Picking the Most Effective Pain Medicine



WE Svetlana Kantorovich, Ph.D.

Director, Clinical & Scientific Affairs Proove Biosciences, Inc.



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PROME

Variations in DNA



- Humans share 99.9% of their DNA
- The remaining 0.1% is what sets us apart from one another
 - Physical appearance
 - Susceptibility to disease
 - Response to medications
- We can detect the sequence of DNA and identify changes that may make one patient more susceptible to a disease, or respond differently to a medication, than another patient.
 - ✓ Reduce trial-and-error
 - Avoid ADEs

SNPs : Single Nucleotide Polymorphisms

- DNA is composed of nucleotides:
- SNPs are <u>polymorphisms</u> at the <u>single</u> <u>nucleotide</u> level
 - Not the same as a mutation!
 A SNP has to be present in at least 1% of population
- Our DNA has ~10 million SNPs.
 - One gene may have 1000s of SNPs
 - Sometimes it is necessary to look at a combination of SNPs together



https://neuroendoimmune.wordpress.com/2014/03/27/dnarna-snp-alphabet-soup-or-an-introduction-to-genetics/

Which SNPs are clinically-relevant?



Pharmacodynamics: Site of action – "What the drug does to the body"



Violin JD et al. 2014. Trends in Pharmacological Sciences. 35(7)



<u>Pharmacokinetics</u>: Metabolism – "What the body does to the drug"

Proove Genetic Testing



Patients on any medication

Patients on or starting opioids

/E Patients on or starting Ibuprofen, Acetaminophen, Gabapentin, or Alprazolam

Patients experiencing pain

Patients on or starting opioids

Patients on or starting NSAIDs

NSAID RISK

OPIOID RISK

PERCEPTION

OPIOID RESPONSE

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Drug Metabolism Genetic Profile





Proportions of drugs metabolized by CYP450

Which SNPs are clinically-relevant?







Drug Metabolism

Intended Use: Avoid ADEs, trial-anderror and effectively choose medications likely to work for patients



Drug Metabolism Genetic Profile



In a prospective study of 122 patients, physicians who used the test rated its Impact Clinical benefit on decision making as 3.88 on a 5-point scale (1.47 points higher on Actionability Decision than controls). 5 patient 5 1.5 Increase in benefit Avg. benefit to MD 4 4 1 Avg. benefit to 3 3 1.0986 3.88 3.8 2 0.5 2 0.7855 0.726 2.7 2.41 1 1 0 Changed dose Explained Explained 0 0 Guided Guided Non-Guided Non-Guided lack of benefit Correlation Physicians who used the test rated its benefit on patient care as 3.80 on a 5-Clinical with point scale (1.10 points higher than controls). Improvement within 60 days Utility Outcomes



Opioid Response

Intended Use: Avoid trial-and-error, ADEs, and effectively choose medications likely to work for patients







Non-Opioid Response

Intended Use: Avoid trial-and-error, ADEs, and effectively choose medications likely to work for patients





Non-Opioid Response Genetic Profile



In a prospective longitudinal study of 6,908 patients across 92 different research sites, physicians who used the test rated its benefit in decision making as a 4.08 on a 5-point scale (1.12 points higher than controls).



Impact

on

Decision

Clinical

Actionability

Objectively Assess Pain Perception





Pain Perception Clinical Utility



Cinical
With
ConditionMarket
COMTDopamine
Epinephrine
Norepinephrine

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COMT Activity	Pain Sensitivity	Clinical Implications
High	Low	Quicker recovery from surgical procedures; lower opioid requirements; under-reporting pain
Moderately High	Moderately Low	Quicker recovery from surgical procedures; lower opioid requirements
Average	Average	Quicker recovery from surgical procedures; lower opioid requirements
Moderately Low	Moderately High	Higher opioid requirements, may be magnifying pain
Low	High	Longer recovery from surgical procedures; higher opioid requirements; pain magnifying

Tammimäki, A. & Männistö, P. T. Catechol-O-methyltransferase gene polymorphism and chronic human pain: a systematic review and meta-analysis. *Pharmacogenet Genomics* **22**, 673-691, doi:10.1097/FPC.0b013e3283560c46 (2012)

McLean, S. A. *et al.* Catechol O-methyltransferase haplotype predicts immediate musculoskeletal neck pain and psychological symptoms after motor vehicle collision. *J Pain* **12**, 101-107, doi:10.1016/j.jpain.2010.05.008 (2011).

Dai F et al. (2010) Association of catechol-O-methyltransferase genetic variants with outcome in patients undergoing surgical treatment for lumbar degenerative disc disease. The Spine Journal 10:949-957.



Pain Perception

Intended Use: Interpret patient's selfreported pain to guide appropriate use of Rx and non-Rx treatment



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Pain Sensitivity Index 2 - APS/LPS = MODERATELY LOW 3 - APS/APS = AVERAGE 5 4 - HPS/LPS = MODERATELY HIGH HPS/APS **High Pain Sensitivity** HPS/APS

- 1 LPS/LPS = LOW- (lowest pain sensitivity)
- 5 HPS/APS & HPS = HIGH (highest pain sensitivity)

Jane Doe is genetically predisposed to high pain sensitivity and may be perceiving an exaggerated level of pain. Patient pain numeric rating scores may be inconsistent with medical evaluations. This patient may take longer to recover from surgical procedures or injuries and continue to experience pain with average doses of pain medication. Consideration of alternative therapies, including cognitive-behavioral therapy, that target altered neurochemistry may be warranted.

Genotype

Catechol-O-Methyltransferase (S-COMT promoter A/G)	A/A
Catechol-O-Methyltransferase (COMT his62his C/T)rs4633	C/C
Catechol-O-Methyltransferase (COMT leu136leu C/G)rs4818	C/C
Catechol-O-Methyltransferase (COMT val108/158met A/G)rs4680	G/G
Serotonin 2a Receptor (HTR2A) rs7997012	G/G
Dopamine Beta Hydroxylase(DBH) visile11115	C/C
Serotonin Transporter (SLC6A4) ····· rs140701	с/т
Methylenetetrahydrofolate Reductase (MTHFR)	G/A
GABA _A Receptor, gamma2 (GABRG2)rs211014	C/C
Opioid Receptor, Mu 1 (OPRM1) rs1799971	A/G

Depression

Additional Factors

Gender Age

- Mental Health

Pain Perception Genetic Profile







Opioid Risk

Intended Use: Stratify risk to cost, effectively use opioids in low risk, monitor/rotate in moderate risk, avoid/limit in high risk







Clinical Validity Correlation with Condition

Individual genes have been independently found to correlate with abuse-related disorders

- Genetic variants are located within four important neurochemical pathways associated with the brain reward pathways
 - Serotonergic
 - Endorphinergic
 - GABAergic
 - Dopaminergic circuits



OPIOID RISK

Correlation Clinical with Validity Condition

Gene

Serotonin 2A Receptor

Disorder

- Drug Abuse⁹

- Serotonin Transporter
- Catechol-O-Methyltransferase

Dopamine D2 Receptor

Dopamine D1 Receptor

Dopamine D4 Receptor

Dopamine Transporter

Dopamine Beta Hydroxylase

Methylene Tetrahydrofolate Reductase

Human Kappa Opioid Receptor

Gamma-Aminobutyric Acid

Human Mu Opioid Receptor

- Alcohol abuse^b • Anxiety⁷
- Depression⁸

- Alcohol abuse¹⁰
- Substance abuse¹¹
- Alcohol abuse¹²
 - Methamphetamine abuse¹³
 - Alcohol, cocaine, nicotine dependence¹⁴
 - Heroin addiction^{15,16}
 - Drug abuse^{1/}
 - Cocaine addiction¹⁸
 - Methamphetamine addiction¹⁹
 - Alcohol abuse²⁰
 - Cocaine addiction^{20,21}
 - Smoking addiction²²
 - Bipolar disorder, depression, schizophrenia²³
 - Alcohol abuse²⁴
 - Alcohol abuse²⁵
 - Methamphetamine dependence²⁶
 - Complex regional pain syndrome²⁷ Heroin dependence²⁸



OPIOID RISK





Clinical Actionability Decision In a prospective longitudinal study of 473 Orthopedic Surgery patients, physicians rated the benefit of the test on decision making and patient care a 4.10/5





Clinical Utility Correlation with Outcomes In a study of 1,781 patients across 76 research sites, physicians who used the test rated it 0.71 points higher on a 5-point scale. Improvement within 60 days

NSAID Risk Genetic Profile



More than 100 million NSAIDs are prescribed each year

Over 100,000 individuals are hospitalized annually for NSAID-related serious complications: >2 billion dollars of healthcare costs

16,500 NSAID-related deaths occur each year



NSAID Risk

Intended Use: Avoid ADEs associated with NSAID use



Bleeding / Ulcer



This patient is predicted to be at elevated risk of developing an NSAID-induced ulcer disease and gastro-intestinal bleeding due to COX-1 and NSAID metabolizing enzyme polymorphisms. Consider treatment to reduce risk of gastric ulcers, such as Proton Pump Inhibitors (PPIs) or Histamine H2-receptor antagonists. Evaluating CYP2C19 and CYP2D6 genetics, respectively, for these treatments with the Proove Drug Metabolism profile can help to make the appropriate selection.

Cardiovascular



This patient has a COX-1 genetic variant that is predicted to be ineffectively regulated with aspirin treatment. If taking aspirin, this patient is at increased risk of experiencing an adverse cardiovascular event due to aspirin resistance. Consider alternatives to aspirin for heart disease and stroke prevention. In general, this patient carries a COMT genotype that confers a higher risk of Coronary Artery Disease and cardiovascular disease (CVD). However, treatment with aspirin and Vitamin E has been shown to prevent incident CVD in patients with this genotype.

Aspirin Resistance



This patient is predicted to be at increased risk of aspirin resistance. Consider an alternative to aspirin for prevention of heart disease and stroke. Aspirin inhibits platelet activation and aggregation via multifactoral mechanisms - including those determined by heritable factors, such as variants in multi-drug resistance efflux pumps and COX1 genes. Aspirin resistance refers to an absence of an expected pharmacological effect and/or poor clinical outcomes, such as recurrent vascular events.

H.Pylori Gastropathies

This patient is not predicted to be at increased risk of developing gastropathies with concomitant NSAID use.



No Predicted Risk



Predicted Risk

Some Predicted Risk



Some Predicted Risk

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Thromb	oembolism
Risk	Q2

Intended Use: Proactive diligence with venous thromboembolism



Report Date May 9, 2016

Proof of Thromboembolism Risk

Proove Thromboembolism Risk Profile (PBIO25)

v.1

Patient Information Patient Name Date of Birth Ethnicity Gender

0k

No Predicted Risk

Jane Doe

Caucasian

Female

Date of Service May 9, 2016 Date Received by Laboratory January 28, 1976 November 24, 2014

Customer ID P-SW20022201 Account Name

Proove Research Institute Physician Name Payne, Doc

This patient does not have an increased genetic risk of experiencing venous thromboembolism events, such as deep vein thrombosis (DVT) and pulmonary embolism (PE). The patient is not a carrier of the Factor II (Prothrombin) or Factor V Leiden risk alleles.

Date of Injury

Invalid date

Genetic Variation Results

Gene	Results
Fartor I	rx179996.5: G/G
Faulor V	-56025: C/C
MTHER	rs1801133: G/A

References

1. Heit et al. A genome-wide association study of venous thromboembolism identifies risk variants in chromosomes 1 g74.2 and 9q.J Thromb Haemost, 7017 Aug; 10(8); 1571-31.

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3. Heit et al. Genetic veriation within the anticoaculant, procoaculant, fibringlytic and innate immunity pathways as risk factors 'or venous thromooembolism. J Thromb Haemost. 2011 Jun;9(6):1133-42.

4. Severinsen et al. Genetic susceptibility, smoking, onesity and risk of venous thromboembolism. Br J Haematol. 2010 Apr 149(2):273-9.

5. Juul et al. Factor V Leicen and the risk for venous thromboempolism in the acult Danish population. Ann Intern Med. 2001 Mar 2.140(5):330-7.

6. Zhang et al. Association between MTHER C677T polymorphism and venues thremboempolism risk in the Crimese population: a meta analysis of 24 case controlled studies. Ang ology, 2015 May;66(5):422-32.

6. Soh'll et al. The genetics of venous thromboembolism. A meta-analysis involving approximately 120,000 cases and 180,000 controls. Thromb Haemost, 2009 Aug; 102(2): 350-70.

8. Simone et al. Risk of venous thromboembol'sm associated with single and combined effects of Factor V Leiden, Prothromoin 20210A and Methylenetetrahydrofolate reductase C677T: a meta-analysis involving over 11,000 cases and 21,000 controls, Eur J Epidemiol, 2013 Aug; 28(8): 621-47.



Laboratory Director: S. Nguyen, M.D., F.C.A.P Proove Blosciences, Inc. - Proove Medical Laboratories, Inc. 26 Technology Drive East, Irvine, CA 92618 - Ph. (855) 775-6832 - Fax (888) 971-4219 - www.proove.com CA State Lab ID No: CLF 4478 CLIA No: 05D0580755

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Future Directions

Can genetic information predict/improve outcomes in Orthopedics?



Thank you!

SKantorovich@proove.com