Non-UHC countries, with the exception of the U.S., reported lower testing per 1,000 compared to UHC countries. Surprisingly, some of the countries that have managed COVID-19 well, such as South Korea, Sri Lanka, and Taiwan, have relatively low testing rates. We cannot dismiss the fact that testing rates are related to the financial status of individual countries, as most of the lower-income countries explored here, such as Egypt, Guatemala, Lesotho, Kenya, and Nigeria, have very low testing rates.

IV. Recovery Rate (%) by UHC Status of the Country

The figure outlines that there may be an association between the recovery rate of a country and its UHC status. The average recovery rate of the UHC countries is 67.59%, and 51.46% for the non-UHC countries. From these points, there is a possible association between the recovery rates of countries with UHC status. Seven of the twelve non-UHC countries recorded a recovery rate below 50%.

Discussion

Our preliminary analysis demonstrated that UHC does not appear to reduce mortality in the COVID-19 pandemic. Our findings suggest that many countries with a CFR greater than five percent were countries with a UHC system. However, countries with UHC had higher recovery rates for COVID-19 than the countries without UHC. This can potentially be explained by the other measures that were included in the analysis such as access to testing. In these measures, the majority of the countries with UHC had greater access to such resources.

Strengths of this study include the use of mixed methodologies. This preliminary study further contributes to the growing scientific literature on COVID-19 and the effectiveness of UHC status during a pandemic.

Although this study evaluates 29 nations from six different continents, this size may not be sufficient to make definite conclusions. Additionally, because COVID-19 is still an ongoing pandemic, our use of a cross-sectional study design represents a major limitation to this study. Another limitation is some nations may not be reporting their case counts and testing rates accurately.

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Three month assessment of post-traumatic stress disorder, depression, and functional recovery in patients hospitalized early in the COVID-19 pandemic in the New Orleans region

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Abstract

It remains unclear whether being hospitalized for COVID-19 is associated with depression, post-traumatic stress syndrome or functional limitations after the acute illness phase. In this study of hospitalized patients early in the pandemic, 30% of patients had moderate to severe depression and 33% had Post Traumatic Stress Disorder at three months post discharge, suggesting that there should be concern over the psychological recovery of COVID-19 patients. Greater than 20 % of patients reported significant or severe limitations in overall functional recovery, while 31% reported occasional limitations in recovery. Being affected by the disease and hospitalized exposes the individual to challenges in their recovery. These factors can predispose individuals to the development of mental symptoms during or after the acute phase of the disease. Patients hospitalized with COVID-19 should be monitored for the development of mental health disorders after discharge. Early interventions developed at discharge, such as a graduated exercise regimens, coping strategies, mental health follow up and protocol driven home safety measures could benefit these individuals.

Methods

Two hundred patients that were discharged from Ochsner main campus hospital in New Orleans during the Months of March and April 2020 with primary diagnosis of COVID-19 were enrolled. The cohort of surveyed patients was equally matched between male and female as well as an equal match of patients discharged home directly or to an in-patient facility. These patients were admitted in the months of April and March and represent some of the initial patients hospitalized for COVID-19 in the New Orleans region.

All patients were mailed a survey three months after their discharge from the hospital. Patients were given one month to complete the survey. This included the Patient's Health Questionnaire-9 depression scale (PHQ9), the Veterans Post-Traumatic Stress Disorder Scale, a Post-COVID-19 Functional Status Scale, and a general survey. These measurements were chosen due to their simplicity, ability to be self-reported, and correlation with recovery from COVID-19. A follow-up phone call was made to encourage completion of the survey.

Discussion

Most people who have coronavirus disease 2019 (COVID-19) recover completely within a few weeks, exhibiting few long term effects [1]. Some patients, even those who had mild versions of the disease, continue to experience symptoms after their initial recovery. This includes a wide variety of psychological manifestations [2].

Older patients, patients with comorbidities and those with more severe clinical courses are the most likely to experience lingering COVID-19 symptoms [3]. A variety of physical complaints have been well documented, as well as a growing body of evidence suggesting psychological and overall functional limitations. In this study, nearly 30% of patients had moderate to severe depression secondary to COVID-19 by the PHQ9 scale (Figure 1). It was also observed that 31% had post-traumatic stress disorder at three months post-discharge, as evidenced by the results of the Veteran's PTSD Scale (Figure 2). This data suggests that there should be concern over the psychological recovery of COVID-19 patients.

Greater than 20% of patients reported significant or severe limitations in overall functional recovery and 31% reported occasional limitations in recovery. Although complete physical recovery is the norm for most COVID-19 patients,

this study demonstrated continued significant functional disability for over 50% of patients three months after discharge from the hospital, as seen in the Post-Covid-19 Functional Recovery Scale depicting limitations in daily life (Figure 3). This is somewhat expected as patients admitted to the hospital have a more severe form of COVID-19 which is associated with persistent long-term symptoms.

The purpose of this study is not to definitively assess the incidence of psychological disease and functional recovery in the recovery of COVID-19 patients, but rather to provide information that may impact the ongoing evolution of discharge planning among hospitalized patients. The scale of the pandemic has necessitated the rapid adaptation of best practices and data on an ongoing basis. Hospitalization is a traumatic event, but possibly even more so for COVID-19 patients. Many of the tools—both formal and informal—used to mitigate the trauma of a hospitalization have not been available during this pandemic. This includes the physical component of family and staff support in the hospital, social support after discharge and having overall confidence in the expertise of the healthcare system. Phone call follow-ups and patient satisfaction surveys have improved many of these areas, but barriers still remain.

Enhancing COVID-19 Psychiatric and Functional Recovery

As with many other aspects of the COVID-19 pandemic, recovery may be a challenge and there is still much to learn. The trauma of a COVID-19 hospitalization and possible post discharge depression will continue to have a significant impact on recovery. After the initial strain on health care systems due to the pandemic, we may now have the opportunity to address some of the long-term recovery issues.

It is suggested that after trauma, there are five essential elements — sense of safety, a calming environment, social connectedness, self-reliance, and optimism — that help buffer against long term adverse effects [4]. It has been a struggle to obtain each of these after a hospitalization for COVID-19 due to system restraints and limited resources. Discharge planning should take each of these areas into account. Safety should be addressed by giving specific protocols for caregiver safety as well as a timeline for reintroduction to society. A plan to limit social isolation should include follow up phone calls and family support. As noted by the results of this study, depression

should be screened for in follow up appointments.

Functional recovery should also be aggressively considered among all patients. Predicting long term functional recovery has proven to be problematic, as even mild cases may have long term limitations. A discharge plan should include a gradual exercise program, simple pulmonary rehab, and possibly reflective mental exercises such as meditation. A protocol driven program that addresses home safety issues may promote self-reliance, optimism and an increased confidence in the healthcare system as a whole.

In this unprecedented pandemic in which many of our initial efforts have focused on technological medical advances, these simple, relatively inexpensive, and personal measures may be of great benefit.

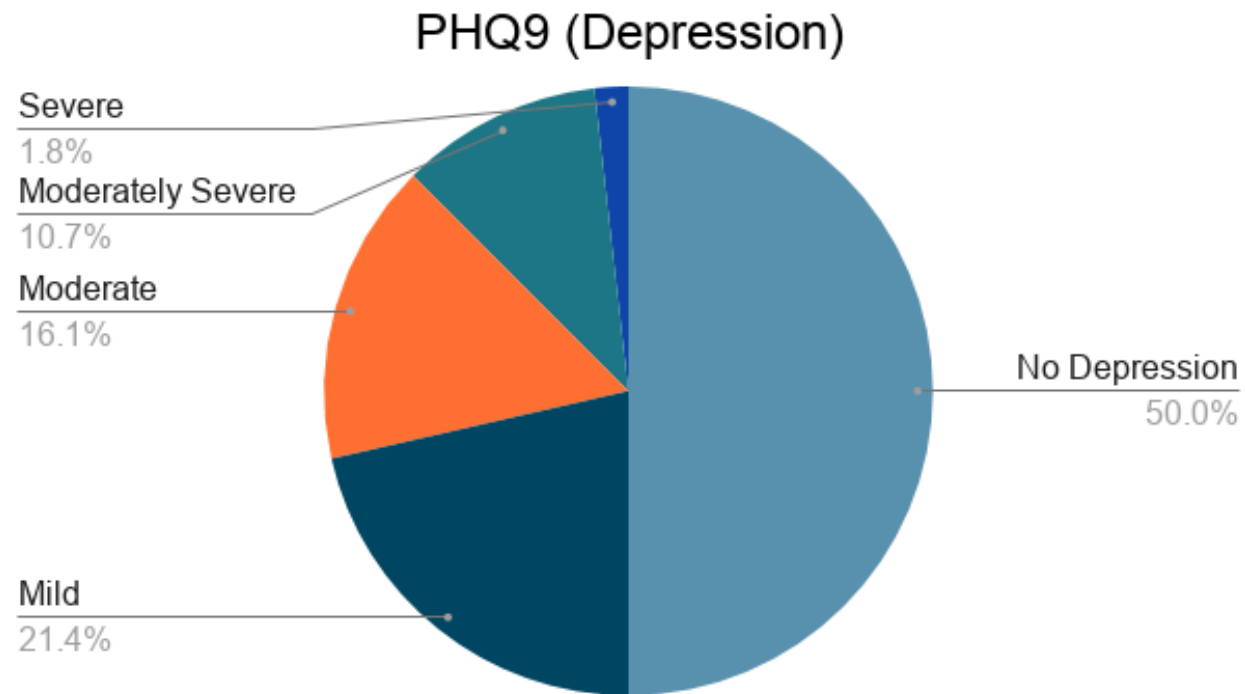


Figure 1 - Percentage breakdown of survey respondents diagnosed with or without PTSD

Veteran's PTSD Scale

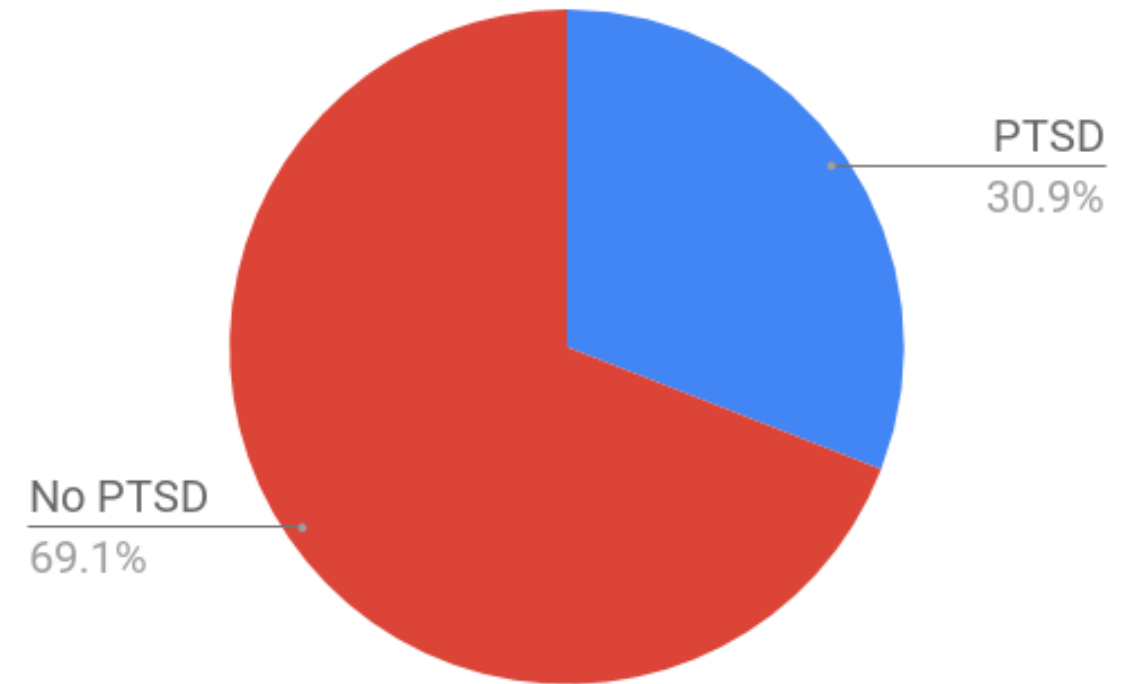


Figure 2 - Percentage breakdown of survey respondents by severity of depression

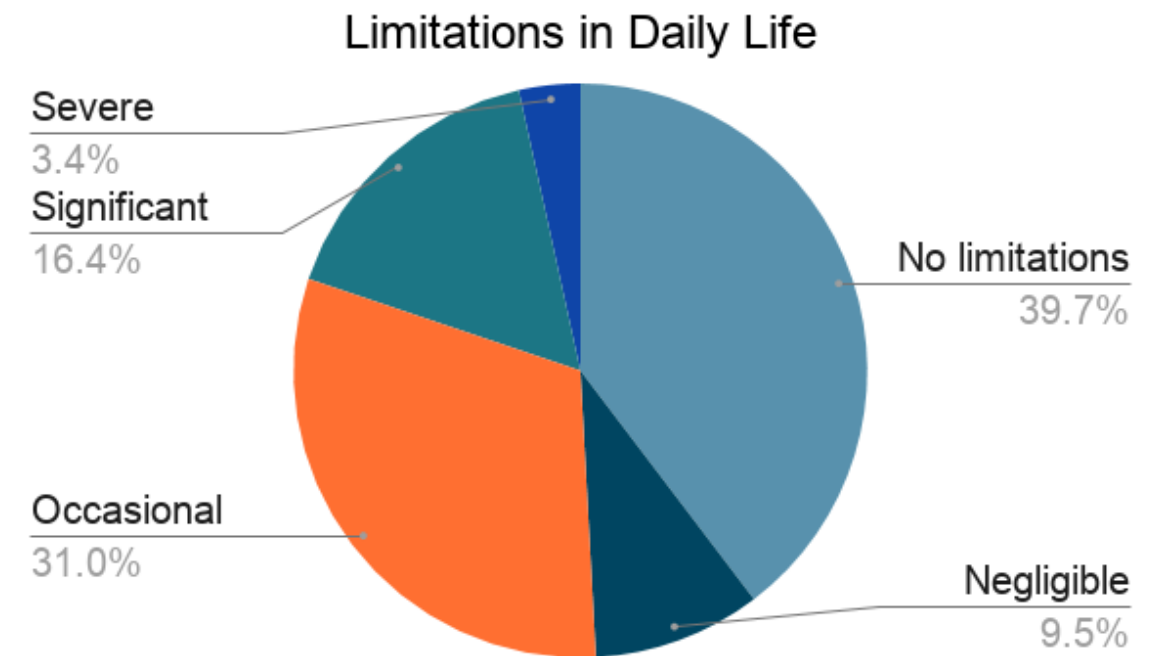


Figure 3 - Percentage breakdown of survey respondents by level of independence in day-to-day life

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Humanities and Social Sciences

Humanitarian Consequences of the bin Laden Manhunt

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Several factors contributed to the CIA's decision to employ a humanitarian cover during the bin Laden manhunt. The hunt was a time-sensitive priority, there was precedent for use of neutral actors by the Agency, and the complicated ties between the humanitarian and national security world would have advantaged this decision.

The bin Laden vaccination campaign is part of a long-standing and ongoing debate regarding the advantages and potential consequences of a neutral cover. The Agency has used actors with a perception of neutrality like journalists, the Peace Corps, and religious figures in covert operations throughout its history. In 1996, the Senate Select Committee on Intelligence held a hearing and suggested that covert activity must have “a very specific and a really high-level showing of necessity before a journalist or Peace Corps operator or clergy would be used by the CIA.” They cited violence against neutral actors, but the 1997 Intelligence Authorization Act allowed the ban on these covers to be waived with presidential approval.

Then-Director of Central Intelligence John Deutch likely would have argued that the bin Laden manhunt presented an exceptional circumstance as bin Laden plotted further attacks and “the Nation would look to the Agency to use all possible measures, all possible means, to detect and deter such an event.” As it has precedent in CIA history and was supported by the Executive, it is not unreasonable that the CIA would make this decision in the very critical hunt.

Fundamental misunderstandings or misinterpretations of the role of humanitarians cause tension between U.S. officials and NGOs. In 2001, then Secretary of State Colin Powell said that NGOs are “force multipliers” and “an

important part of our combat team” in the GWOT. Powell received pushback from the NGO community for his comments, as they caused concern about the neutrality of U.S.-based humanitarian organizations. The model of “humanitarian soldiers” further complicates the landscape, as militaries actively engage in humanitarian work with a political goal. This visual connection between humanitarian activity and American forces in Afghanistan had grave consequences, as aid worker killings rose during the mid 2000s.

Many humanitarian organizations receive the bulk of their funding from the U.S. government, amidst both unspoken and overt pressure to comply with U.S. policy objectives. Save the Children USA receives 61% of its funding from the U.S. government. The International Rescue Committee receives 76% from the government, and CARE USA receives 83%. In 2004, former USAID chief administrator, Andrew Natsios, “threatened to ‘tear up’ contracts with NGOs and ‘find new partners’ should NGOs not be supportive of U.S. policy objectives.” The exploitation of this connection during the bin Laden manhunt shattered the already fragile trust of humanitarians in Pakistan. The consequences of the CIA's vaccination campaign include restrictions on humanitarian access and increased violence against humanitarians that detract from public health efforts.

For many in Pakistan, this operation confirmed long-standing suspicions that humanitarians were tools of western governments. Pakistan expelled Save the Children in 2012, with Interior Minister Chandry Nisar Ali Khan saying,

Local NGOs that use foreign help and foreign funding to implement a foreign agenda in Pakistan should be scared. We will not allow them to work here whatever connections they enjoy, regardless of the outcry.... Let me clarify: offices of any international NGO found doing anti-Pakistan activities would be shut down.

Save the Children staff were given a week to vacate and their building was chained closed. Pakistan canceled agreements with at least 15 foreign charities that it believed were involved with foreign intelligence-gathering efforts in the Federally Administered Tribal Areas (FATAs). The perceived actions and affiliation of even one NGO can affect many others in the region.

Also, the Pakistani Taliban used the revelation to further anti-vaccine propaganda, and more than 60 polio vaccine workers have been killed by the

Pakistani Taliban since the raid. A Johns Hopkins University study states that between 1997 and 2005, 320 humanitarian workers were killed. However, in 2011 alone, 308 aid workers were killed, wounded, or captured — “the greatest number on record” according to the British Medical Journal. The number has continued to rise, and according to Humanitarian Outcomes’ 2014 Aid Worker Security Report, 2013 “set a new record for violence against civilian aid operations, with 251 separate attacks affecting 460 aid workers.” Pakistan was named among the top five most violent countries for aid workers by Humanitarian Outcomes. In 2019, a mob set fire to a government health facility administering polio drops in Abbottabad where the 2011 vaccine campaign occurred.

Increasing violence and restrictions against NGOs also contributes to long-term negative impacts on public health initiatives in Pakistan. In 2011, Pakistan had 650 polio cases - the most in the world. Seventy-three percent of these cases are linked to the FATAs that have a strong Taliban presence and history of conflict with Pakistan’s central government. Taliban rhetoric has further hurt the Global Polio Eradication Initiative. A Taliban fatwa (religious edict) issued in June 2012 read, “polio agents could also be spies as we have found in the case of Dr. Shakil Afridi has surfaced. Keeping these things in mind we announce to stop the polio dosage.” This suggests a potentially causal relationship between the blurring of humanitarian and intelligence-gathering lines and long-term consequences for Pakistan’s public health.

The violence, program setbacks, and access restrictions are part of the ethical and operational dilemmas faced by humanitarians. Their primary protection is supposed to be the Humanitarian Principles. However, “neutrality” is more of an ideal than a reality, and humanitarians must make choices between the Principles, their security, and the effectiveness of their programming. Strict adherence to the principles of humanitarianism is meant to prevent organizations from having to make these decisions. However, in the complicated and clandestine world of future operations, planners on all sides have the responsibility to consider these consequences. The future of humanitarianism depends on these challenges being met.

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Westernizing Fashions: The Nationalization of Gender Identity in Early Modern Russia

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Field: Slavic Studies

Abstract

This study examines the roots of contemporary Russian gender identity by evaluating the influence of 18th century cultural reformations on 19th century national identity development. Beginning in the early 18th century, old traditions of Russian Patriarchal Orthodoxy were discouraged by Peter the Great, who believed that Russia needed to advance from a "backward" country by emulating the cultures of Western European nations. The result of these discouraged patriarchal traditions was a patina of feminine liberation, which became the status quo of Russian society, notably during the period of Catherine the Great (1762-69). Her death in the late 18th century marked the beginning of a reactionary conservative culture, which preached against Russia's Westernization. They believed that Russian society was suffering because it was attempting to emulate Europe, a task that was both unachievable and undesirable. To combat the "evil West," they conceptualized the Russian Empire as a separate entity from the rest of Europe, one that could not be evaluated by the same metrics of success as its peers. But because of the foreign academic training of the Russian elite, there was no realistic way for them to "unlearn" their thought paradigms; Western traditions had already gripped Russian society in such a way that they were either considered "normal," or a Westernized version of the Russian tradition existed. This paper applies this theory of religion, sexuality, gender, and culture to the development of Russian fashion culture during the 18th and 19th centuries and demonstrates the cultural implications of both tradition and advancement.

Gender and National Identity During the Early 19th Century

In the beginning of the 19th century, Russian Orthodoxy stipulated that both women and men should dress modestly, so as to keep their focus on their faith and devotion to God. Yet Russian aristocrats, especially Russian aristocratic women, did not follow this provision. Because their wealth and status had to be demonstrated when they were allowed to be publicly visible, they turned to the latest French trends. But as European fashions became increasingly in style, only the poor or staunchly Orthodox (i.e. Old Believers) held fast to the archaic styles of fashion.

However, the choice not to don the latest vogues could also have meant that one was taking pride in their cultural heritage. The empress Catherine II promulgated the idea that one should not be ashamed of their *Russianness*, and frequently made it apparent through her wardrobe: if not a Russian soldier's uniform, she often wore a Russian dress. Her dedication to make the citizens of her empire take more pride in their native fashion manifested through restrictions on importing Western fashion [1]. She hoped Russians would modify their own clothing to be more Western, but nevertheless maintain a distinct Russian style. Her dress of choice was a "sarafan francisé (Frenchified sarafan) ... a low-cut dress which had long-slit, hanging sleeves, and a short train" [2]. However, after Catherine II's death, European fashion went through drastic cultural changes.

Changing Fashions in the 19th Century

As Russia attempted to de-Europeanize in the early 19th century, the role of the French language was removed from the realm of fashion. Since Paris was the global hub of fashion, monolingual, aristocratic Russian women were unable to participate in Western cosmopolitanism. Thus, domestic Russian cosmopolitanism, mainly through fashion journals, developed to meet this demand. Aesthetics were mainly promoted through fashion journals, which up until 1831 were only focused on Western fashion. All the journals were in French, and advocated for a Eurocentric view of the garment world. If women wanted to participate in this cosmopolitanism, they had to learn French. In the 19th century this became a problem, as speaking French in aristocratic circles was increasingly frowned upon.

As the main target audience of fashion journals, Russian women were perceived to be the arbiters of Russian language; they were targeted to advance

Slavophilic thought. Since women were intended to be domestic and docile, and give all of their attention to the social spheres available to them, they had the ability to decide what was socially "in vogue." As the national opinion on the French language reversed, women wanted to look into the newest fashions, but only in Russian.

The problem of a lack of Russian fashion present in journals was solved by Elizaveta Safonova, who in 1831 published a journal called *Vaza*, or *The Vase*, which included a section on the fashions of Saint Petersburg [3]. Although this did alleviate the amount of global dissonance the women of Russia felt, it did not eliminate the usage of French in Russian journals. Olga Vassilieva-Codognet writes that, "the amount of French varies very much from one journal to another, ranging from whole pages... to just a few words..." [4]. Since Russian women, who wanted to read the journals, were finding them increasingly inaccessible, journal publishers either used calques (borrowed transliteration), putting the Russian translation after the French, or placing the French word in brackets after the Russian [5].

In early 19th century Russia, it was uncommon for a woman to be running a journal, let alone a business. Elizaveta Petrovna had some independence outside of the household, which was previously unheard of. Because there were women owning and operating businesses, the national perspective on the role of the woman had certainly not regressed to Pre-Petrine standards; the loss of access to the throne did not entail that the subjugation of women was absolute.

Hence, Russian society was able to have its cake and eat it too: Russian ladies could access the cosmopolitanism of France without having to learn French, simultaneously embracing Westernization while viewing it through the lens of the Russian language. Cosmopolitanism, however, further subjugated the women of Russia into gentle positions, encouraged them to browse fashion magazines, and retain their docile role. Although women did not enjoy the same freedoms as they did in the 18th century, they were overall allowed greater flexibility than their pre-Europeanization counterparts.

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United States Baseball's Exploitation of Latin America and its Athletes

Author: Ingrid Ren

Baseball, internationally seen as America's favorite pastime, is also feverishly followed as the favorite sport of Latin American countries Cuba, the Dominican Republic, and Venezuela. Since baseball was first introduced to Latin America through Cuba in the late 19th century, Latin American baseball players have been recruited to American leagues and today make up over a quarter of the Major League and around half of the Minor League, with one out of ten Major League players coming from the Dominican Republic (Ruck). However, underneath this high representation of Latino baseball players lie dirty, American recruitment tactics and a history of exploiting Latin America. Driven by baseball's popularity and status in the U.S., a network of American and Latino baseball recruiters target young, Latino boys and exploit them in inhumane academies across Latin America and the Caribbean, lured by the promise of attaining fame and wealth in the United States. In order to understand the existence of these baseball academies, this paper will study how the historic presence of the United States military in Latin American countries, alongside promoting the existing popularity of baseball in the area, creates a precedent of American exploitation of the economy and land that extends to an exploitation of young, Latino boys.

A Ramseyan Resolution of Ontological Commitment in First-Order Paraphrases of Beauty Judgments

Author: Ben Zimmerman
Field: Philosophy

The sentence “that painting is beautiful” seems simple, but what does the sentence actually say? Does it declare that the painting has the property of beauty? Does it posit that the gestalt of the painting’s features makes it beautiful? Or is it a personal statement about how the painting struck the viewer? As I will explain, each potential answer hinges on a presupposition about the nature of beauty.

Using first-order logic as an investigative medium, I demonstrate how presuppositions of beauty figure into the meaning of sentences such as “that painting is beautiful” (call such sentences ‘beauty judgments’).

Conventionally, simple copular descriptive statements, like the above beauty judgment, can be translated into first-order logic as follows:

“x is beautiful” is rendered as Bx

“Some person is beautiful” (i.e., there is some x who is a person and who is beautiful) as $\exists x(Px \wedge Bx)$

“Every person is beautiful” as $\forall x(Px \supset Bx)$, where $P\textcircled{1}$ means “ $\textcircled{1}$ is a person” and $B\textcircled{1}$ means “ $\textcircled{1}$ is beautiful”

While these standard paraphrasing methods work just fine with statements like “some cat is not blue,” which would be written $\exists x(Cx \wedge \sim Bx)$,

when it comes to beauty judgments, these standard paraphrasing strategies fail.

To best understand why, one can look to discussions of the predicability of existence. If a logic allows existence as predicate such that, e.g., $x!$ means “x exists,” then existence is being treated as a property. This treatment is problematic because it is then quite difficult to say what existence adds to a bundle of other properties. Are we to say that there are quiescent agglomerations waiting for existence to be added to them before they can become actual things? But then how could properties exist as unrealized potentials before existence is predicated of them? Attempts to paraphrase beauty judgments (e.g., “x is beautiful”) run into similar difficulties.

Like existence, beauty is a fairly abstract concept (a “theoretical term,” to use Ramsey’s locution). It is difficult to say how a beautiful unicorn (u_1) might differ from a not-beautiful unicorn (u_2) if they otherwise have the exact same properties. It cannot be that, on the most inclusive catalog of properties, u_1 is the same as u_2 : if this were the case, they would have to have the same beauty status by Leibniz’s law of the identity of indiscernibles. It would not, moreover, solve the problem to append Bu_1 (where Bx : “x is beautiful”) to a description of u_1 because, just as we were led to ask how existence could be added to an agglomeration of properties without changing the other elements, we would have to ask how beauty could magically be added to an agglomeration.

The only common alternative would be to take the modified sentence “unicorns [1] are beautiful” and symbolize it with the universal affirmative form: $\forall x(Ux \supset Bx)$ [2]. But this schematization reflects a characterization of beauty as simply a nominal category to which any “beautiful” thing belongs. For many-over-one epistemologies, the understanding reflected in this symbolization might be totally satisfactory (though it certainly would not be for any one-over-many Platonist).

But whether you think instantiations of a property should have a unifying form (eidos) or not, conceiving of beauty as an index of beautiful objects makes for a sort of Euthyphro dilemma: Does a beautiful object encode beauty because it belongs to the class of beautiful objects, or does it belong to

the class of beautiful objects because it encodes beauty?

On top of all the objections that have been made, the apparent necessity of using material implication is troubling given the nature of its truth-functionality (viz., an implicative schema can be false if and only if its antecedent is true while its consequent is false). The schema does not preclude something that is not a unicorn from being beautiful. While this may seem perfectly reasonable given that we wish to deem a number of things beautiful, we have left logical room for the possibility of an object whose sole characteristic is being beautiful, and that is of course nonsensical.

If one wishes to say that something is beautiful—and to do so using the language of first order logic—one is forced to use predicative expressions. In light of everything discussed so far, this limitation seems like an insurmountable obstacle. However, that misperception is due to the fact that every treatment of the beauty predicate up to this point has committed us to an ontological characterization of beauty as a property no different from, e.g., texture.

There is, however, a way to use the beauty predicate without abasing beauty's ethereal ontic status. As Frank Ramsey famously suggested, “a judgment ha[s] no single object, but is a multiple relation of the mind or mental factors to many objects, those, namely, which we should ordinarily call constituents of the propositions judged” [3]. In other words, we can expand our conception of beauty to a theoretical quality we have epistemic access to only through its “structural” properties: we eliminate direct reference to the unobservable aspect and “connect the theoretical content... with observable behavior” [4].

In order to do this logically, one “[takes] all the sentences affirmed in a scientific theory that use some term (e.g. ‘quark’), replac[es] the term by a variable, and existentially quantif[ies] into the result” [5]. This makes a Ramsey sentence. So, if we wish to use the Ramsey-Lewis method of defining theoretical terms for the issue at hand, we must find a description of beauty that defines it in light of a complex chain of effects that it produces.

To this end, I have selected a quatrain of Charles Baudelaire’s “Hymne à la Beauté” which Alexander Nehamas quotes in the epigraph to his book *Only a Promise of Happiness*. The poem reads:

“Who cares if you come from paradise of hell, / appalling **Beauty**, artless and monstrous scourge, / if **only your eyes, your smile or your foot reveal / the Infinite I love and have never known**” [6].

Now, we select the parts of the stanza that are logically relevant (the bolded portion) and rephrase them using language more conducive to first-order paraphrasing:

Beauty is such that: if there is a thing (x) that is beautiful, then its eyes, its smile, or its foot imply the revelation of an infinity such that the infinity is loved by x but was not heretofore known to x, and for any thing (y) such that •the eyes of y, the smile of y or the foot of y imply the revelation of an infinity such that the infinity is loved by y but was not heretofore known to y,• then y is identical to x.

Now let: $B^{\textcircled{1}}$ mean “ $\textcircled{1}$ is beautiful”; $P^{\textcircled{1}\textcircled{2}}$ mean “ $\textcircled{1}$ is a property of $\textcircled{2}$ ” (e.g., P_{ex} : “eyes of x”); $R^{\textcircled{1}\textcircled{2}}$ mean “ $\textcircled{1}$ is revealed to $\textcircled{2}$ ”; $L^{\textcircled{1}\textcircled{2}}$ mean “ $\textcircled{1}$ loves $\textcircled{2}$ ”; $K^{\textcircled{1}\textcircled{2}}$ mean “ $\textcircled{1}$ is heretofore known to $\textcircled{2}$ ”; e mean “eyes”; s mean “smile”; and lastly let f mean “foot.” Additionally, define the function $\Psi^{\textcircled{1}}$ as equivalent to $((P_{e\textcircled{2}} \supset R^{\infty\textcircled{2}}) \vee (P_{s\textcircled{1}} \supset R^{\infty\textcircled{2}}) \vee (P_{f\textcircled{1}} \supset R^{\infty\textcircled{2}})) \wedge (\infty = (L^{\textcircled{1}\infty} \wedge \sim K^{\infty\textcircled{2}}))$.

Now, with x as the beautiful object, we get the Ramsey sentence:

$$\exists x \exists e \exists s \exists f \exists \infty [B_x \leftrightarrow [((P_{ex} \supset R^{\infty x}) \vee (P_{sx} \supset R^{\infty x}) \vee (P_{fx} \supset R^{\infty x})) \wedge (\infty = (L_{x\infty} \wedge \sim K^{\infty x})) \wedge \forall y (\Psi_y \supset (y=x))]]]$$

This schema skirts all of the issues that have previously been discussed. All it essentially says is that beautiful objects are those objects which precipitate the observable effects described above. Now we have a deductively evaluable argument, logically defining beauty, and if that isn’t valuable—

aside from what its structure shows us about what we mean when we call something beautiful (as well as how we make sense of such beauty judgments)—then little of logic is.

References

1. A generic equivalent to saying “all unicorns” or “every unicorn,” &c.
2. “For all individuals, if x is a unicorn, then x is beautiful.” However, n.b., the “if..., then” construction here does not signify causal implication but rather material implication.
3. Ramsey, 1927a, 154, as quoted in; MacBride, Fraser, Mathieu Marion, María José Frápolli, Dorothy Edgington, Edward Elliott, Sebastian Lutz, and Jeffrey Paris. “Frank Ramsey.” Stanford Encyclopedia of Philosophy. Stanford University, August 14, 2019. <https://plato.stanford.edu/entries/ramsey/>.
4. Ladyman, James. “Structural Realism.” Stanford Encyclopedia of Philosophy. Stanford University, January 10, 2014. <https://plato.stanford.edu/entries/structural-realism/#ESRRamSen>.
5. “Ramsey Sentence.” Oxford Reference. Oxford University Press, November 3, 2019. <https://www.oxfordreference.com/view/10.1093/oi/authority.20110803100403458>.

