Project Notes:

Project Title: How Modifications in Ethnic Diet Can Alter Drug Efficiency in Individuals
Name: Patel, Saara

Contents:

Knowledge Gaps:

This list provides a brief overview of the major knowledge gaps for this project, how they were resolved and where to find the information.

Knowledge Gap	Resolved By	Information is located	Date resolved
Why is the pharmacogenetics technology underutilized?	Reading a journal article	In my project notes	08-20-2025
How can I inhibit a gene?	Article from Gordon Library	In my project notes	9-1-2025
What is Watson-Crick base-pairing?	Reading a library article	In project notes	9-13-2025
How can I measure plant protein content?	Reading a journal article about an at-home method	In my project notes	9-27-2025
What animal to use as a model for humans in terms of genetic material?	Talking to a peer/classmate.	Information is not written.	10-6-2025
What is the broad effect of the implementation of pharmacogenetics	Reading a journal article	In my project notes	10-8-2025
Where kolaviron is accessible	Researching where the ingredient can be found (scientific websites, supermarkets)	Information is not written.	10-23-2025
What is RT-PCR	Looking at Sci-Lit presentations and other procedures available online	Information is not written.	11-6-25
What primers are needed for RT-PCR, and what genes should I be focusing on	Looking at pre-existing studies on 1) what genes are known to be affected by the ingredients I am studying, and 2) studies that have listed primer sequences for the same genes	In a private Google document that I have created	11-11-25
What other bioactive	Google search of	In all MSEF and grant	11-16-25

ingredients can I use in my experiment?	related articles	documentation	
Dosages needed for ellagic acid (enough to provide effects but not toxicity)	Reading a journal article	In a private Google document I have created, and in an email to Dr. C	11-24-25
How oxidative stress is relieved in Drosophila on a curcumin diet	Reading a journal article	Information is not written.	11-30-25
Why does an increase in locomotion occur even when ethanol consumption is higher	Reading a journal article	Information is not written.	12-10-25
What are the ortholog genes for human CYP3a4 and CYP3a5 metabolism genes?	Using search engines, such as Google	Information is in a private Google Doc	1-7-26
What are the minor allele frequencies of CYP genes in Asia and the Middle East?	Reading journal articles on MAF values	Information is logged in a private Google Doc	1-22-26
What is the standard lab procedure used to isolate RNA?	Reading journal articles	Information is not written.	2-1-26

Literature Search Parameters:

These searches were performed between 8/13/2025 and 2/10/2026.
List of keywords and databases used during this project.

Database/search engine	Keywords	Summary of search
PubMed Database	plateau, clopidogrel, *CYP2C19*, allele, genotype, phenotype	In this search I learned of clopidogrel, which is a drug. It also revealed that in gene variation of CYP2C19 affects how we digest/absorb/react to the drug. The search related pharmacogenetics to ethnicity and frequency of genes in a population.
Gordon Library	Drosophila, CYP family, inhibitor, drug, medicine	This search presented me with research that correlated drosophila, fruit flies, with humans. Many described the use of drosophila as a model organism for humans, despite their size.
Gordon Library	CRSIPR, blue-light, precision, gene-editing, cells	This search yielded results surrounding how genes can be inhibited using CRISPR. It also came up with articles surrounding how this technology can be taken to the next step with UV light.
Gordon Library	CYP genes, RT-PCR, gene-specific primers	The search yielded results surrounding articles that have already done RT-PCR on the genes I have identified and provided the forward and reverse reactions for me to use as reference
Gordon Library	Geographic ingredient, CYP inhibitor, Middle East	This search mainly yielded results on ellagic acid, which is a compound native to the middle East and has known effects on CYP alleles. Its dosage in Drosophila is normally 200µg.
Gordon Library	RTPCR, gene primers, RNA isolation	This search yielded results for lab procedures using RNA

		isolation for future use in RT-PCR.

Article #1 Notes: Personalizing Medicine with Clinical Pharmacogenetics

Source Title	Personalizing Medicine with Clinical Pharmacogenetics
Source citation (APA Format)	Scott S. A. (2011). Personalizing medicine with clinical pharmacogenetics. *Genetics in medicine : official journal of the American College of Medical Genetics*, 13(12), 987–995. https://doi.org/10.1097/GIM.0b013e318238b38c
Original URL	https://www.gimjournal.org/article/S1098-3600(21)03612-1/fulltext
Source type	Journal
Keywords	Clinical pharmacogenetics, pharmacogenomics, genetic testing, personalized medicine, molecular genetics
#Tags	
Summary of key points + notes (include methodology)	Pharmacogenetics, first looked into in the 1950s, involves the specialization of medicine to a person's genetic information, resulting in optimal treatment and few adverse effects. Using this information, it is possible to look at variations in their DNA to identify risks or changes needed to their treatment plan- for example, in terms of dosages- but this technology is still working to be further implemented. Variations in genes, such as for the CYP gene, which has large effects on metabolism rates, ranging from poor to ultra-rapid, code for different phenotypes that respond to medication differently. Different ethnicities will also play a role in PGx results. The study performed found that Asians and African-Americans are prone to the reduced function alleles, and the Ashkenazi Jewish population needs higher dosages of warfarin, a drug to prevent blood clots. Slowly, but surely, this advancement in the medical field is growing. The FDA has worked to edit the labels of drugs to include new pharmacogenetic information. It is still being decided how the cost of this new option will be treated by insurance, but its accuracy and validity (analytic, clinical, ethical, legal, and social) are the first steps towards making it a reality. As of right now, for diseases other than Mendelian ones, which are multifactorial, the tests performed are not always as beneficial as hoped. In addition to that, education among clinical professionals is vital to boosting its use.
Research Question/Problem/ Need	What is pharmacogenetics, and why is it not more widely utilized?
Important Figures	

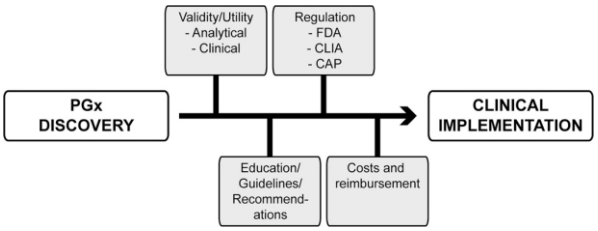


Figure 1 This is a chart of the current challenges and barriers to clinical implementation of pharmacogenetics.

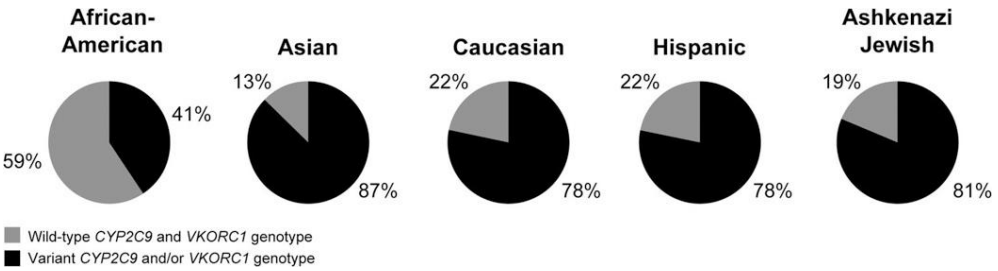


Figure 2 Population frequencies of wild-type CYP2C9. Thers is a significantly higher frequency of African-Americans who are wild-type for both CYP2C9 and VKORC1.

Drug(s)	Gene(s)	FDA drug label section with pharmacogenomic information	Reference	Organization
Abacavir	*HLA-B*5701*	Boxed warning, contraindications, warnings and precautions, patient counseling information	Becquemont et al.[8]	ESF-UB
Azathioprine/ 6-mercaptopurine	*TPMT*	Dosage and administration, warnings and precautions, drug interactions, adverse reactions, clinical pharmacology	Becquemont et al.[8]	ESF-UB
			Relling et al.[72]	CPIC[9]
Clopidogrel	*CYP2C19*	Boxed warning, dosage and administration, warnings and precautions, drug interactions, clinical pharmacology	Holmes et al.[73]	ACCF/AHA
			Becquemont et al.[8]	ESF-UB
			Scott et al.[74]	CPIC[9]
Codeine	*CYP2D6*	Warnings and precautions, use in specific populations, clinical pharmacology	Crews et al.[75]	CPIC[9]
Flucloxacillin	*HLA-B*5701*	—	Becquemont et al.[8]	ESF-UB
Irinotecan	*UGT1A1*	Dosage and administration, warnings, clinical pharmacology	EGAPP Working Group[76]	EGAPP[77]
Selective serotonin reuptake inhibitors (SSRIs)	*CYP2C19/CYP2D6*	For selected SSRIs, see FDA Biomarker Table[a]	EGAPP Working Group[78]	EGAPP[77]
Statins	*SLCO1B1*	—	Becquemont et al.[8]	ESF-UB
Tacrolimus	*CYP3A5*	—	Becquemont et al.[8]	ESF-UB
Tamoxifen	*CYP2D6*	—	Becquemont et al.[8]	ESF-UB
Warfarin	*CYP2C9/VKORC1*	Dosage and administration, precautions, clinical pharmacology	Flockhart et al.[79]	ACMG
			Becquemont et al.[8]	ESF-UB
			Johnson et al.[80]	CPIC[9]
Multiple (53 drugs)	Multiple (11 genes)	For selected drugs, see reference and FDA Biomarker Table[a]	Swen et al.[10]	KNMP-PWG

Figure 3 These are guidelines, recommendations, and statements on pharmacogenetic.

VOCAB: (w/definition)

Mendelian disease- Diseases that occur due to a mutation in a single gene
Whole-exome- Regions of the genome for responsible coding proteins
DTC- (direct to consumer) companies that sell straight to the consumers of the products
Porphyria- a rare group of genetic disorders that affects the production and path of a critical part of the hemoglobin, also known as the heme. It is a buildup/clog of toxins in the body.

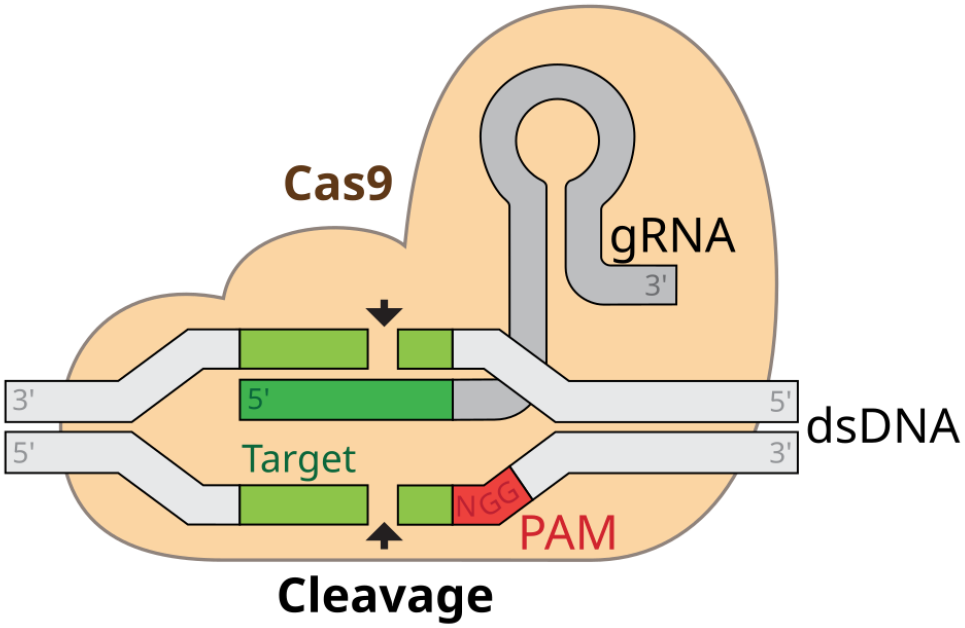
	pharmacokinetic measurements- A measurement that encompasses the four main parameters of absorption, distribution, metabolism, and excretion of drugs in the body.
Cited references to follow up on	Relling MV, Altman RB, Goetz MP, Evans WE. Clinical implementation of pharmacogenomics: overcoming genetic exceptionalism. *Lancet Oncol.* 2010;11:507–509. doi: 10.1016/S1470-2045(10)70097-8. [DOI] [PMC free article] [PubMed] [Google Scholar] Kroetz DL, Yee SW, Giacomini KM. The pharmacogenomics of membrane transporters project: research at the interface of genomics and transporter pharmacology. *Clin Pharmacol Ther.* 2010;87:109–116. doi: 10.1038/clpt.2009.226. [DOI] [PMC free article] [PubMed] [Google Scholar] 12.Ng PC, Murray SS, Levy S, Venter JC. An agenda for personalized medicine. *Nature*. 2009;461:724–726. doi: 10.1038/461724a. [DOI] [PubMed] [Google Scholar]
Follow up Questions	How does this impact the complexity, timeline, and effectiveness of medical treatment? The cost? What other factors weigh into pharmacogenetics (weight, age, height, etc…)? How would pharmacogenetics change the industry of over-the-counter medicine? How does a PGx test work? Cost? Efficacy?

- Genetic testing has increased due to mutations of Mendelian diseases
    - Mendelian diseases are diseases that occur from a single gene
- One of the main ways testing has been implemented is through technology
    - Diagnostic confirmation
    - Prenatal testing
    - Population screening
- Pharmacogenetics was established in 1950
- This idea was not implemented until very recently and is still not very widely used
- The FDA is slowly starting to expand on specific drugs
- Doctors still don't use it much, even though there has been evidence from various studies that the tool has led to better health outcomes
- There needs to be a lot more universal education on how to use the guidelines properly
- It is undetermined how much of the cost will be covered by insurance
- 1978 was the first year of the DNA-based test for sickle cell

- There was screening for autosomal recessive disorders such as cystic fibrosis, thalassemia, and hemoglobinopathies
- Screening for ethnic panels
    - The response people have to drugs can depend on race
    - Environment and allele frequencies can depend on different locations
    - Warfarin: worse for African Americans because they are less likely to carry specific alleles
- Future use of pharmacogenetics could be:
    - to find variants associated with different diseases
    - Finding a specific patient's risk for other diseases
    - Be more universal- be clinically implemented
- In order to be implemented and used, the use of pharmacogenetics must pass the criteria of "Analytic validity, Clinical validity, Clinical utility, and associated Ethical, legal, and social implications".

Article #2 Notes: CRISPR Explained: Gene Editing and the Future of Medicine

Source Title	CRISPR Explained: Gene Editing and the Future of Medicine
Source citation (APA Format)	Tuhin, M. (2025, July 13). *CRISPR explained: Gene editing and the Future of Medicine. Science News Today.* https://www.sciencenewstoday.org/crispr-explained-gene-editing-and-the-future-of-medicine
Original URL	https://www.sciencenewstoday.org/crispr-explained-gene-editing-and-the-future-of-medicine
Source type	Science News Article
Keywords	CRISPR, gene, mutation, environment, food security, ethics
#Tags	
Summary of key points + notes (include methodology)	CRISPR stands for "Clustered Regularly Interspaced Short Palindromic Repeats." With this technology, which is commonly referred to as scissors for DNA, scientists can precisely edit the genome of a given organism. New genes can be added, and mutations can be corrected. Though its uses are vast, one promising area of study that it could be applied to is the medical field. CRISPR can be used to cure genetic diseases by editing the underlying mutation. An example of this is sickle cell anemia. Scientists are able to make changes to the patients' hematopoietic cells, correcting the shape of their blood cells. Other conditions that this technology could apply to are cystic fibrosis, muscular dystrophy, and Huntington's disease.

	CRISPR's use spans far past the medical setting. It is also thought to be a tool for solving food insecurity. By editing the genomes of plants, scientists are able to make plants more resilient to their environment and nutritious. As populations are increasing, plants having the ability to survive through droughts and disease would be a game changer. Similarly, animals like pigs have been modified to survive factors that have threatened their existence in the past. While CRISPR offers the possibility of editing embryos, many people question its efficacy, creating tension. Another obstacle is the tools' availability. Even if the technology were to be proved 100% safe, the cost and accessibility could be challenging in many areas of the world. Despite all CRISPR's benefits, its use must be regulated and further researched.
Research Question/Problem/ Need	What are the mechanics of CRISPR and how can it be used globally?
Important Figures	 *Figure 4 This is a diagram of the CRISPR Cas-9 Editing System.*
VOCAB: (w/definition)	NHEJ - an imprecise way of repairing cut DNA. The broken ends are reattached and often disable the function of the gene, HDR- precise insertion of a correction or new gene that fixes a mutation. hematopoietic cells - cells that produce blood cells dystrophy - when an organ or tissue is dysfunctional
Cited references to follow up on	N/A
Follow up Questions	How effective is this technology? What research needs to be done to expand this knowledge to other diseases or disorders?

	What is stopping the creation of edited plants, assuming there are fewer ethical concerns? Is a medical CRISPR solution uniform for each patient with the same disorder, or does it vary?

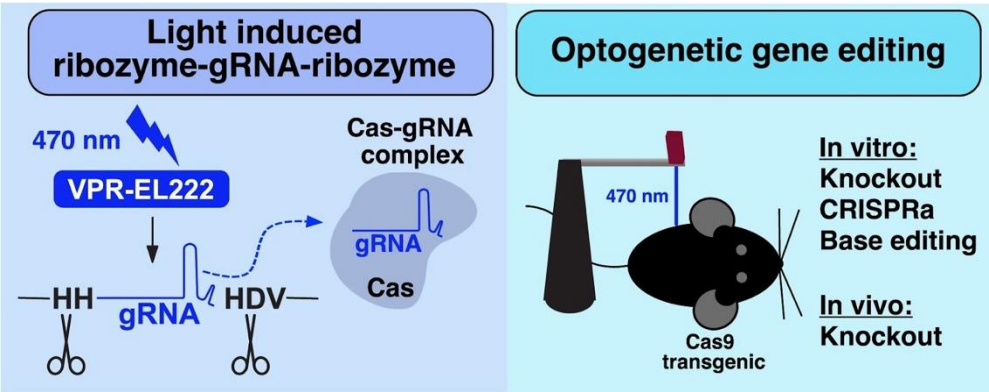
Article #3 Notes: CRISPR Beef Cattle Get FDA Green Light

Source Title	CRISPR Beef Cattle Get FDA Green Light
Source citation (APA Format)	Nature Publishing Group. (2022). CRISPR beef cattle get FDA green light. *Nature News*. https://doi.org/10.1038/s41587-022-01297-zz
Original URL	https://www.nature.com/articles/s41587-022-01297-z
Source type	Science News Journal
Keywords	Cattle, animals, products, environment, FDA, CRISPR
#Tags	
Summary of key points + notes (include methodology)	CRISPR allows genetic changes to be made in organisms. One of its uses is in plants and animals to allow them to live longer, be more resistant to change, and improve quality. This combination of abilities is applicable in multiple different world-wide issues faced today. It is especially important considering the growing population and increasing hunger rates that exist. In March of 2022, this technology was used on cattle. The PRLR-SLICK cattle were edited to have a specific protein for a shortened prolactin receptor and also a phenotype that makes their coat slicker. These changes allow them to withstand and survive through different climates that would otherwise put them in immense danger (or even threaten them to become extinct). After being genetically modified to be better suited to their environment (tropical heat), the studies conducted found that the products that came from the cattle also seem to be perfectly healthy, earning its approval from the FDA. When given the full sequence of the DNA, the FDA found several errors that were announced to be unintentional; however, it was determined that they pose no risk to the cattle, products, or environment. As this technology is still new and battling ethical concerns, it is still in its early stages of development. Two other genetically compromised animals that have been approved so far are salmon and pigs.
Research Question/Problem/ Need	How has CRISPR been used to impact plants and animals in relation to food?
Important Figures	N/A
VOCAB: (w/definition)	Prolactin - a protein that is expressed in many glands and tissues of the human body Intergenic regions - the DNA that is found between genes Recombinetics - a leading company in animal gene editing
Cited references to follow up	N/A

on	
Follow up Questions	What are the long-term effects of eating these edited products? Why were the unintentional edits made? Can they become harmful over time? What are other reasons to genetically modify animals, other than food?

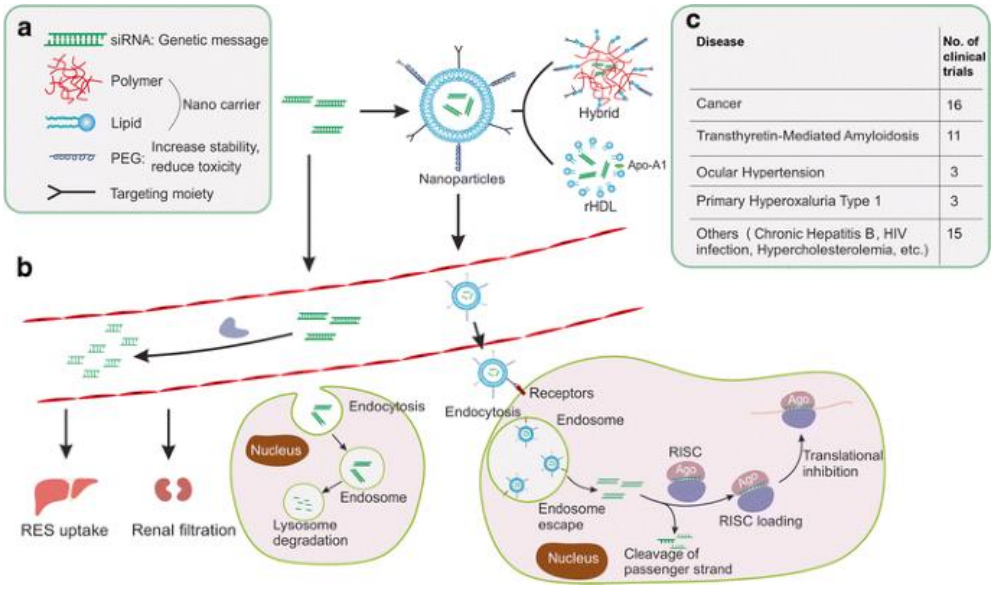
Article #4 Notes: New Light-Controlled CRISPR Tool Enhances Precision in Genetic Research

Source Title	New Light-Controlled CRISPR Tool Enhances Precision in Genetic Research
Source citation (APA Format)	Sten, A. S. (2025, March 28). *New Light-Controlled CRISPR Tool Enhances Precision in Genetic Research.* Phys.org. https://phys.org/news/2025-03-crispr-tool precision-genetic.html
Original URL	https://phys.org/news/2025-03-crispr-tool-precision-genetic.html
Source type	Science News Article
Keywords	Mice, CRISPR, UV-light, gene-editing, cells
#Tags	
Summary of key points + notes (include methodology)	While CRISPR's uses have been being researched, a new way to control it has been discovered. This breakthrough allows CRISPR, which is thought to be scissors for genes, to be even more controlled. One of the technology's biggest advantages is its ability to act precisely. It can cut specific genes in a way that will not disrupt other genes (in certain cases). By using blue UV light, scientists can zone in on a specific section of the genome without having to worry about the rest. This new discovery is now nicknamed BLU-VIPR. The use of light can also control when the change takes place, which again, unlocks a whole new world of possibilities for the technology. With this new discovery, scientists can hold off on the gene editing until the light is shone. This method was proved to be effective when tested on the lymph nodes of mice. Researchers say that this new breakthrough will create a ripple effect in the scientific field and help to create more breakthroughs about genetics. This sector of CRISPR still needs more work, but it has the potential to be turned into a new industry, especially one that allows the editing software to be used in more complex scenarios. In the future, scientists are working to edit multicellular organisms in more precise manners. They also want to expand the system to target other immune cells rather than be limited to T cells.
Research Question/Problem/ Need	What changes does the scientific breakthrough of the use of UV-light when working with CRISPR make to the technology?

Important Figures	 *Figure 5 A diagram following the process of BLU-VIPR, a method allowing scientists to control the CRISPR to a higher degree using light.*
VOCAB: (w/definition)	BLU-VIPR - name given to the method that allows light to control CRISPR Transcription activation domain - the places where transcription factors bind to complexes, activating transcription Gene knockout - the act of removing or inactivating a gene from a genome Vitro- a process done outside of an organism- for example, a beaker or test tube
Cited references to follow up on	Diego Velasquez Pulgarin et al, *Light-induced expression of gRNA allows for optogenetic gene editing of T lymphocytes in vivo*, Nucleic Acids Research (2025). DOI: 10.1093/nar/gkaf213
Follow up Questions	How were the mice tested? What was the delay time? In what situations would using UV light make a significant difference? What amount/strength/duration of UV light would be needed? Is it safe for humans, knowing that UV light is dangerous in large amounts?

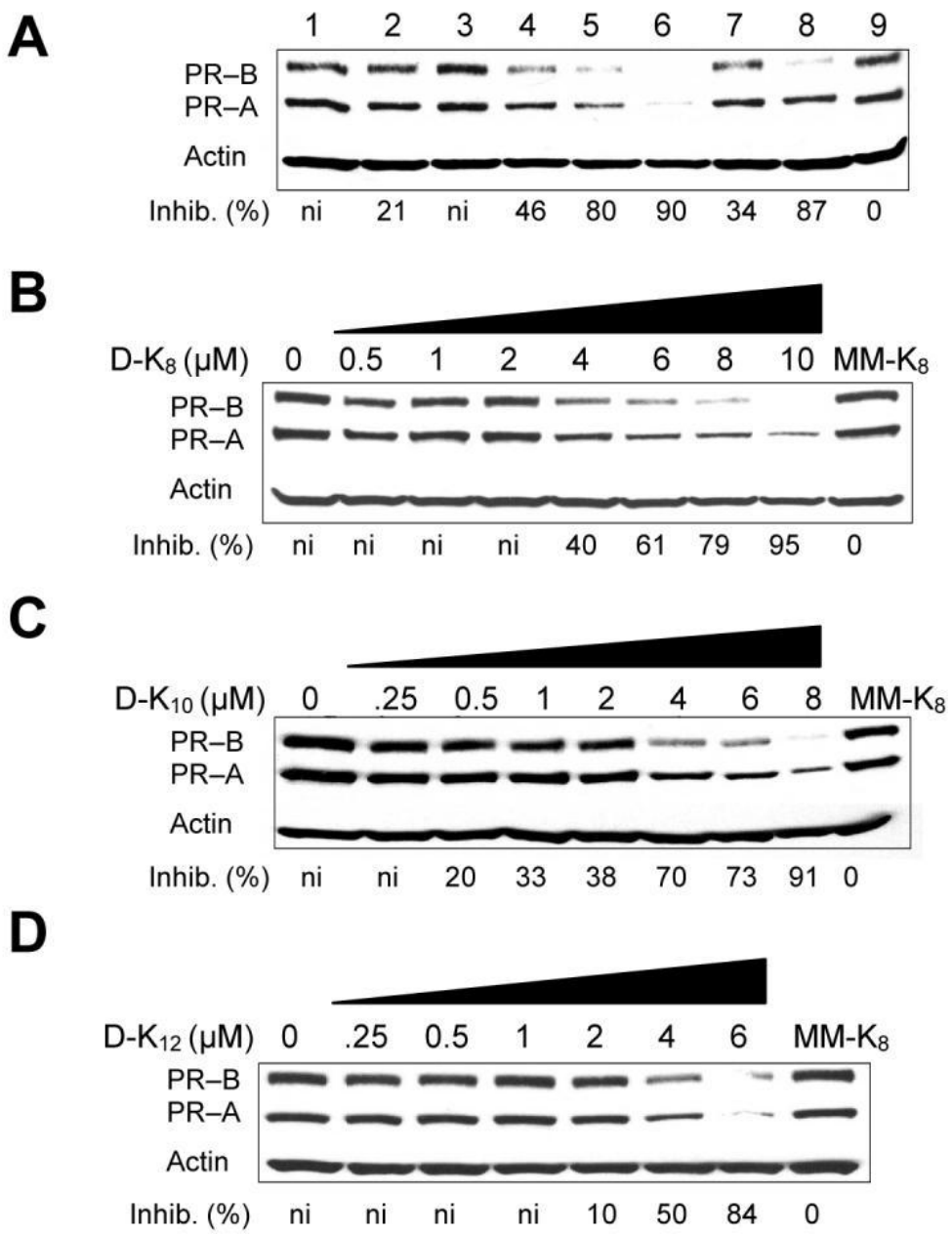
Article #5 Notes: RNA Interference-based Therapy and its Delivery Systems

Source Title	RNA Interference-based Therapy and its Delivery Systems
Source citation (APA Format)	Chen, X., Mangala, L.S., Rodriguez-Aguayo, C. et al. (2018). RNA interference-based therapy and its delivery systems. *Cancer Metastasis* Rev 37, 107–124. https://doi-org.ezpv7-web-p-u01.wpi.edu/10.1007/s10555-017-9717-6
	https://link-springer-com.ezpv7-web-p-u01.wpi.edu/article/10.1007/s10555-017-9717-6
Source type	Journal Article
Keywords	Gene Delivery, Nucleic Acid Therapeutics, RNA Interference, RNA Nanotechnology, RNAi Therapy, siRNA
#Tags	
Summary of key points + notes (include methodology)	RNA interference is the process by which RNA molecules stop a specific sequence of RNA from being translated. This could be crucial in the study of medicine, especially due to its precision. While other approaches exist, they are not well-regulated, as it is hard to identify agents that will inhibit protein function. Using RNAi can even help decode something as big as cancer. Researchers have found that the silencing of Lgr5 would “eliminate” gastric cancer. It could also be used to stop drug resistance. This is effective due to the technology’s precision, low-cost, and ability to block multiple pathways at the same time. Later, this strategy could be applied towards making personalized medicine. Other huge medical diseases that could depend on this process are cardiovascular disease and diabetes. Scientists are also looking into its use on stem cells. While it all sounds promising, there are some cons too. First of all, the delivery of this therapy is often complicated. Its characteristics are also quite unfavorable. Its weight, low stability, negative charge, and high structural stiffness make it difficult for the process to occur in the cytoplasm, as they do not transport well there.
Research Question/Problem/ Need	What is RNAi and its components, and how can it be used medically?

Important Figures	 *Figure 6 This diagram shows the components of a designed nanoparticles for RNAi delivery, the process of RNAi. and also other clinical application of siRNA-based drugs.*
VOCAB: (w/definition)	Demethylation- The act of adding a hydrogen atom to a molecule to remove a methyl group. Endogenous – A symptom that is not the result of an external factor. Adjuvants- A group of substances used to increase the effectiveness of a drug, often used in vaccines.
Cited references to follow up on	Mansoori, B., Sandoghchian Shotorbani, S., & Baradaran, B. (2014). RNA interference and its role in cancer therapy. *Advanced Pharmaceutical Bulletin,* 4(4), 313–321. https://doi-org.ezpv7-web-p-u01.wpi.edu/10.5681/apb.2014.046. Rao, D. D., Vorhies, J. S., Senzer, N., & Nemunaitis, J. (2009). siRNA vs. shRNA: similarities and differences. *Advanced Drug Delivery Reviews, 61*(9), 746 759. https://doi-org.ezpv7-web-p-u01.wpi.edu/10.1016/j.addr.2009.04.004. Weiss, W. A., Taylor, S. S., & Shokat, K. M. (2007). Recognizing and exploiting differences between RNAi and small-molecule inhibitors. *Nature Chemical Biology, 3*(12), 739–744. https://doi-org.ezpv7-web-pu01.wpi.edu/10.1038/nchembio1207-739.
Follow up Questions	1. What are the adverse side effects that come with using RNA interference? 2. Once the RNA molecules are in your system, how long does it take to block the respective enzymes? 3. Could it be used on the spot, or only as a preventative measure? 4. Is this a temporary or permanent solution to silencing a gene?

Article #6 Notes: Inhibiting Gene Expression with Peptide Nucleic Acid (PNA)–Peptide Conjugates that Target Chromosomal DNA

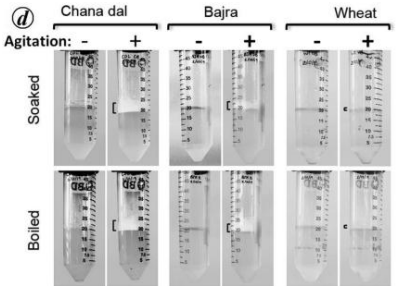
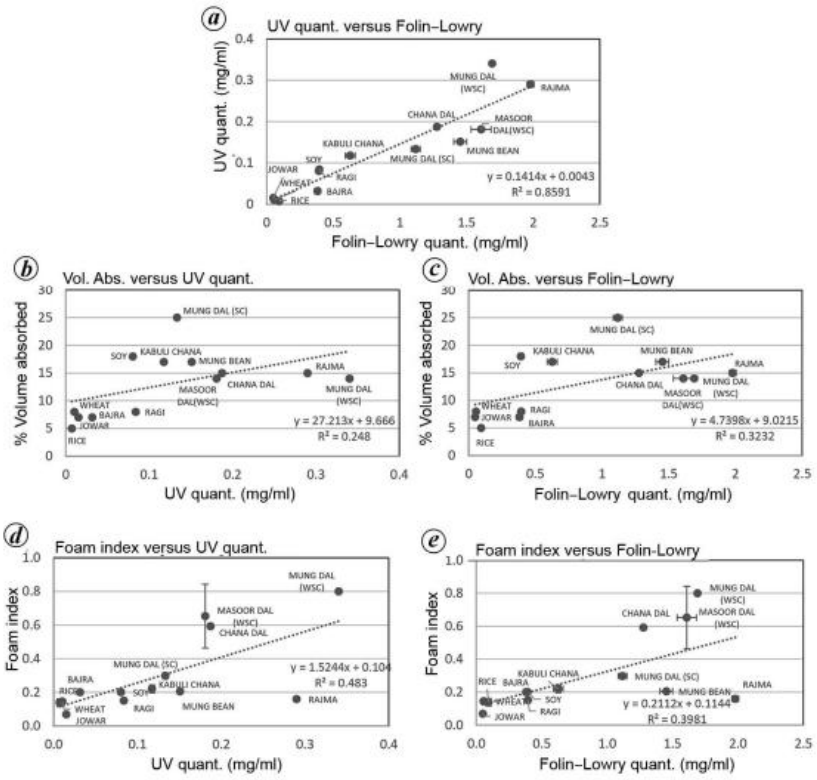
Source Title	Inhibiting Gene Expression with Peptide Nucleic Acid (PNA)–Peptide Conjugates that Target Chromosomal DNA
Source citation (APA Format)	Hu, J., & Corey, D. R. (2007). Inhibiting gene expression with peptide nucleic acid (PNA)--peptide conjugates that target chromosomal DNA. Biochemistry, 46(25), 7581–7589. https://doi.org/10.1021/bi700230a
Original URL	**https://pubs.acs.org/doi/10.1021/bi700230a**
Source type	Journal Article
Keywords	Peptide nucleic acids, Watson-Crick base-pairing, agPNA, gene expression, inhibition, peptide
#Tags	
Summary of key points + notes (include methodology)	Peptide nucleic acids recognize complementary DNA sequences, making them important for exploring cell structure, but they need more work before being widely available. This breed of nucleic acids is able to invade double-stranded DNA. In addition, peptides possess the ability to alter the transport of molecules into cells (endocytosis). The journal tests 36 different agPNA-peptide conjugates in combination with cationic amino acids, such as arginine or lysine in order to look at their role in inhibiting genes. While it became apparent that these additives were not required in gene inhibition, it was observed that by having them, the potency of the agPNA was increased. In their experiment, they looked at breast cancer cells. They added the different conjugates to the cells to measure the effects of potency. They found that the PNA that had mismatched bases and a missing attached peptide did not behave as expected, and did not inhibit the gene. This told them that in order for the process to work, an import peptide is necessary. They also confirmed previous studies that mentioned how adding calcium (+2) increases the ability of the PNA to inhibit the gene. Therefore, there findings can be summarized as: PNA conjugates allow for gene inhibition and are improved with the use of hydrophobic groups.
Research Question/Problem/ Need	Can agPNA peptide conjugates enter cells, target DNA, and block the expression of those genes?

Important Figures	 *Figure 7 This is a western blot analysis of the inhibition of PR protein expression by agPNA−lysine conjugates.*
VOCAB: (w/definition)	Cationic- anything that carries a positive charge endocytosis – a process of a cell bringing a large molecule into itself confluence- the process of combining or merging oligonucleotides- short strands of DNA used as building blocks for long DNA strands.
Cited references to follow up on	Kaihatsu K, Janowski BA, Corey DR. Recognition of chromosomal DNA with PNAs. Chem. Biol. 2004;11:749–758. doi:10.1016/j.chembiol.2003.09.014 Tyler BM, Jansen K, McCormick DJ, Douglas CL, Boules M, Stewart JA, Zhao L, Lacy

	B, Cusack B, Fauq A, Richelson E. Peptide nucleic acids targeted to the neurotensin receptor and administered i.p. cross the blood–brain barrier and specifically reduce gene expression. *Proc. Natl. Acad. Sci. U S A*. 1999;96:7053–8. doi: 10.1073/pnas.96.12.7053 Kaihatsu K, Huffman K,E, Corey DR. Intracellular uptake and inhibition of gene expression by PNAs and PNA–peptide conjugates. *Biochemistry*. 2004;43:14340–14347. doi: 10.1021/bi048519l
Follow up Questions	Are the effects of this process long-term or short-term? Does the addition of agents and hydrophobic groups depend on the cells in which they are inhibiting? How can this process be translated into a human in terms of application methods? How do the delivery methods of PNAs affect the potency of their effect?

Article #7 Notes: Foam index as a surrogate measure of protein content: an exploratory and inexpensive laboratory-free tool for students

Source Title	Foam index as a surrogate measure of protein content: an exploratory and inexpensive laboratory-free tool for students
Source citation (APA Format)	Chauhan, A. (2023). Total Leaf Protein Content: A Measure to Study the Phytotoxic Effects of Sulfur Dioxide on Crop Plants. *International Journal for Research in Applied Science and Engineering Technology*, *11*(3), 911–915. https://doi.org/10.22214/ijraset.2023.49559
Original URL	https://www.currentscience.ac.in/Volumes/128/05/0495.pdf
Source type	Journal Article
Keywords	Froth, grains, home lab, nutrition, protein estimation
#Tags	
Summary of key points + notes (include methodology)	A way to measure the protein content that is at home-friendly is by using a method called blanching. This includes soaking grains until they release protein into a supernatant. These two, when combined, release a type of foam, which can be qualitatively measured. There are two other main ways to measure protein content. One uses ultra-violet absorption, the other being the Folin-Lowry method. This journal also experimented with a type of dye formulated to separate the foam that is truly protein from the foam that isn't. Specifically, these methods were used in rice, wheat, and maize. This is because it is widely recognized that protein is a must-have in a person's diet. However, other ways of generally measuring protein are not one hundred percent reliable due to other factors, like temperature, cultivation methods, and environments. The research was mainly important because it is an experiment that is easily conductible at home and also accounts for communities that may be less fortunate and need a high nutritional source.
Research Question/Problem/ Need	How can the nutritional protein content of raw food be measured at home?

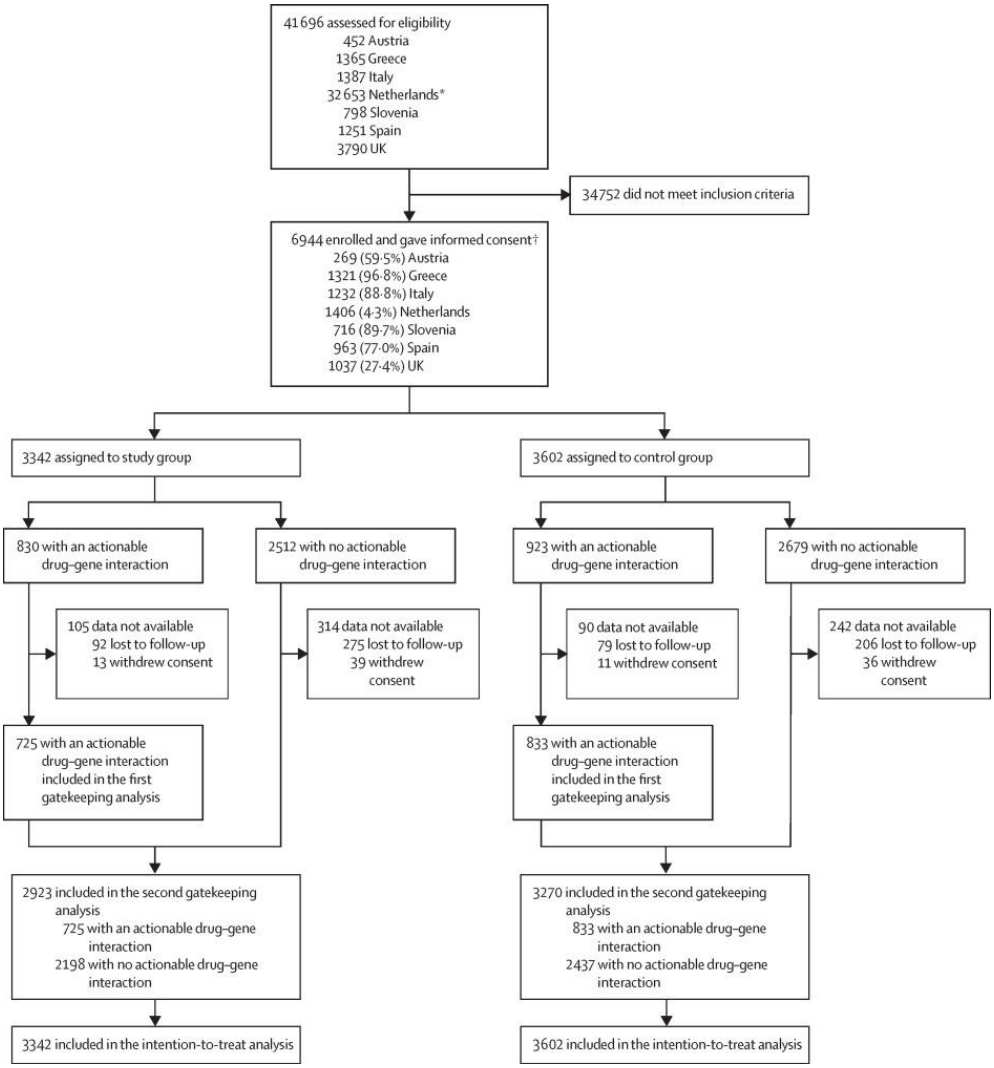
Important Figures	 *Figure 8 Picture of the 3 grain extracts obtained by either soaking the grains overnight (soaked) or by blanching the soaked grains in boiling water.*  *Figure 9 The correlation of soaked grain extracts to standard methods of protein estimation using the Folin-Lowry method.*
VOCAB: (w/definition)	Vernier calipers- a measurement instrument that takes a precise recording of something's dimensions Spectrophotometry- a measurement of the amount of light something absorbs or transmits Aliquot- a smaller sample taken from a chemical sample.
Cited references to follow up on	Wolfe, R. R., Baum, J. I., Starck, C. and Moughan, P. J., Factors contributing to the selection of dietary protein food sources. *Clin. Nutr.*, 2018, 37(1), 130–138; https://doi.org/https://doi.org/10.1016/ j.clnu.2017.11.017. Xiong, X., Ho, M. T., Bhandari, B. and Bansal, N., Foaming properties of milk

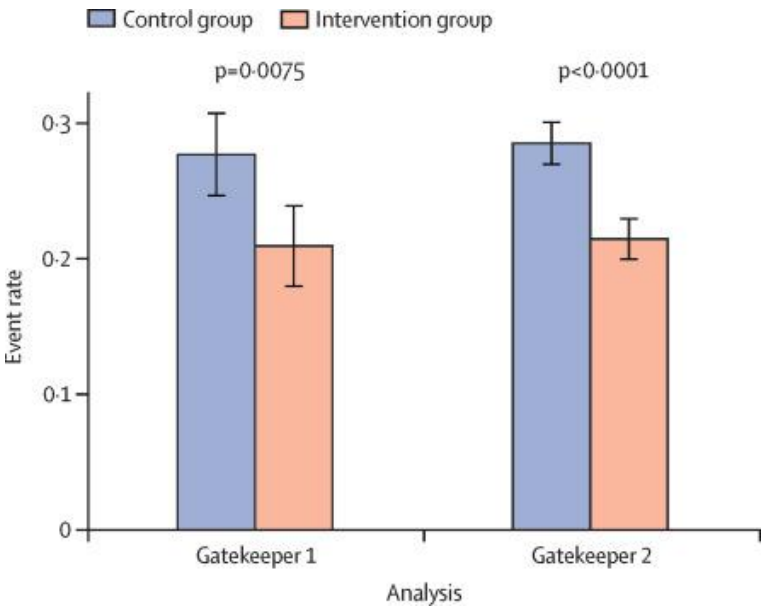
	protein dispersions at different protein content and casein to whey protein ratios. *Int. Dairy J.,* 2020, 109, 104758; https://doi.org/10.1016/j.idairyj.2020.104758. Waniska, R. D. and Kinsella, J. E., Foaming properties of proteins: evaluation of a column aeration apparatus using ovalbumin. *J. Food Sci.,* 1979, 44(5), 1398 1402; https://doi.org/10.1111/j.1365-2621. 1979.tb06447.x.
Follow up Questions	Does this process also work for other foods, such as plants? How does the process of the protein being produced as foam compare to how our body naturally digests protein? What are the effects of different nutrients (given to the plant as it grows) on the amount of protein it will produce?

Article #8 Notes: A 12-gene pharmacogenetic panel to prevent adverse drug reactions: an open-label, multicentre, controlled, cluster-randomised crossover implementation study

Article notes should be on separate sheets

Source Title	A 12-gene pharmacogenetic panel to prevent adverse drug reactions: an open-label, multicentre, controlled, cluster-randomised crossover implementation study
Source citation (APA Format)	Swen, J. J., van der Wouden, C. H., Manson, L. E., Abdullah-Koolmees, H., Blagec, K., Blagus, T., Böhringer, S., Cambon-Thomsen, A., Cecchin, E., Cheung, K.-C., Deneer, V. H., Dupui, M., Ingelman-Sundberg, M., Jonsson, S., Joefield-Roka, C., Just, K. S., Karlsson, M. O., Konta, L., Koopmann, R., … Rajasingam, A. (2023). A 12-gene pharmacogenetic panel to prevent adverse drug reactions: An open-label, multicentre, controlled, cluster-randomised crossover implementation study. *The Lancet*, *401*(10374), 347–356. https://doi.org/10.1016/S0140-6736(22)01841-4
Original URL	https://www-sciencedirect-com.ezpv7-web-p-u01.wpi.edu/science/article/pii/S0140673622018414
Source type	Journal Article
Keywords	Pharmacogenetic testing, drug therapy, pharmacogenetic panel, genetic testing, adverse drug reactions
#Tags	
Summary of key points + notes (include methodology)	It had already been established that testing patients for genetic data prior to being medicated has been proven useful and beneficial. However, the researchers were unsure if testing a wide array of these pharmacogenes (genes that affect the four-stage process of drugs) before the patient even needed them would give them even further insight as to the medication they would need. To research this, the study looked at 18 hospitals, 9 community health centers, and 28 community pharmacies in European countries. They looked for 50 germline mutations in a total of 12 genes. The people who had a variant that was significant enough to hinder treatment were given a new plan based on the DPWG recommendation (which swayed away from standard care). Other patients were put into a control group. These people were only given the standard care, which did not account for any genetic testing. The analysis performed depended on comparing the outcomes of the people who had genetic testing and changes to their treatment to the people who did not. If this proved to be statistically significant, then further

	analysis was conducted for the remaining data collected from the study. They found that 21.5% of patients who were in the study group had an ADR, while 28.6% of the control group also did. This allowed them to hypothesize that genetically testing patients for a large array of genes that have the potential to stop drug efficiency did, in fact, have an impact, and reduced major side effects.
Research Question/Problem/ Need	Can testing patients for broad genetic testing instead of focused genetic testing have any benefits for drug prescription?
Important Figures	 *Figure 10 A visual flow chart of the selection process that the researchers followed to assign both control and study groups*

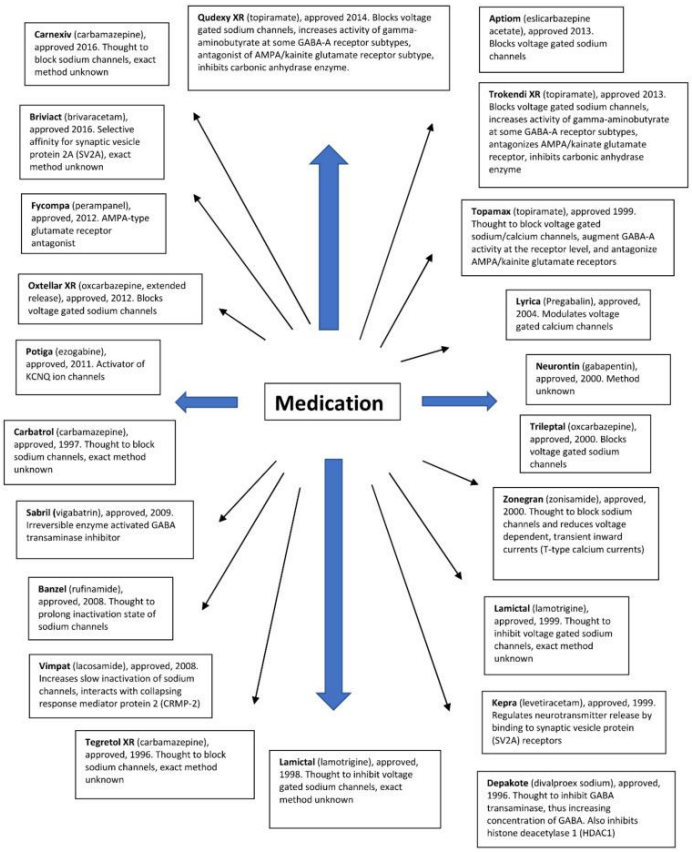
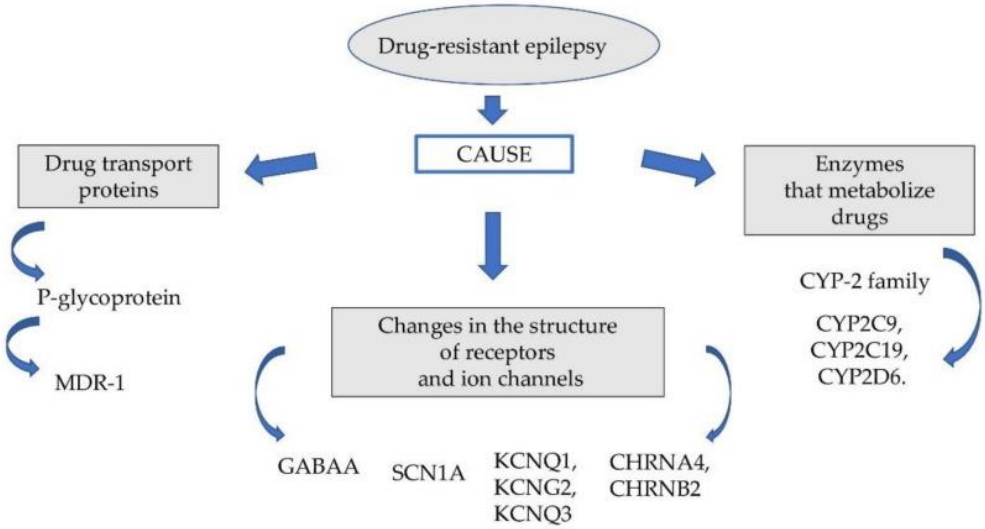
	 *Figure 11 Graph representing both phase 1 and phase 2 of the experiment. The difference in the percentage of people with adverse drug reactions and those who did not react remains fairly constant for both sample sizes.*
VOCAB: (w/definition)	Germline- reproductive cells, opposite of somatic DPWG- Dutch Pharmacogenetics Working Group Drug disposition- the process of how a drug works in the body and gets eliminated. It follows a process of absorption, distribution, metabolism, and excretion. Consortia- an association between multiple partners Oestrogen- reproductive hormone
Cited references to follow up on	DMF Claassens, GJA Vos, TO Bergmeijer, *et al.* A genotype-guided strategy for oral P2Y(12) inhibitors in primary PCI *N Engl J Med*, *381* (2019), pp. 1621-1631 LM Henricks, C Lunenburg, FM de Man, *et al.* DPYD genotype-guided dose individualisation of fluoropyrimidine therapy in patients with cancer: a prospective safety analysis *Lancet Oncol*, 19 (2018), pp. 1459-1467 PCD Bank, KE Caudle, JJ Swen, *et al.* Comparison of the Guidelines of the Clinical Pharmacogenetics Implementation Consortium and the Dutch Pharmacogenetics Working Group *Clin Pharmacol Ther*, 103 (2018), pp. 599 618
Follow up Questions	What other “broad” genes exist that would be useful to add to their array? What were the drug effects that were present? In those who were in the study group, was their severity lessened? What was the cost and time frame of the experiment? How feasible would it be to implement in the medicine field?

- A test of 12 genes that looked for 50 variations in patients
- They looked at a sample of people from 18 hospitals, 9 health centers, and 28 pharmacies
- Tested in 7 European countries
- Followed the guidelines of the Dutch Pharmacogenetics Working Group
    - This group is interested in implementing the tool into standard care, educating doctors, and also making guidelines for the variations of genetic information people may have (what to do in the treatment if – if true)
- Patients who enrolled could not be:
    - less than 18
    - already involved with genetic testing for their index drug
    - treated for less than a week
    - could not have any kidney or liver issues
- Physicians were given a survey and then a crash course on how to handle the patients under these specific guidelines
- Patients were checked on during a twelve-week window—at 0 weeks, 3 weeks, 7 weeks, and 12 weeks
- Tested 6944 people and split them into a control and a study group
    - They used the chi-squared and the Wilcoxon statistical methods to measure how fair their baseline was. They were hoping for p-values greater than 0.05.
- The people in the study group who required more specific care would get it, while no one in the control group got special care (they followed the standard of care)
- They tested for 12 genes that are common and have an MAF value greater than 1% so that 90-90% of people would have at least one gene that was actionable, no matter who they sampled for the experiment
- This experiment is the first to conduct a large-scale panel genetic test that looks at not just single genes and drug combinations
- They used gatekeeping and only looked at one part of the study, then, if it was statistically significant, they looked at the rest of the data
- They just looked at the people who had actionable genes in both the control and study groups in order to get the stronger scenario
- They used a 10-question global health score to assess patient social, mental, and physical wellbeing and compare it to the number of adverse drug reactions they would have
- They used the Liverpool Causality Assessment tool to determine if the drug was the main factor
- They used the National Cancer Institute - Common Terminology Criteria for Adverse Events to grade how severe each reaction was to provide consistency
- Had a random 10% of data rechecked by the Netherlands Pharmacovigilance Center, and using Cohen's Kappa, were able to figure out how accurate and unbiased their data was
- 93.5% of patients had a variant
- Most common variation: CYP2D6 (44.6%) and lease common variation: HLA-B*57:01 (4.1%)
- Results
    - 30% fewer ADRs, younger = slightly higher risk, higher health score = less risk, more allergies = higher risk, more comedications = higher risk

Article #9 Notes: Pharmacogenetics of Drug-Resistant Epilepsy

Article notes should be on separate sheets

Source Title	**Pharmacogenetics of Drug-Resistant Epilepsy**	
Source citation (APA Format)	Smolarz, B., Makowska, M., & Romanowicz, H. (2021). Pharmacogenetics of Drug-Resistant Epilepsy (Review of Literature). *International Journal of Molecular Sciences*, *22*(21), 11696. https://doi.org/10.3390/ijms222111696	
Original URL	https://www.mdpi.com/1422-0067/22/21/11696	
Source type	Journal Article	
Keywords	pharmacogenetics; drug-resistant epilepsy; genes; CYP2 family; MDR-1; GABA receptors; ion channels	
#Tags		
Summary of key points + notes (include methodology)	Epilepsy, a neurological disorder causing seizures due to electrical activity in the brain, is highly expensive to treat and can also be resistant to treatment. In fact, 30% of patients with this disorder do not have a response to treatment. This is a result of the genetic makeup of patients with this issue. Patients have different SNPs that affect the proteins responsible for drug efficacy. Some of the most vital gene mutations in this study were CYP2C9, CYP2C19, MDR1, and MRP. By working to uncover the mystery of this, doctors and scientists can further understand why two patients experiencing similar symptoms and seizures have distinct and different reactions to the same medication or treatment plan. When the scientists honed in on enzymes that metabolize drugs, they focused on the CYP families. These enzymes came in variants that are responsible for the metabolism of the medicine the patients are given in their treatment. These changes in genetic information also translated to their treatment plans as well. Sixty patients were examined by a researcher, who concluded that the dose of CYP2C9*3 necessary to treat patients was 37% lower compared to the dose in patients with CYP2C9*1. In addition, another experiment was conducted in which younger kids who had epilepsy and were drug resistant (meaning that their treatment did not work for them), the SNPs identified that coded for reduced activity were those in the CYP family and were linked to poor metabolism. To date, the FDA has approved 23 drugs for the treatment of epilepsy, each of which tackles the problem in a slightly different way.	
Research Question/Problem/ Need	What is the role of pharmacogenetics in those who have resistant epilepsy?	

Important Figures	 *Figure 12 A list of antiepileptic drugs and their mode of action.*  *Figure 13 The factors affecting drug-resistant epilepsy.*
VOCAB: (w/definition)	Antiepileptic- a drug used to treat epilepsy Idiosyncrasy- a distinct mode of behavior belonging to a specific person Etiopathogenesis- the process from the cause of a disease up until the development and progression

	Myoclonal- a sudden twitch or shock	

Cited references to follow up on	Margineanu D.G., Klitgaard H. Mechanisms of drug resistance in epilepsy: Relevance for antiepileptic drug discovery. Expert Opin. Drug Discov. 2009;4:23–32. doi: 10.1517/17460440802611729. [DOI] [PubMed] [GoogleScholar] Regesta G., Tanganelli P. Clinical aspects and biological bases of drug-resistant epilepsies. Epilepsy Res. 1999;34:109–122. doi: 10.1016/S0920 1211(98)00106-5. [DOI] [PubMed] [Google Scholar] Marchi N., Hallene K.L., Kight K.M., Cucullo L., Moddel G., Bingaman W., Dini G., Vezzani A., Janigro D. Significance of MDR1 and multiple drug resistance in refractory human epi-leptic brain. BMC Med. 2004;2:37. doi: 10.1186/1741 7015-2-37. [DOI] [PMC free article] [PubMed] [Google Scholar]	
Follow up Questions	What are the environmental factors that lead to population-specific minor allele frequencies? Are these genes the most problematic for other resistant diseases? Is there a difference in looking at early onset epilepsy versus older people who are resistant?	

Article #10 Notes: Implementing Pre-Emptive Pharmacogenetics: Impact of Early Pharmacogenetic Screening in a Pediatric Oncology Cohort of 1,151 Subjects

Source Title	**Implementing Pre-Emptive Pharmacogenetics: Impact of Early Pharmacogenetic Screening in a Pediatric Oncology Cohort of 1,151 Subjects**
Source citation (APA Format)	Bernsen, E. C., Verwiel, E. T. P., van der Lee, M., Swen, J. J., Santoso, M., Brigitha, L. J., Admiraal, R., Tops, B. B. J., Huitema, A. D. R., Kemmeren, P., Hehir-Kwa, J. Y., Hanff, L. M., & Diekstra, M. H. M. (2025). Implementing pre-emptive pharmacogenetics: Impact of early pharmacogenetic screening in a pediatric oncology cohort of 1,151 subjects. *Clinical Pharmacology & Therapeutics*, *118*(2), 438–448. https://doi.org/10.1002/cpt.3685
Original URL	https://ascpt-onlinelibrary-wiley-com.ezpv7-web-p-u01.wpi.edu/doi/full/10.1002/cpt.3685
Source type	Journal Article
Keywords	Pediatric oncology, individualized medicine, drug dosing, genetic profiling, CPIC, DPWG, molecular diagnosis, anticancer
#Tags	
Summary of key points + notes (include methodology)	This study used PGx screening on its patients. They did this so they could improve the way they treat oncology cases both safely and more accurately. Unfortunately, there are not many guidelines or much focus on the cancer field when it comes to pharmacogenetics. Some of the drugs that are being researched, such as medicines like thiopurines, irinotecan, capecitabine, and 5-fluorouracil, do offer more insight into this problem. In the study, they looked at 1,151 patients. They then focused on 10 genes and 28 drugs, all of which were specifically defined by both the Clinical Pharmacogenetics Implementation Consortium (CPIC) and the Dutch Pharmacogenetics Working Group (DPWG). A limited list of these drugs was allopurinol, phenytoin, amitriptyline, proton pump inhibitors, codeine, paroxetine, voriconazole, tramadol, tacrolimus, rasburicase, and 6-mercaptopurine. By doing this, they were able to conclude that the use of genetic screening improved approximately 16% of patients and their treatment plans. Those in the field are arguing for a greater implementation of pharmacogenetics as it could help medical staff to identify gene-drug interactions and improve the long-term effects of treatments.
Research Question/Problem/ Need	How can genetic screening of patients improve drug accuracy and dosing for pediatric oncology patients?

Important Figures

Gene	Pharmacogenetic-sensitive drug	Indication drug in pediatric oncology	Recommendation available	
			CPIC	DPWG
ABCG2	Allopurinol	Lowering high uric acid levels due to tumor lysis		√
CYP2C9	Ibuprofen (NSAID)	Pain	√	
	Celecoxib (NSAID)	Pain	√	
	Phenytoin	Epilepsy	√	√
CYP2C19	Voriconazole	Invasive aspergilloses	√	√
	Omeprazole (PPI)	Nausea or gastric reflux	√	√
	Pantoprazole (PPI)	Nausea or gastric reflux	√	√
	Citalopram (SSRI)	Antidepressant	√	√
	Escitalopram (SSRI)	Antidepressant	√	√
	Sertraline (SSRI)	Antidepressant	√	√
	Nortriptyline (TCA)	Antidepressant	√	√
	Imipramine (TCA)	Antidepressant		√
	Amitriptyline (TCA)	Neuropathic pain	√	√

Figure 14 A list of gene-drug pairs and drug indication in pediatric oncology in reference to the CPIC and DPWG.

	Total (*n* = 1,151)
	Age at diagnosis (years)
	Median (range) 7.0 (0–22)
	0–1 101 (8.8%)
	1–11 614 (53.3%)
	12–22 436 (37.9%)
	Sex
	Female 519 (45.1%)
	Male 632 (54.9%)
	Tumor type
	I. Leukemias, myeloproliferative diseases, and myelodysplastic diseases 257 (22.3%)
	II. Lymphomas and reticuloendothelial neoplasms 92 (8.0%)
	III. Central nervous system and miscellaneous intracranial and intraspinal neoplasms 272 (23.6%)
	IV. Neuroblastoma and other peripheral nervous cell tumors 85 (7.4%)
	V. Retinoblastoma 0 (0.0)
	VI. Renal tumors 91 (7.9%)
	Figure 15 Baseline characteristics for the experiment.
VOCAB: (w/definition)	pharmacodynamics – the mechanism of action of drugs in the body. There are four stages: absorption, distribution, metabolism, and excretion CPIC- Clinical Pharmacogenetics Implementation Consortium – an organization that works in tandem with DPWG to create pharmacogenetic guidelines Polypharmacy- the concurrent use of various medications by a single patient (can lead to health complications)
Cited references to follow up on	Evans, W.E. & Relling, M.V. Pharmacogenomics: translating functional genomics into rational therapeutics. *Science* **286**, 487–491 (1999). Schulpen, M. *et al*. Significant improvement in survival of advanced stage childhood and young adolescent cancer in The Netherlands since the 1990s. *Eur. J. Cancer* **157**, 81–93 (2021). Bosma, P.J. *et al*. The genetic basis of the reduced expression of bilirubin UDP glucuronosyltransferase 1 in Gilbert's syndrome. *N. Engl. J. Med.* **333**, 1171 1175 (1995).
Follow up Questions	Why is there such a small priority for drugs regarding cancer if it is such a prominent and detrimental disease that kills so many?

	How would ethnicity affect these results (or the 16%)? What is the reason for using whole genome sequencing and not a panel test? Which drugs were the more prominent? Which genes had the largest frequency in the sample?

Article #11 Notes: A Survey of Human Disease Gene Counterparts in the Drosophila Genome

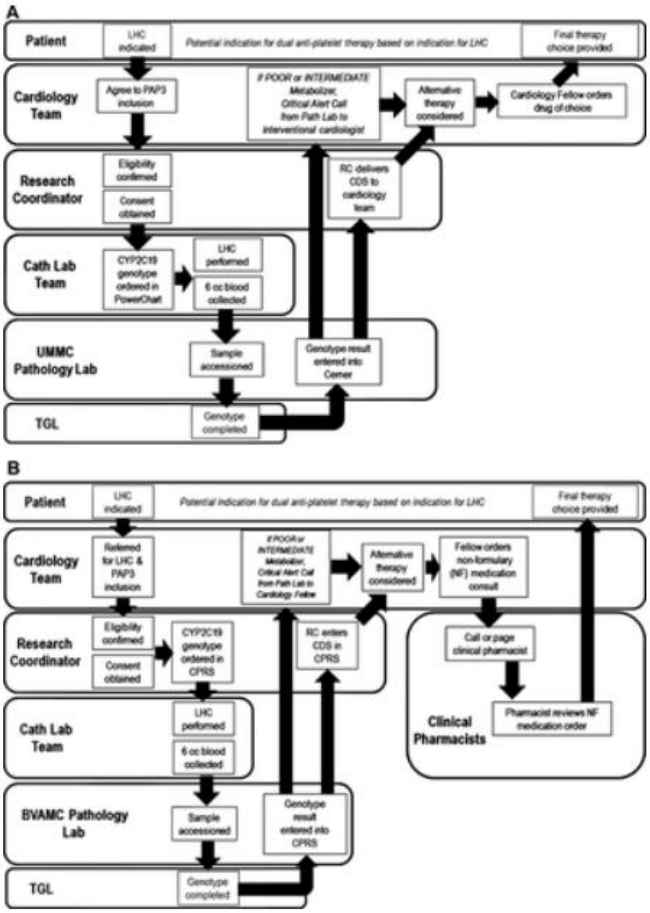
Source Title	A Survey of Human Disease Gene Counterparts in the Drosophila Genome
Source citation (APA Format)	Mark E. Fortini, Marian P. Skupski, Mark S. Boguski, Iswar K. Hariharan; A Survey of Human Disease Gene Counterparts in the Drosophila Genome. J Cell Biol 24 July 2000; 150 (2): F23–F30. doi: https://doi.org/10.1083/jcb.150.2.F23
Original URL	https://rupress.org/jcb/article-abstract/150/2/F23/47917/A-Survey-of-Human-Disease-Gene-Counterparts-in-the?redirectedFrom=fulltext
Source type	Journal Article
Keywords	Drosophila, human genes, disease, function
#Tags	
Summary of key points + notes (include methodology)	This study compared a whole genome sequence of humans and compared it to that of Drosophila, or fruit flies. Prior knowledge points out that somewhere between 50% and 75% of genes in humans are conserved in the flies. This study found that out of 287 human disease genes, 178 of them were conserved, making up about 62%. To do this, they looked at 287 genes that are known to cause disease. They were cross-checked with OMIM and other medical literature and reviews. These genes only included those that have mutations or deletions in humans. Those that were proven through indirect sources, like cell culture or yeast experiments, were not included in their research. After this process, the genes that were researched accounted for a wide array of diseases. For example, those of cancer, neurological, cardiovascular, metabolic, renal, endocrine, hematologic, immune, and malformation syndromes. Then, they use a tool named BLASTSTP to compare the human proteins to yeast, worms, and flies. To evaluate data, they used E-values and a database called InterPro. What they found in their research is that cancer genes were highly preserved, as well as neurological, endocrine, and metabolic ones. Hematologic and Immune genes were very poorly conserved. So while Drosophila may be a good model organism for the studies of neurological diseases, cancer, malformation syndromes, and metabolic disorders, it may not be the best choice for immune, hematologic, and certain endocrine diseases.
Research Question/Problem/ Need	What is the percent similarity between human and drosophila genes?

Important Figures	 *Genes that were present versus absent in Drosophila*
VOCAB: (w/definition)	Paralogs- A gene that is a duplication of an ancestral gene (homologous). E-Values- A statistical method that quantifies the minimum strength of association between events. A lower value is more significant. OMIM- Online Mendelian Inheritance in Man
Cited references to follow up on	Banfi S., Borsani G., Rossi E., Bernard L., Guffanti A., Rubboli F., Marchitiello A., Giglio S., Coluccia E., Zollo M. Identification and mapping of human cDNAs homologous to Drosophila mutant genes through EST database searching.

	Nat. Genet. 1996;13:167–174. doi: 10.1038/ng0696-167. [DOI] [PubMed] [Google Scholar] Berkeley Drosophila Genome Project. Sequence similarities of human inherited disease genes with Drosophila DNA 1999. http://www.fruitfly.org/sequence/human2fly.html [Google Scholar] Fortini M.E., Bonini N.M. Modeling human neurodegenerative diseases in Drosophila on a wing and a prayer. *Trends Genet*. 2000;16:161–167. doi: 10.1016/s0168-9525(99)01939-3. [DOI] [PubMed] [Google Scholar]
Follow up Questions	How does the presence of sequence gaps affect the results of the study or the percent similarity? Do the results have any implications for evolutionary tinkering? What do these findings say about past evolution? How can we use Drosophila to model humans in terms of disease and medicine? Could we test for potential treatments?

Article #12 Notes: Implementation of pharmacogenetics: The University of Maryland personalized anti-platelet pharmacogenetics program

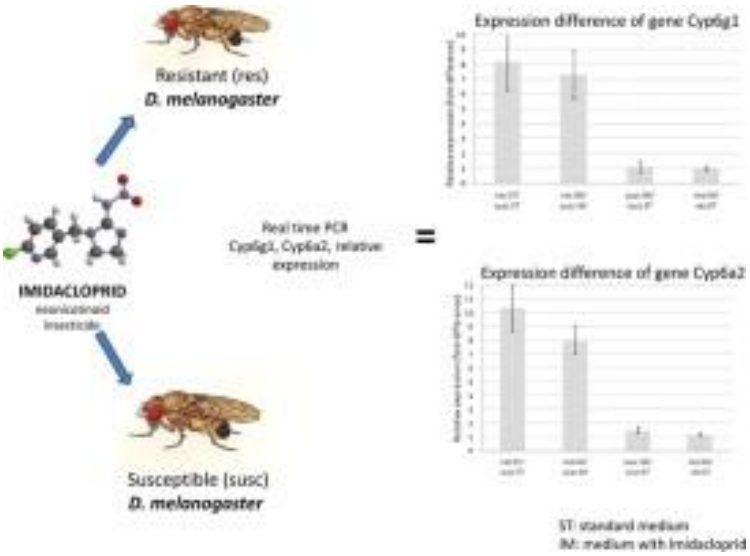
Source Title	Implementation of pharmacogenetics: The University of Maryland personalized anti-platelet pharmacogenetics program
Source citation (APA Format)	Shuldiner, A. R., Palmer, K., Pakyz, R. E., Alestock, T. D., Maloney, K. A., O'Neill, C., Bhatty, S., Schub, J., Overby, C. L., Horenstein, R. B., Pollin, T. I., Kelemen, M. D., Beitelshees, A. L., Robinson, S. W., Blitzer, M. G., McArdle, P. F., Brown, L., Jeng, L. J., Zhao, R. Y., … Vesely, M. R. (2014). Implementation of pharmacogenetics: The University of Maryland personalized anti-platelet pharmacogenetics program. *American Journal of Medical Genetics Part C: Seminars in Medical Genetics, 166*(1), 76–84. https://doi.org/10.1002/ajmg.c.31396
Original URL	https://onlinelibrary-wiley-com.ezpv7-web-p-u01.wpi.edu/doi/full/10.1002/ajmg.c.31396
Source type	Journal Article
Keywords	Pharmacogenetics, barriers, antiplatelet, CYP2C19, drug-gene pairs, genomic medicine, myocardial infarction
#Tags	
Summary of key points + notes (include methodology)	The University of Maryland implemented PAP3, a process in which those struggling with cardiac issues can take a genetic test for the CYP2C19 gene and receive results within 5 hours of taking the test in order to determine the right treatment plan for them. They do this by consulting the CPIP guidelines. To model this, they looked at clopidogrel, a drug that prevents blood clots and works in tandem with the CYP2C19 gene (which codes for metabolization). Those who have variants in this gene may not react to the medicine as well, thus giving them a higher risk of having a future heart problem. While there are ways to work around this, like prescribing a different medicine, many come with their own side effects. For example, Prasugrel and ticagrelor give patients a higher risk of bleeding. Though there is evidence proving that genotype testing can overall improve treatment options for patients, due to a lack of education and efficacy questions, it has not been further utilized. For both locations looked into, The University of Maryland Medical Center and The Baltimore VA Medical Center, CYP2C19 testing was ordered for patients with heart conditions, they were tested, treatment changes were made, providers were educated on pharmacogenetics, and the effectiveness of the process was analyzed. Testing was done through a blood sample, and the turnaround time was roughly 5 hours. While the CPIC guidelines

	were given as a tool, providers were not obligated to follow. By doing this, 32% of the patients had actionable drug-gene interactions, 63% of which were given new treatment plans.
Research Question/Problem/ Need	How can genetic testing for the CYP2C19 gene improve antiplatelet therapy based on the Clinical Pharmacogenetics Implementation Consortium guidelines?
Important Figures	 *The workflow for CYP2C19 genetic testing at different sites (A and B).*
VOCAB: (w/definition)	Auspices- support or partnership/sponsorship of another person or organization Metabolite- substances produced or used during the body's breakdown of food or drugs Percutaneous coronary intervention- the buildup of plaque in the arteries
Cited references to follow up on	Brandt JT, Close SL, Iturria SJ, Payne CD, Farid NA, Ernest CS II, Lachno DR, Salazar D, Winters KJ. 2007. Common polymorphisms of *CYP2C19* and *CYP2C9* affect the pharmacokinetic and pharmacodynamic response to clopidogrel but not prasugrel. *J Thromb Haemost* **5**: 2429–2436. Crews KR, Gaedigk A, Dunnenberger HM, Klein TE, Shen DD, Callaghan JT, Kharasch ED, Skaar TC. 2012. Clinical Pharmacogenetics Implementation

	Consortium (CPIC) guidelines for codeine therapy in the context of cytochrome P450 2D6 (*CYP2D6*) genotype. *Clin Pharmacol Ther* **91**: 321–326. Johnson JA, Gong L, Whirl-Carrillo M, Gage BF, Scott SA, Stein CM, Anderson JL, Kimmel SE, Lee MT, Pirmohamed M, Wadelius M, Klein TE, Altman RB. 2011. Clinical Pharmacogenetics Implementation Consortium Guidelines for *CYP2C9* and *VKORC1* genotypes and warfarin dosing. *Clin Pharmacol Ther* **90**: 625–629.
Follow up Questions	How would the results have changed if insurance hadn't been an issue for the patients? How does genetically testing those who are poor metabolizers help them? What are the alternatives other than prasugrel and ticagrelor? What is the difference between CPIP and DPWG guidelines? What statistical methods were used to determine the efficiency of the results?

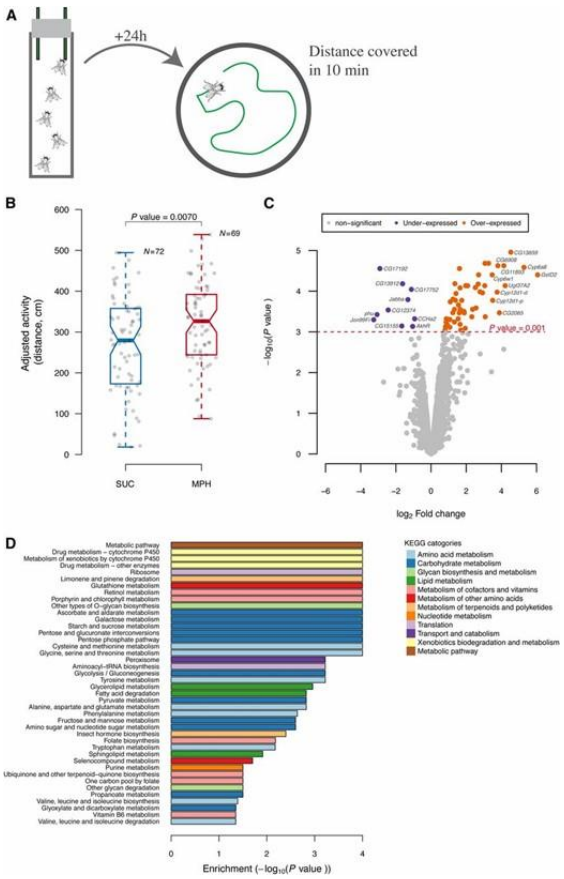
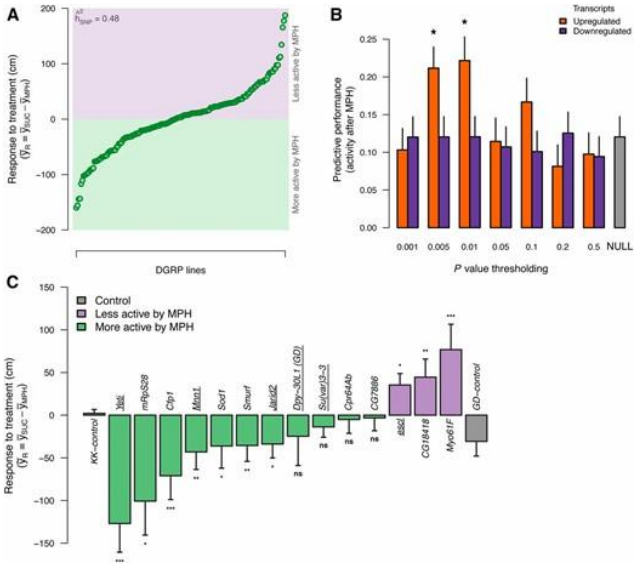
Article #13 Notes: Imidacloprid does not induce Cyp genes involved in insecticide resistance of a mutant *Drosophila melanogaster* line

Source Title	Imidacloprid does not induce Cyp genes involved in insecticide resistance of a mutant Drosophila melanogaster line
Source citation (APA Format)	Kalajdzic, P., Markaki, M., Oehler, S., & Savakis, C. (2013). Imidacloprid does not induce Cyp genes involved in insecticide resistance of a mutant Drosophila melanogaster line. *Food and Chemical Toxicology*, *60*, 355–359. https://doi.org/10.1016/j.fct.2013.07.080
Original URL	https://www.sciencedirect.com/science/article/pii/S0278691513005358?via=ihub
Source type	Journal article
Keywords	Imidacloprid, Cytochrome P450, Induction, D. melanogaster
#Tags	
Summary of key points + notes (include methodology)	Imidacloprid is a type of neonicotinoid, which is an umbrella insecticide. Using these often kills or paralyses insects. These chemicals target their nicotinic acetylcholine receptor. Ethical concerns have risen over its use, as though it is effective at ridding unwanted insects, we think it also has harmful effects on organisms that it is not supposed to have. The CYP family, cytochrome P450 monooxygenases, is responsible for detoxifying these agents and can often be overexpressed. The exposure to specific chemicals has the ability to grow the insects' insecticide resistance through upregulation of CYP genes. For this study in particular, it was unknown if the toxin Imidacloprid could do this. In order to test this, the researchers had two groups of fruit flies. One group was known to be resistant to the chemicals, thus having a larger baseline expression of the CYP genes. Then, they had a control group. This control group consisted of Drosophila wild-type flies. Both groups were treated exactly the same. They were kept at 24 degrees Celsius, given cornmeal-agar-yeast for food, and day/night cycles of 12 hours at a time. Then each group was exposed to the chemical, except their doses differed depending on underlying resistance. After their RNA was extracted, a PCR test was performed. By looking at the breakdown of expressive genes, they noticed no major increase. This let them determine that the exposure to imidacloprid had no effect on the resistance of the chemical or CYP genes.
Research Question/Problem/ Need	Can the use of Imidacloprid, an insecticide, induce P450 genes in Drosophila?

Important Figures	 *The two groups of flies studied and their difference in expression*
VOCAB: (w/definition)	Neurotoxins- A toxin affecting the nervous system Xenobiotics- a substance that is found in an organism, but is not naturally produced Agarose-gels- A gel made from dissolving agarose powder in a liquid, creating a 3D structure with channels that allow the separation of molecules.
Cited references to follow up on	Beckingham, K. M. (2005). Drosophila melanogaster--the model organism of choice for the complex biology of multi-cellular organisms. Gravitational and Space Biology Bulletin : *Publication of the American Society for Gravitational and Space Biology., 18*(2), 17–29. Chintapalli, V. R., Wang, J., & Dow, J. A. (2007). Using FlyAtlas to identify better drosophila melanogaster models of human disease. *Nature Genetics*, *39*(6), 715–720. https://doi.org/10.1038/ng2049 Willoughby, L., Chung, H., Lumb, C., Robin, C., Batterham, P., & Daborn, P. J. (2006). A comparison of drosophila melanogaster detoxification gene induction responses for six insecticides, caffeine and phenobarbital. *Insect Biochemistry and Molecular Biology*, *36*(12), 934–942. https://doi.org/10.1016/j.ibmb.2006.09.004
Follow up Questions	How can the issue of harming other organisms, such as bees, be mitigated? How long were the groups exposed to the toxin? Could varying exposure duration change induction levels in the Drosophila? Do these results hold true for all other classes of neonicotinoids as well, or just imidacloprid?

Article #14 Notes: Genetic Signatures of Drug Response Variability in Drosophila melanogaster

Source Title	Genetic Signatures of Drug Response Variability in Drosophila melanogaster
Source citation (APA Format)	Palle Duun Rohde, Iben Ravnborg Jensen, Pernille Merete Sarup, Michael Ørsted, Ditte Demontis, Peter Sørensen, Torsten Nygaard Kristensen, Genetic Signatures of Drug Response Variability in *Drosophila melanogaster*, *Genetics*, Volume 213, Issue 2, 1 October 2019, Pages 633 650, https://doi.org/10.1534/genetics.119.302381
Original URL	https://academic.oup.com/genetics/article/213/2/633/5930595
Source type	Journal Article
Keywords	Ritalin, ADHD, Drosophila Genetic Reference Panel, cross-generational effects, locomotor activity
#Tags	
Summary of key points + notes (include methodology)	In this study, the researchers look at a population of people who have ADHD. This disorder is characterized as a common mental disorder that commonly affects children. Tell-tale signs of having ADHD would be the lack of ability to focus, sit still, and think through things completely before acting on them. A common medication used to treat those with this disorder is methylphenidate (MPH or Ritalin). This study wanted to determine how different genotypes react to this medicine. They chose to model this through Drosophila because many of their neurological genes are conserved and show similarity to humans. To do this, they examined wild-type Drosophila and exposed them to Ritalin or sucrose, which acted as a control in this experiment. Then they looked at the distance they moved in ten minutes, also known as their locomotor activity. Then, they did a transcriptome analysis of the entire genome to see if the expression of any of the genes changed at all. Another method they used was a measurement from parent to the offspring. They first treated the flies with methylphenidate, and then they bred offspring. Those babies were left unexposed to the medicine. Then the behavior of these offspring was tested using a gene expression analysis. Based on these results, the researchers were able to determine that the use of MPH increases locomotor activity, the gene expression in Drosophila was manipulated with the use of the MPH, the behavioral response of the flies varied by genotype, and there were cross-generational effects between parent and offspring.
Research Question/Problem/ Need	How can preexisting medical knowledge regarding genetics be deepened with the use of Drosophila as a model?

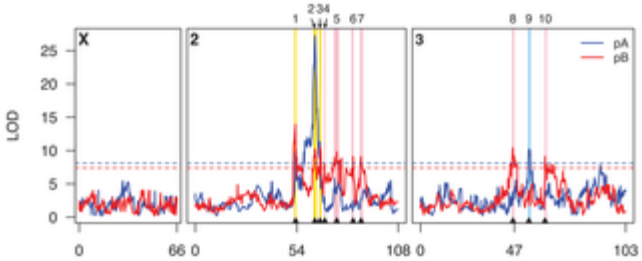
Important Figures	 *Locomotor and transcriptomic effects of MPH in a WT D. melanogaster population*  *Genotypic characterization of response to MPH*
VOCAB: (w/definition)	Intrinsic- something that is essential Serotonergic- related to the serotonergic system that regulates mood, sleep, and

	cognitive ability Dopaminergic- structures involved with dopamine- a controller of mood and reward Putative- commonly accepted
Cited references to follow up on	Andretic, R., van Swinderen, B., & Greenspan, R. J. (2005). Dopaminergic modulation of arousal in drosophila. Current Biology, 15(13), 1165–1175. https://doi.org/10.1016/j.cub.2005.05.025 Archer, T., Oscar-Berman, M., & Blum, K. (2011). Epigenetics in Developmental Disorder: ADHD and Endophenotypes. *Journal of Genetic Syndromes & Gene Therapy*, *2*(104). *Bhaskara, S., Dean, E. D., Lam, V., & Ganguly, R. (2006). Induction of two cytochrome P450 genes, CYP6A2 and CYP6A8, of drosophila melanogaster by caffeine in adult flies and in cell culture. Gene, 377, 56–64. https://doi.org/10.1016/j.gene.2006.02.032*
Follow up Questions	Were there any sex-specific differences in behavioral or transcriptomic responses? How was the methylphenidate concentration and exposure duration determined to measurable behavioral changes without introducing toxicity? How would the age of the Drosophila affect their genetic and behavioral changes?

Article #15 Notes: Identifying Loci Contributing to Natural Variation in Xenobiotic Resistance in Drosophila

Source Title	Identifying Loci Contributing to Natural Variation in Xenobiotic Resistance in Drosophila
Source citation (APA Format)	Najarro, M. A., Hackett, J. L., Smith, B. R., Highfill, C. A., King, E. G., Long, A. D., & Macdonald, S. J. (2015). Identifying Loci Contributing to Natural Variation in Xenobiotic Resistance in Drosophila: e1005663. *PLoS Genetics*, *11*(11). https://doi.org/10.1371/journal.pgen.1005663
Original URL	https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005663
Source type	Journal article
Keywords	interindividual genetic variation, toxins, xenobiotics, polymorphisms, caffeine, cytochrome P450
#Tags	
Summary of key points + notes (include methodology)	In this study, the researchers want to determine how genetic variation influences drug digestion, especially in the field of detoxification. They model this using caffeine as their xenobiotic of choice. To do this, they looked at the phenotypes of about 1,700 genotypes in Drosophila, fruit flies, that code for caffeine resistance. They used the DSPR, or Drosophila Synthetic Population Resource, and the DGRP, or Drosophila Genetic Reference Panel, as well. The researchers exposed the Drosophila to levels of caffeine while maintaining specific controls. For example, they kept the gender and age of the Drosophila constant throughout the trials. Then, they measured their survival time under the stress they were under. From here, they formulated 10 QTLs or quantitative trait loci. Many of these were located on the chromosomes 2L, 2R, and 3R; however, 3R was the strongest, so the researchers paid special attention to the genes on this one. Many of these QLTs were related to the cytochrome P450 enzymes (related to metabolism). Specifically, they looked at the Cyp12d1 gene and the Cyp6d5 gene. After, they looked at the individual gene expression using a PCR (polymerase chain reaction) test. With the use of RNAi, or RNA interference, the gene reduces caffeine resistance. This allowed the researchers to hypothesize that this gene could have a role in the digestion of drugs. When they tested for heritability, their H-squared value fell within the range of 0.50 to 0.55. This was significant because it informed the scientists that half of the variation they encountered was actually a result of genetic differences.
Research Question/Problem/ Need	How do structural variations of the Cyp12d1 gene contribute to drug resistance in Drosophila?

Important Figures



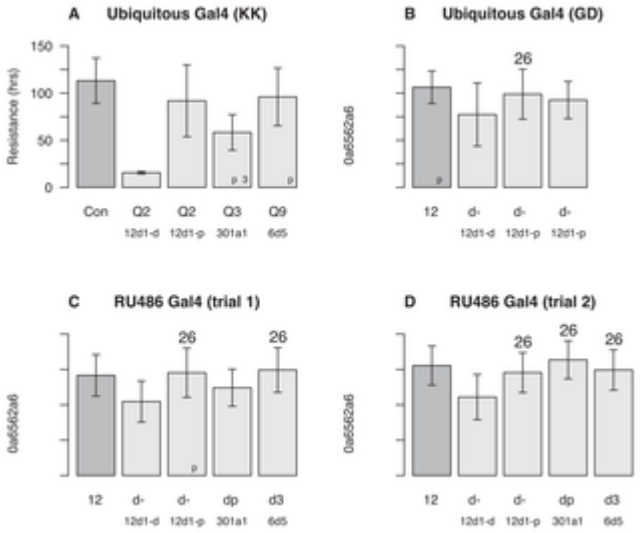
Genome scan for caffeine resistance

Name (Chr)	Panel	LOD score	Peak cM (2-LOD CI)[a]	Peak Mb (2-LOD CI)[a]	Number of genes[b]	Percent of H^2 [c]
Q1 (*2L*)	pA	9.9	53.3 (53.1–53.6)	18.74 (18.22–19.26)	123	5.5
	pB	14.0	53.2 (52.8–53.3)	18.52 (17.65–18.72)	81	7.7
Q2 (*2R*)	pA	27.2	63.6 (63.3–63.8)	7.07 (6.90–7.16)	36	14.4
	pB	10.3	63.6 (62.9–64.3)	7.06 (6.68–7.43)	122	5.7
Q3 (*2R*)	pA	11.3	66.1 (65.8–66.3)	8.36 (8.21–8.49)	65	6.3
	pB	10.6	66.3 (66.2–66.8)	8.49 (8.43–8.74)	48	5.9
Q4 (*2R*)	pB	8.1	68.8 (68.5–69.2)	9.65 (9.54–9.81)	26	4.5
Q5 (*2R*)	pB	9.8	75.2 (73.6–76.3)	11.49 (11.11–11.76)	68	5.4
Q6 (*2R*)	pB	9.1	83.9 (82.9–84.1)	13.77 (13.46–13.83)	69	5.1
Q7 (*2R*)	pB	9.1	88.1 (87.5–89.0)	15.23 (15.02–15.58)	74	5.0
Q8 (*3L*)	pB	10.4	46.4 (46.0–47.1)	20.56 (19.89–24.36)	398	5.8
Q9 (*3R*)	pA	10.2	54.4 (54.1–55.2)	9.87 (9.73–10.41)	79	5.7
Q10 (*3R*)	pB	9.1	62.5 (62.4–63.4)	14.01 (13.98–14.36)	61	5.1

[a] 2-LOD CI indicates the 2-LOD support interval of the QTL. Physical positions are given based on release 5 of the *Drosophila* reference genome.
[b] The number of protein-coding genes in the 2-LOD support interval.
[c] The proportion of the phenotypic variance due to each QTL comes directly from the linear model used for mapping (page 77 of [76]). The percentage of the broad-sense heritability (H^2) is simply this estimate divided by the broad-sense heritability of the mean measure of caffeine resistance.

doi:10.1371/journal.pgen.1005663.t001

Qualitative chart of mapped caffeine resistance QTL



Effects of RNA interference on single genes

VOCAB: (w/definition)

QTL - Quantitative Trait Loci- a statistical method used to map portions of the genome that influence traits that are quantitative, such as height or weight
DSPR- Drosophila Synthetic Population Resource, or a panel of recombinant inbred lines
Elucidate- to make clear
Danaus Plexippus- monarch butterfly

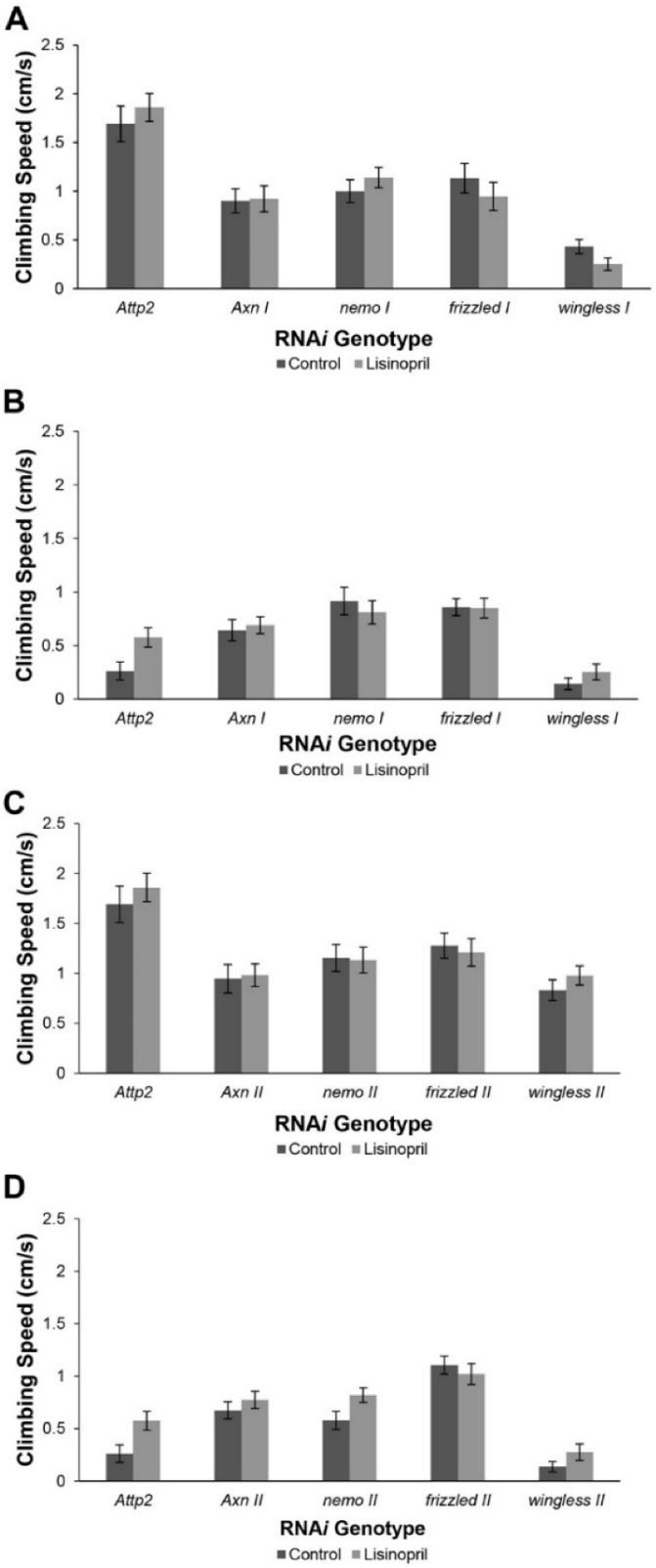
Cited references to follow up on	Zhong, W., Maradit-Kremers, H., St. Sauver, J. L., Yawn, B. P., Ebbert, J. O., Roger, V. L., Jacobson, D. J., McGree, M. E., Brue, S. M., & Rocca, W. A. (2013). Age and Sex Patterns of Drug Prescribing in a Defined American Population. *Mayo Clinic Proceedings*, *88*(7), 697–707. https://doi.org/10.1016/j.mayocp.2013.04.021 Li, X., Schuler, M. A., & Berenbaum, M. R. (2007). Molecular Mechanisms of Metabolic Resistance to Synthetic and Natural Xenobiotics. *Annual Review of Entomology*, *52*(1), 231–253. https://doi.org/10.1146/annurev.ento.51.110104.151104 Daborn, P. J., Yen, J. L., Bogwitz, M. R., Le Goff, G., Feil, E., Jeffers, S., Tijet, N., Perry, T., Heckel, D., Batterham, P., Feyereisen, R., Wilson, T. G., & Ffrench Constant, R. H. (2002). A Single P450 Allele Associated with Insecticide Resistance in Drosophila. *Science (American Association for the Advancement of Science)*, *297*(5590), 2253–2256. https://doi.org/10.1126/science.1074170
Follow up Questions	What are the main differences between the DSPR (Drosophila Synthetic Population Resource) and the DGRP (Drosophila Genetic Reference Panel)? What are the pros and cons of using RNA interference (RNAi) versus CRISPR? Why was caffeine used as a model xenobiotic? What is the justification behind that?

Article #16 Notes: Genome-Wide Analysis in Drosophila Reveals the Genetic Basis of Variation in Age-Specific Physical Performance and Response to ACE Inhibition

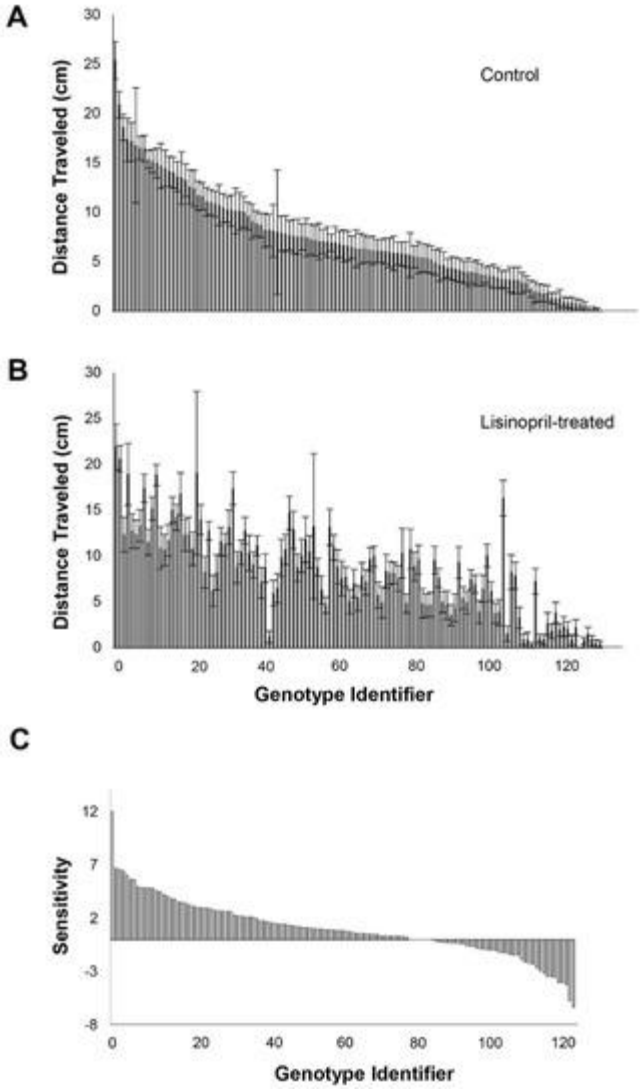
Source Title	Genome-Wide Analysis in Drosophila Reveals the Genetic Basis of Variation in Age-Specific Physical Performance and Response to ACE Inhibition
Source citation (APA Format)	Gabrawy, M. M., Khosravian, N., Morcos, G. S., Morozova, T. V., Jezek, M., Walston, J. D., Huang, W., Abadir, P. M., & Leips, J. (2022). Genome-Wide Analysis in Drosophila Reveals the Genetic Basis of Variation in Age-Specific Physical Performance and Response to ACE Inhibition. Genes, 13(1), 143. https://doi.org/10.3390/genes13010143
Original URL	https://www.mdpi.com/2073-4425/13/1/143
Source type	Journal Article
Keywords	Aging, personalized medicine, frailty, Lisinopril
#Tags	
Summary of key points + notes (include methodology)	Angiotensin-converting enzyme inhibitors are also referred to as ACE'is. One of the medications belonging to this category is Lisinopril, which is used in people who have high blood pressure, or hypertension. The effects of the medication vary slightly when it comes to treating different people. One of the main hypotheses for this is because of the genetic variation that exists between people. To model this, they used Drosophila as a test subject. These fruit flies were chosen due to having an ACE homolog. In the experiment, they wanted to measure the climbing speed and the endurance of the flies. Then, they wanted to further analyze how age has an effect on this. Then, they also wanted to test the genes they found and use RNA interference knockdown in order to determine if changing the expression of the genes would have any effect on the response the fly had to the ACEi. To do this, they narrowed in to 126 genomes using the Drosophila Genetic Reference Panel, or the DGRP. For each genotype, they looked at the flies' stats for how fast they could climb and how long they could keep it up after being treated with Lisinopril. Then they found a Sensitivity index regarding each other the genotypes (this was a measurement of how responsive each other's genotypes were to the medication). By doing this, they found confirmation that the genetic differences that make up an organism have an impact on the response the organism has to the medication, in this case, Lisinopril. They also found that the younger flies could climb about 50% as fast as the older flies could, giving the researchers insight into the role of age.
Research Question/Problem/	How does the use of angiotensin-converting enzyme inhibitors improve physical

Need	performance with genetically distinct individuals?

Important Figures



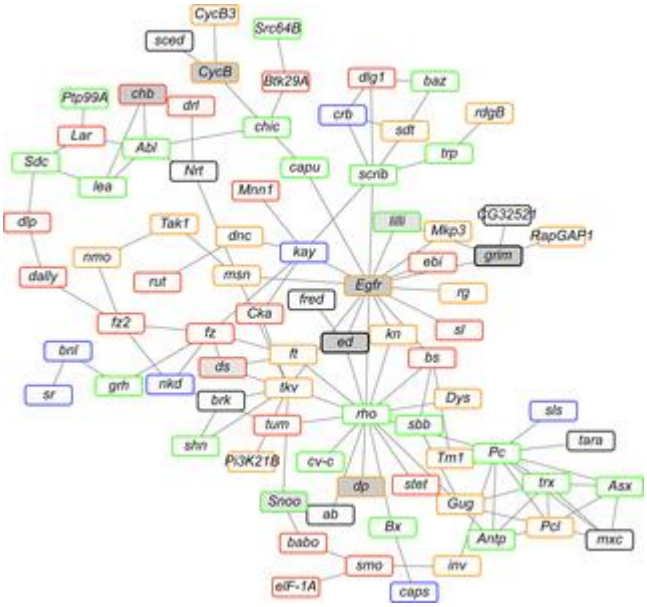
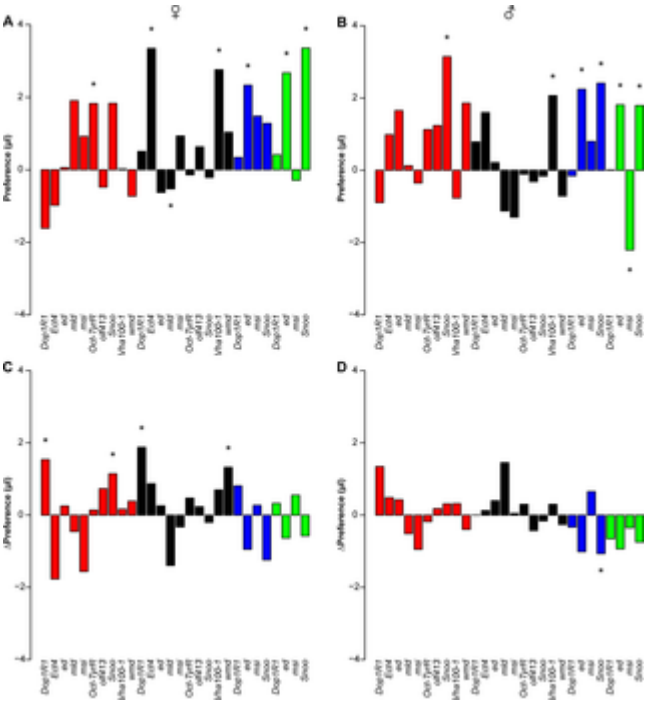
The effect of Lisinopril treatment on the climbing speed of the Drosophila

	 *The effect of Lisinopril on endurance, sensitivity, and the magnitude of response at an old age*
VOCAB: (w/definition)	Hypertension- high blood pressure, when the force of blood against artery walls is too high Ortholog- a gene in separate species that evolved from a common species Stringent- to be strict or precise.
Cited references to follow up on	Buford, T. W., Manini, T. M., Hsu, F.-C., Cesari, M., Anton, S. D., Nayfield, S., Stafford, R. S., Church, T. S., Pahor, M., & Carter, C. S. (2012). Angiotensin Converting Enzyme Inhibitor Use by Older Adults Is Associated with Greater Functional Responses to Exercise. *Journal of the American Geriatrics Society (JAGS)*, *60*(7), 1244–1252. https://doi.org/10.1111/j.1532-5415.2012.04045.x

	Cesari, M., Pedone, C., Antonelli Incalzi, R., & Pahor, M. (2010). ACE-Inhibition and Physical Function: Results From the Trial of Angiotensin-Converting Enzyme Inhibition and Novel Cardiovascular Risk Factors (TRAIN) Study. *Journal of the American Medical Directors Association*, *11*(1), 26–32. https://doi.org/10.1016/j.jamda.2009.09.014 Akif, M., Georgiadis, D., Mahajan, A., Dive, V., Sturrock, E. D., Isaac, R. E., & Acharya, K. R. (2010). High-Resolution Crystal Structures of Drosophila melanogaster Angiotensin-Converting Enzyme in Complex with Novel Inhibitors and Antihypertensive Drugs. *Journal of Molecular Biology*, *400*(3), 502–517. https://doi.org/10.1016/j.jmb.2010.05.024
Follow up Questions	How does the interaction between age, treatment plans, and genotypes found in Drosophila tell us about personalized medicine in humans? What was the sample size used in the experiment? What is the ideal age for the response to Lisinopril? How did the researchers decide which genes to include in their research?

Article #17 Notes: Genetics of cocaine and methamphetamine consumption and preference in Drosophila melanogaster.

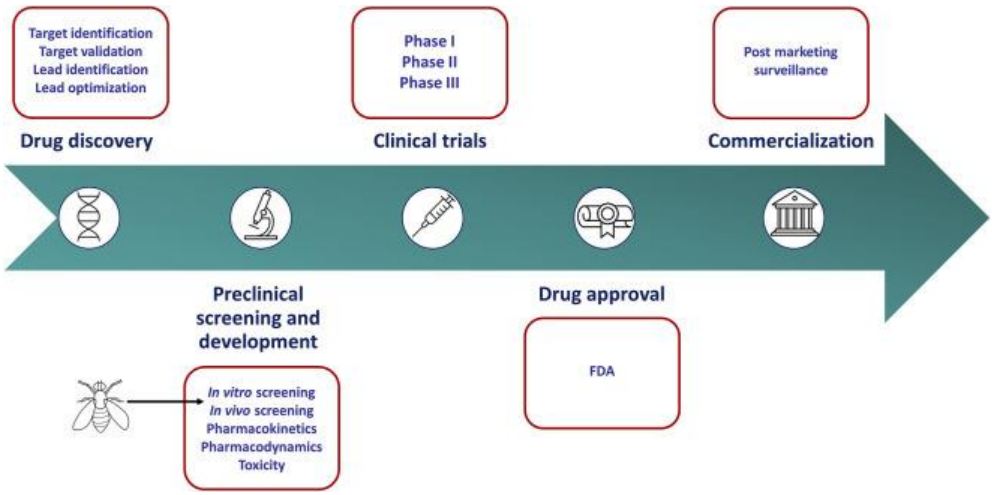
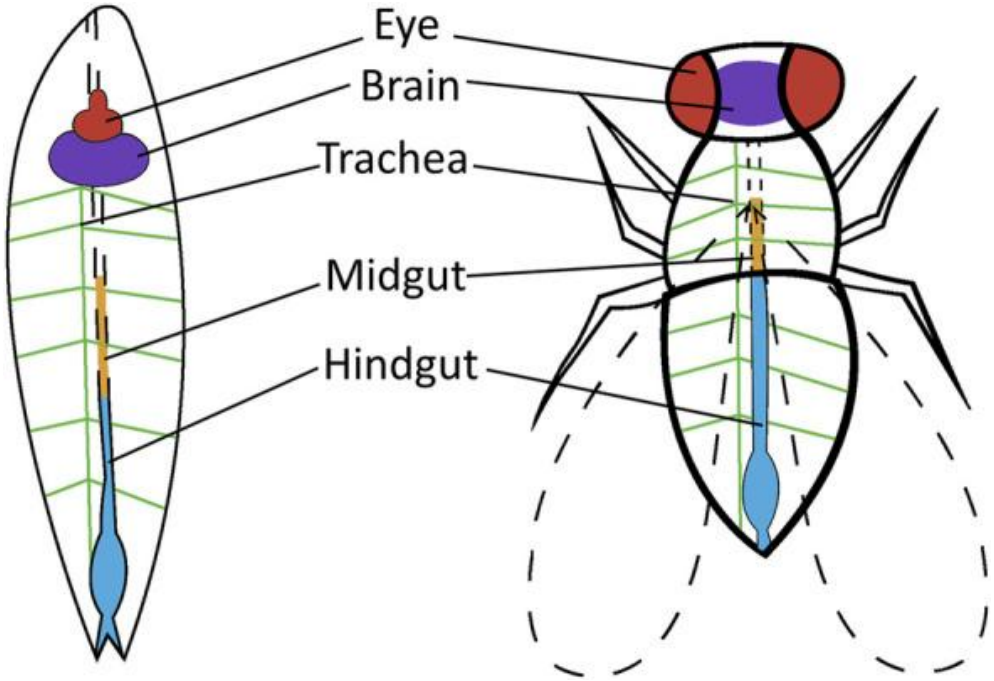
Source Title	Genetics of cocaine and methamphetamine consumption and preference in Drosophila melanogaster.
Source citation (APA Format)	Highfill, C. A., Baker, B. M., Stevens, S. D., Anholt, R. R. H., & Mackay, T. F. C. (2019). Genetics of cocaine and methamphetamine consumption and preference in Drosophila melanogaster. *PLoS Genetics*, *15*(5), e1007834. https://doi.org/10.1371/journal.pgen.1007834
Original URL	https://go-gale-com.ezpv7-web-p-u01.wpi.edu/ps/i.do?p=OVIC&u=mlin_c_worpoly&id=GALE%7CA587702554&v=2.1&it=r&sid=summon&aty=ip
Source type	Journal Article
Keywords	Cocaine, substance use, health, methamphetamine, genetic variation, RNA interference
#Tags	
Summary of key points + notes (include methodology)	In this study, the researchers were interested in discovering how a person's genetic information influences their traits when it comes to addiction. They found that this concept was too complicated to look at in humans, so they decided to model this in Drosophila instead. This was sensible because the two organisms share many of the same homologs. To do this experiment, the scientists looked at 46-48 genetic variants, which they found using the DGRP, or the Drosophila Genetic Reference Panel. Then, they had a study group and a control group. One group was given sucrose (5%) for food; this was the control group. The other was given a concoction of sucrose and one of the drugs of choice (either cocaine or methamphetamine). The flies were then left at their own will for about a day. The scientists. After this duration was over, we also looked at how much of this feeder substance was consumed in order to investigate preferred intake further. They calculated this by reading and noting the change in volume of the food and dividing that by the number of flies that were feeding on it. When this experiment was done, male Drosophila and female Drosophila were separated. This would allow them to track any gender-specific differences. After all this was done, they identified polymorphisms in the Drosophila impacting their results. Then, they used RNA interference to inhibit them, and tested the flies response again. What the researchers noticed was that some of the flies were very drawn to the drugs, while others behaved the opposite. Many of the genes responsible for this had to do with the genes that control reward and motivation

Research Question/Problem/ Need	How do genetic differences in individuals characterize their addiction-related behaviors?
Important Figures	 *A map of all significant genetic interaction for cocaine and methamphetamine traits*  *The differences in cocaine preference and change in cocaine preference found between the third and first exposures between RNAi and control genotypes.*
VOCAB: (w/definition)	Dimorphism- two separate forms of 1 species Biogenic amines- organic nitrogen compounds that are found in organisms Mesolimbic- a circuit in the brain responsible for reward and motivation

	Endosymbiont- organism that lives inside or another
Cited references to follow up on	Horne, M. K., Lee, J., Chen, F., Lanning, K., Tomas, D., & Lawrence, A. J. (2008). Long-term administration of cocaine or serotonin reuptake inhibitors results in anatomical and neurochemical changes in noradrenergic, dopaminergic, and serotonin pathways. Journal of Neurochemistry, 106(4), 1731–1744. https://doi.org/10.1111/j.1471-4159.2008.05534.x Hall, F. S., Drgonova, J., Jain, S., & Uhl, G. R. (2013). Implications of genome wide association studies for addiction: Are our a priori assumptions all wrong? *Pharmacology & Therapeutics (Oxford)*, *140*(3), 267–279. https://doi.org/10.1016/j.pharmthera.2013.07.006 Agrawal, A., & Lynskey, M. T. (2008). Are there genetic influences on addiction: evidence from family, adoption and twin studies. *Addiction (Abingdon, England)*, *103*(7), 1069–1081. https://doi.org/10.1111/j.13600443.2008.02213.x
Follow-up Questions	Did the males or females have any preference for how much they took of the laced food in order to fulfill their "reward"? Why was the heritability range so large (40%)? What was the preference between the two drugs? Were the preferred intakes different? What was the specific process used for RNA interference? How does the reward system in flies correlate with/connect to the one in humans? How are they the same? How are they different?

Article #18 Notes: Drosophila melanogaster: A platform for anticancer drug discovery and personalized therapies

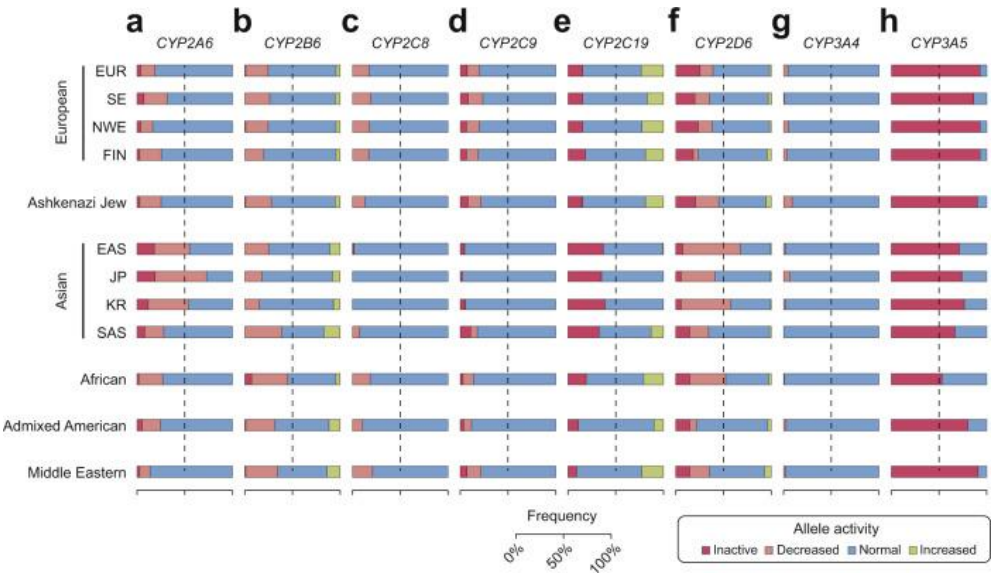
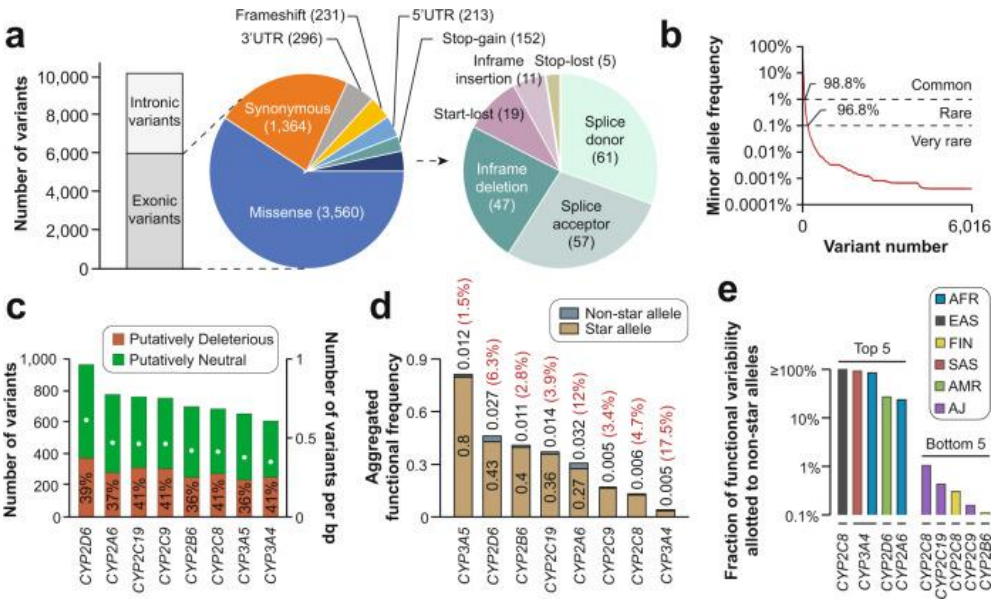
Source Title	Drosophila melanogaster: A platform for anticancer drug discovery and personalized therapies
Source citation (APA Format)	Munnik, C., Xaba, M. P., Malindisa, S. T., Russell, B. L., & Sooklal, S. A. (2022). Drosophila melanogaster: A platform for anticancer drug discovery and personalized therapies. *Frontiers in Genetics*, *13*, 949241. https://doi.org/10.3389/fgene.2022.949241
Original URL	https://pmc.ncbi.nlm.nih.gov/articles/PMC9393232/
Source type	Journal Article
Keywords	Drosophila melanogaster, cancer models, high-throughput screening, drug discovery, personalized therapy
#Tags	
Summary of key points + notes (include methodology)	In this study, the researchers were concerned about the unfeasibility of many cancer drug discoveries. Often, they fail when they are brought to actual human patients. To help combat these issues, the scientists decided to look closely at Drosophila. Part of their justification for doing this was not only the similarity between human and Drosophila genes, but also that their lifespan is a lot shorter than that of humans, and that the experiment would be relatively cheap/cost-effective. The researchers looked at different types of cancers individually. For example, colorectal cancer, lung cancer, thyroid cancer, and brain cancer. Using an upstream activation sequence (UAS), they were able to model different tumors, reflecting human cancer. They specifically manipulated the genes of the flies to include mutations associated with cancers. To do this, they would overexpress genes, suppress them, and combine mutations. Their methodology was particularly interesting. The researchers of the study first examined the genes of actual patients with cancer. Consequently. They examined the particular genes/mutations that are distinct to the disease. Only then did they go and attempt to replicate these changes in Drosophila. This process took place over the span of about a month or a month and a half. After this, they fed the flies food that had dissolved compounds in them to be absorbed by the gut. Then, the scientists looked at what their survival rate would be with the intake of the drug. They specifically looked at lifespan, tumor size, and abnormal behavioral changes.
Research Question/Problem/ Need	How can using Drosophila as a model for human cancer pathways bring light to how we can better translate cell-culture to humans?

Important Figures	 *Flowchart of the drug discovery and development*  *Drosophila tissue and organs*
VOCAB: (w/definition)	Colorectal- affecting the colon and the rectum Adenoid cystic carcinoma- cancer affecting your glandular tissues Apoptosis- the death of cells
Cited references to follow up on	Aritakula, A., & Ramasamy, A. (2008). Drosophila-based in vivo assay for the validation of inhibitors of the epidermal growth factor receptor/Ras pathway. Journal of Biosciences, 33(5), 731–742. https://doi.org/10.1007/s12038-008-0093-9 Ashburn, T. T., & Thor, K. B. (2004). Drug repositioning: identifying and developing new uses for existing drugs. *Nature Reviews. Drug Discovery*, *3*(8), 673–683.

	https://doi.org/10.1038/nrd1468 Bangi, E., Murgia, C., Teague, A., Sansom, O., & Cagan, R. (2015). Abstract PR03: Identifying biomarkers of drug response and resistance using personalized Drosophila models of colorectal cancer. *Clinical Cancer Research*, *21*(4_Supplement), PR03–PR03. https://doi.org/10.1158/1557-3265.PMS14-PR03
Follow up Questions	How were the correct dosages determined for the compounds? How were the scientists sure that the data collected on thyroid cancer was feasible, considering Drosophila do not have thyroids? How ethical is this process? Could it be replicated within reason? Does this system only work for the cancers listed? What would this process look like for other diagnoses? Were females and males separated during experimentation? Were there any differences in their response or tolerance?

Article #19 Notes: The genetic landscape of major drug metabolizing cytochrome P450 genes—an updated analysis of population-scale sequencing data

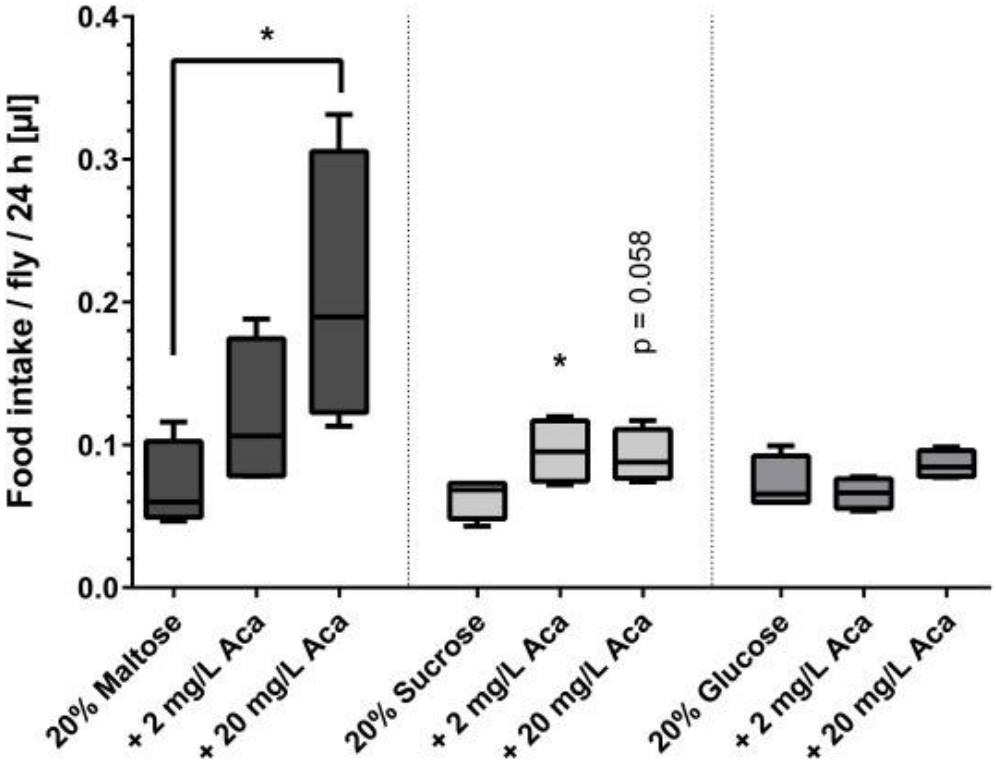
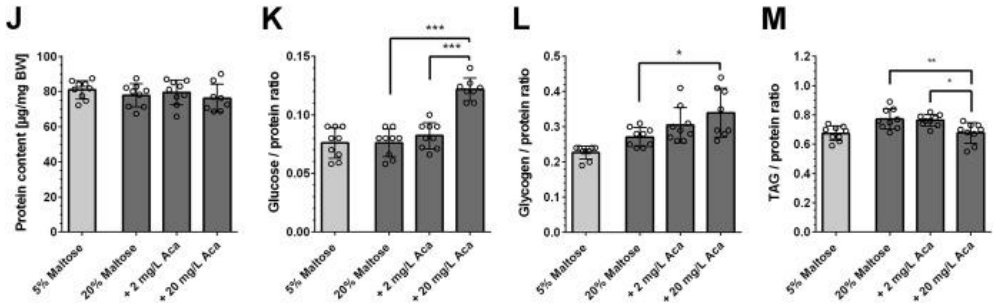
Source Title	The genetic landscape of major drug metabolizing cytochrome P450 genes—an updated analysis of population-scale sequencing data
Source citation (APA Format)	Zhou, Y., & Lauschke, V. M. (2022). The genetic landscape of major drug metabolizing cytochrome P450 genes—an updated analysis of population-scale sequencing data. The Pharmacogenomics Journal, 22(5–6), 284–293. https://doi.org/10.1038/s41397-022-00288-2
Original URL	https://www-nature-com.ezpv7-web-p-u01.wpi.edu/articles/s41397-022-00288-2
Source type	Journal Article
Keywords	Predictive markers, genetic markers, CYP genes, human population
#Tags	
Summary of key points + notes (include methodology)	The cytochrome enzymes come in various variants. However, this study decided to focus on eight major ones that greatly influence the way drugs are metabolized. These eight are CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, CYP3A4 and CYP3A5. Due to the way these alleles influence the way our bodies digest medicine and the pharmacokinetic cycle, they are commonly referred to as star alleles. For this study, the researchers looked at a group of individuals from 12 different populations to ensure diversity in their data. This accounted for a total of 141,614 different people. Then they looked closely at any variants. Were they exonic, deleterious, or neutral? How closely related were they to star alleles? Were they caused by any other variations? They next looked at the change that was made to the metabolism rate. Are they poor, normal, or rapid? When they collected all of their data, they found that out of about 10 thousand of them, 6 thousand were exonic, and their MAF value (minor allele frequency) was very low as well. The remaining 4 thousand variants were more likely to be deletions than to have no major change in phenotype. As prior knowledge has already pointed out, it has been confirmed that, apart from CYP genes, there are a number of other genes that are contributing factors to the way we digest medicine. What the study found was that some populations showed specific patterns. For example, a specific population that has the gene for poor metabolism might have different medical doing preferences compared to another, which had a faster metabolism.
Research Question/Problem/ Need	What is the frequency and how does the expression of various CYP variants in individuals affect distinct populations?

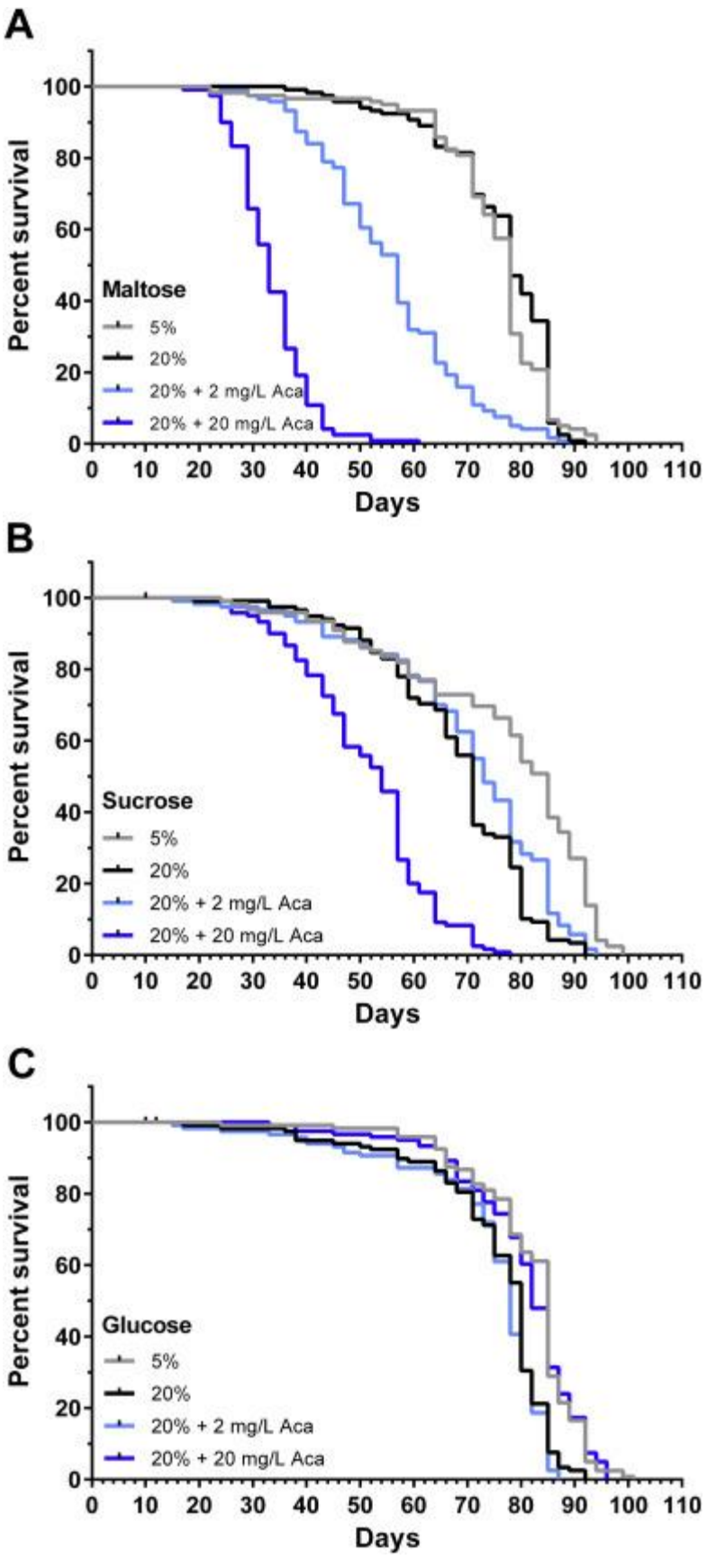
Important Figures	 *Frequencies of inactive (dark red), reduced activity (light red), normal (blue) and increased activity (green) alleles in the CYP family*  *The distribution of CYP drug metabolizing variants*
VOCAB: (w/definition)	Star alleles- a name for a haplotype that is a description of a pattern defined by genetic variation Population admixture- The process of two separate and distinct populations interbreeding Genetic drift- a change in the frequency of an allele that is random from generation to generation Disequilibria- lack of stability in terms of demand
Cited references to follow up on	Zanger, U. M., & Schwab, M. (2013). Cytochrome P450 enzymes in drug metabolism: Regulation of gene expression, enzyme activities, and impact of

	genetic variation. Pharmacology & Therapeutics (Oxford), 138(1), 103–141. https://doi.org/10.1016/j.pharmthera.2012.12.007 Zhou, Y., & Lauschke, V. M. (2022). Population pharmacogenomics: an update on ethnogeographic differences and opportunities for precision public health. *Human Genetics*, *141*(6), 1113–1136. https://doi.org/10.1007/s00439-021-02385-x Machiela, M. J., & Chanock, S. J. (2015). LDlink: a web-based application for exploring population-specific haplotype structure and linking correlated alleles of possible functional variants. *Bioinformatics*, *31*(21), 3555–3557. https://doi.org/10.1093/bioinformatics/btv402
Follow up Questions	How does this sample size account for the population of the community that might be a minority? Were there any patterns noted of combinations of multiple gene variations that worked together in different populations? How does the respective environment of these populations contribute to their expressed phenotype? How does diet impact the results found?

Article #20 Notes: A diet-based Drosophila melanogaster model for the in vivo pharmacological evaluation of α-glucosidase inhibitors

Source Title	A diet-based Drosophila melanogaster model for the in vivo pharmacological evaluation of α-glucosidase inhibitors
Source citation (APA Format)	Lüersen, K., Nevermann, S., Nebendahl, M., Olufolabo, K. O., Oguntimehin, S. A., Moody, J. O., & Rimbach, G. (2025). A diet-based Drosophila melanogaster model for the in vivo pharmacological evaluation of α-glucosidase inhibitors. European Journal of Pharmacology, 1005, Article 178028. https://doi.org/10.1016/j.ejphar.2025.178028
Original URL	https://www.sciencedirect.com/science/article/pii/S0014299925007824?via%3Dihub
Source type	Journal Article
Keywords	Acarbose; Drosophila melanogaster disease model; Drug discovery; Metabolic diseases; Morus mesozygia; α-glucosidase
#Tags	
Summary of key points + notes (include methodology)	The researchers of this study wanted to look at how medical preferences are dependent on diet in Drosophila. They did this in such a small organism because it would make whole-organism screening a lot easier. They are also a lot easier to work with than humans due to the ability people have to manipulate their genetic material. The researchers who conducted the study chose distinct compounds that relate to levels of obesity. Examples of these were types of sugars, like glucose, fructose, maltose, or sucrose. These compounds were mixed into the normal food given to the flies. All flies were given a standard inhibitor. Acarbose was mixed into all food sources as well. Another thing they tested was looking at root bark extracts to see if they would act as an inhibitor. After being consumed by the Drosophila, the scientists looked at how their behavior changed. Specifically, they looked at how long the fly survived, the adverse effects of the feeding solution, and other impacts of the fly phenotypes. With this information, they were able to fine-tune their dosage approximations. Using this, they could increase or decrease them as necessary. What the scientists found was that eating more sugar increased fat storage, the Drosophila had slower development if the inhibitor caused toxic side effects (also meaning that their lifespan is shorter), and there was reduced activity (though the acarbose was an effective inhibitor). However, the results that were reported with the root bark inhibitor varied. It effectively reduced build-up, but also minimized side effects, unlike acarbose.

Research Question/Problem/ Need	How well does a neutral inhibitor like acarbose compare to an inhibitor such as Morus mesozygia in terms of dietary factors that reflect obesity?
Important Figures	 *Description of how acarbose-supplementation leads to enhanced food intake of high-maltose diet-fed Drosophila*  *Effect of acarbose on Drosophila larval development*

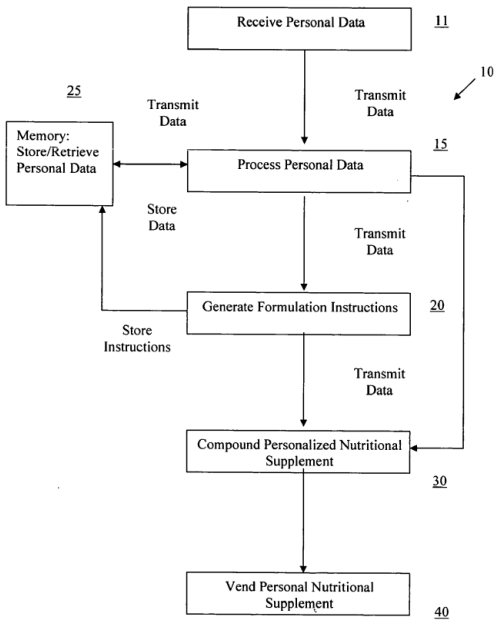

A
Percent survival
Maltose
5%
20%
20% + 2 mg/L Aca
20% + 20 mg/L Aca
Days
B
Percent survival
Sucrose
5%
20%
20% + 2 mg/L Aca
20% + 20 mg/L Aca
Days
C
Percent survival
Glucose
5%
20%
20% + 2 mg/L Aca
20% + 20 mg/L Aca
Days

	What is the effect of acarbose on the lifespan of female Drosophila?
VOCAB: (w/definition)	Diurnal- daily or during the day α-compound- a position in a molecule that is adjacent to a specific functional group Neurodegeneration- the loss of function in neurons that leads to eventual death.
Cited references to follow up on	Agrawal, N., Pallos, J., Slepko, N., Apostol, B. L., Bodai, L., Chang, L.-W., Chiang, A. S., Thompson, L. M., Marsh, J. L., & Housman, D. E. (2005). Identification of Combinatorial Drug Regimens for Treatment of Huntington's Disease Using Drosophila. Proceedings of the National Academy of Sciences - PNAS, 102(10), 3777–3781. https://doi.org/10.1073/pnas.0500055102 Al-Anzi, B., Sapin, V., Waters, C., Zinn, K., Wyman, R. J., & Benzer, S. (2009). Obesity-Blocking Neurons in Drosophila. *Neuron (Cambridge, Mass.)*, *63*(3), 329–341. https://doi.org/10.1016/j.neuron.2009.07.021 Alfahel, R., Sawicki, T., Jabłońska, M., & Przybyłowicz, K. E. (2023). Anti Hyperglycemic Effects of Bioactive Compounds in the Context of the Prevention of Diet-Related Diseases. Foods, 12(19), 3698. https://doi.org/10.3390/foods12193698
Follow up Questions	How do the disaccharide and monosaccharide diets give confirmation of the impact on the compounds? What are the major differences between administration strategies? Would any differences occur between oral intake and through a needle? What research needs to be done before confirming the use of the root extract in daily application? How do these results translate to humans? How was acarbose chosen as a control?

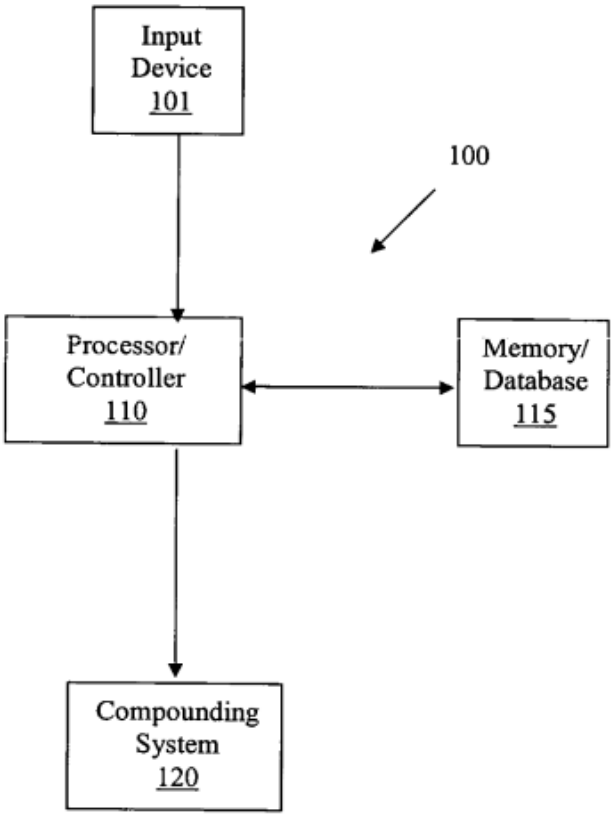
Patent #1 Notes: Personalized Nutritional Supplement

Source Title	Personalized nutritional supplement
Source citation (APA Format)	Koekkoek, R. (2006). *Personalized nutritional supplement* (United States Patent No. US20060099310A1). https://patents.google.com/patent/US20060099310A1/en#patentCitations
Original URL	https://patents.google.com/patent/US20060099310A1/en
Source type	Patent
Keywords	Personalized nutrition, nutrigenetics, dietary supplements, dispensing system, metabolic profiling, data
#Tags	
Summary of key points + notes (include methodology)	This patent is for a method/system that allows people to get dispensed medicine based on their genetic information. This is done through data collection. The system looks at a series of personal data. For example, weight, age, diet, comedications, and preexisting goals the users have set for themselves. Then, loaded into the system, is known pharmacogenetic information. This includes information on pre-known interactions between nutrients and genes as well as nutrients and drugs. The software combines these two categories of data in order to create a profile for the user. Then, the device is able to spew out the correct medicine based on the results of the computed software. The device is capable of dispensing various forms of medication, such as pills that are capsulated or powders. One of the best features of the system is that the information that the user inputs into the system can be updated as new health tests turn up. For example, you can change your overall goals to be more attainable, or maybe even more challenging. Or, if you were to go to the doctors and get a blood level test done, this information could also be inputted into the system.
Research Question/Problem/ Need	What would a system that customizes individuals medicinal needs based on stores genetic data and dispenses them look like?

Important Figures



Flowchart showing the process that device follows in order to supply the user with personalized medication.

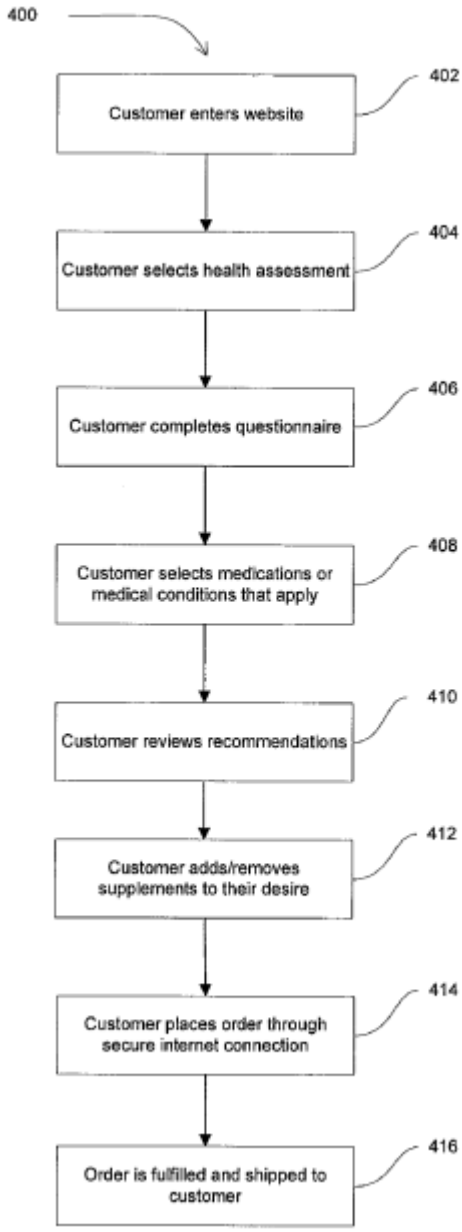


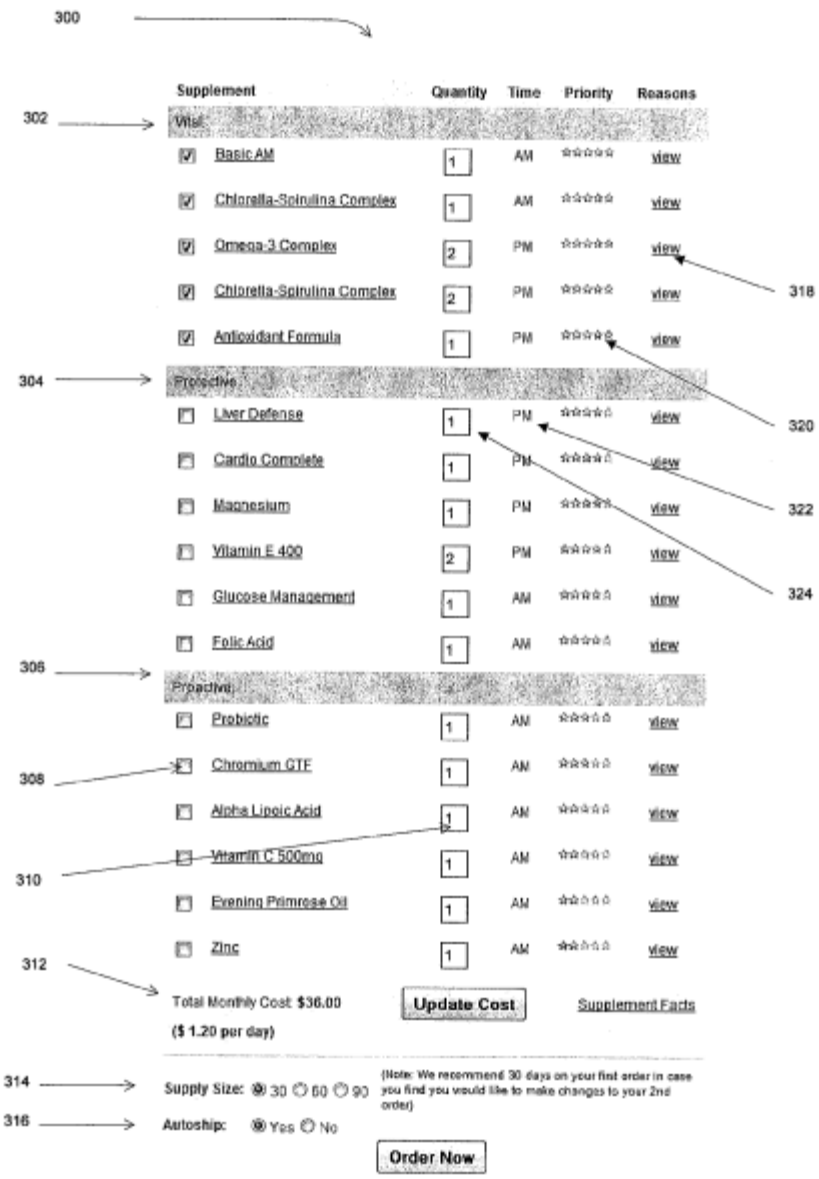
How the compounding system responds to input

VOCAB: (w/definition)	Nutrigenomics- study of the interaction between nutrition and genes Antiquated- outdated Nutraceuticals- food with medical benefits Excipients- inactive substances used as the medium for drugs
Cited references to follow up on	Dopson, M., Davis, J., & Gunwall, R. (2006). Nutritional supplement composition and method (United States Patent No. US20060062827A1). https://patents.google.com/patent/US20060062827A1/en Wilmott, J. M., Aust, D. T., & Crawford, T. K. (2004). Method for producing customized cosmetic and pharmaceutical formulations on demand (United States Patent No. US6782307B2). https://patents.google.com/patent/US6782307B2/en Reese, R. (2004). Pharmaceutical system in which pharmaceutical care is provided by a remote professional serving multiple pharmacies (United States Patent No. US6711460B1). https://patents.google.com/patent/US6711460B1/en
Follow up Questions	What human pharmacogenetic guidelines does the device use for data? What are the ethical concerns of the usage of this device? How reliable are the results? Have there been tests? How would this be tested? What is the cost of implementing this? What are privacy concerns?

Patent #2 Notes: Composition and method to optimize and customize nutritional supplement formulations by measuring genetic and metabolomic contributing factors to disease diagnosis, stratification, prognosis, metabolism, and therapeutic outcomes

Source Title	Composition and method to optimize and customize nutritional supplement formulations by measuring genetic and metabolomic contributing factors to disease diagnosis, stratification, prognosis, metabolism, and therapeutic outcomes
Source citation (APA Format)	Blum, K., Meshkin, B., & Downs, B. (2006). Composition and method to optimize and customize nutritional supplement formulations by measuring genetic and metabolomic contributing factors to disease diagnosis, stratification, prognosis, metabolism, and therapeutic outcomes (United States Patent No. US20060062859A1). https://patents.google.com/patent/US20060062859A1/en
Original URL	https://patents.google.com/patent/US20060062859A1/en
Source type	Patent
Keywords	Metabolomics, biochemical, polymorphisms, enzyme activity, detox, hormonal, diet
#Tags	
Summary of key points + notes (include methodology)	This method looks at data that constructs the user's biochemical buildup. The creator of this patent argued that most supplements do not account for personalization. For example, enzyme activity. This activity can directly correlate to how fast or slow someone processes drugs. Factors like genes, enzymes, and lifestyle, all affect the metabolism rate someone might have. For example, their blood type, levels of hormones, and different variants they carry in their DNA. Then, a computer takes this information and analyzes it. It does this, then looks at data databases and finds if the user is missing nutrients or if they are intaking too many of a certain nutrient. It cross-checks its finding with the users age, weight, diet, comedications and other medical history. Through this, dosages are made and computed. These nutrients include a wide variety, such as vitamins, minerals, proteins, fates, and even herbs. Not only this, but the algorithm looks at a number of other things. First, it looks at the price of the medication. Then, it also shows the quantity of the medication needed by the user. Lastly, it displays a rating of the level of necessity. So, on a scale of 1-5, the site conveys to the individual how large their need for that nutrient is. How essential is it for them to have? After this whole process, the user must order all their supplements.

Research Question/Problem/ Need	Can custom formulations of medicine be made for individuals through genetic, biochemical, and metabolic data?
Important Figures	 *The process a user must go through in order to purchase and receive their personalizes supplements*



The user interface: an example of the results a user might be shown

VOCAB: (w/definition)	Homeopathic- an alternative approach to medicine Erroneous- incorrect Methylation- the process of adding a methyl group to a molecule Serum HDL levels- the level of high-density lipoprotein in the blood
Cited references to follow up on	Ifland, J. R. (2009). Methods and devices for maintaining a diet free from refined foods (World Intellectual Property Organization Patent No. WO2009009485A1). https://patents.google.com/patent/WO2009009485A1/en Stefanon, B. (2010). Determining nutrients for animals through gene expression (United States Patent No. US20100151062A1). https://patents.google.com/patent/US20100151062A1/en

	Sullivan, P. (2011). *Method for personalized nutritional supplements* (United States Patent No. US20110054928A1). https://patents.google.com/patent/US20110054928A1/en
Follow up Questions	What is the cost of this site and are there any customer benefits? How does it work with insurance companies? Has the system been tested scientifically? Can the system tell the user how long they should be consuming that vitamin? Are there any adverse effects or risk? How is this combatted?