Clinical Appropriateness Guidelines

Pharmacogenomic Testing and Genetic Testing for Thrombotic Disorders

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Table of Contents

Scope

Pharmacogenomic testing broadly describes how one's genome, or multiple genes, can influence drug response while more targeted pharmacogenetic testing describes genotyping a specific gene to predict response to certain medications. This document addresses pharmacogenomic testing for the purpose of informing medication selection, dosage, and risk of adverse side effects. It also addresses genetic testing to predict risk of thrombosis. This guideline does not address tumor testing performed to direct treatment decisions (see Clinical Appropriateness Guideline Molecular Testing of Solid and Hematologic Tumors and Malignancies). All tests listed in these guidelines may not require prior authorization; please refer to the health plan.

Appropriate Use Criteria

Pharmacogenomic Testing

Pharmacogenetic testing of common variants associated with drug metabolism is medically necessary when either of the following criteria is met:

- All of the following:
  - The individual is a candidate for a targeted drug therapy associated with a specific genotype
  - The results of the pharmacogenetic test will directly impact clinical decision-making and clinical outcome for the individual
  - Published, peer-reviewed studies have proven that identifying the specific genetic variant improves clinical outcomes
- Identification of the genetic variant is required or recommended in a specific population prior to initiating therapy with the target drug as noted by the U.S. Food and Drug Administration (FDA)-approved prescribing label

Multi-gene pharmacogenomic genotyping assays in which each included target does not meet the above criteria are not medically necessary.

Thrombophilia Testing

Testing for common variants in Factor V Leiden (F5) and prothrombin (F2) is medically necessary for any of the following indications:

- Pregnant woman who has a personal history of a venous thromboembolism (VTE)
- In an individual with an unprovoked VTE (e.g. not associated with fracture, surgery, prolonged immobilization, cancer) when test results will impact long term medication management and at least one of the following:
  - There is concern for homozygous F2 or F5 or compound heterozygous F2/F5

  - The annual risk of recurrent VTE is estimated to be between 5% and 10%
- Individual who has a first-degree relative with F5 or F2 thrombophilia and one of the following:
  - Surgery is planned
  - Patient is pregnant
  - Females considering estrogen contraception or hormone replacement therapy if results would influence decision to use estrogen

The following test, including but not limited to, is not medically necessary:

- MTHFR

CPT Codes

The following codes are associated with the guidelines in the document. This list is not all inclusive.

Covered when medical necessity criteria are met:

81225	CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *8, *17)
81226	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *5, *6, *9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN)
81240	F2 (prothrombin, coagulation factor II) (eg, hereditary hypercoagulability) gene analysis, 20210G>A variant
81241	F5 (coagulation factor V) (eg, hereditary hypercoagulability) gene analysis, Leiden variant
81306	NUDT15 (nudix hydrolase 15) (eg, drug metabolism) gene analysis, common variant(s) (eg, *2, *3, *4, *5, *6)
81335	TPMT (thiopurine S-methyltransferase) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3)
81381	HLA Class I typing, high resolution (ie, alleles or allele groups); one allele or allele group (eg, B*57:01P), each
81404	UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg, hereditary unconjugated hyperbilirubinemia [Crigler-Najjar syndrome]) full gene sequence

0034U	TPMT (thiopurine S-methyltransferase), NUDT15 (nudix hydroxylase 15) (eg, thiopurine metabolism), gene analysis, common variants (ie, TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5)
0070U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, common and select rare variants (ie, *2, *3, *4, *4N, *5, *6, *7, *8, *9, *10, *11, *12, *13, *14A, *14B, *15, *17, *29, *35, *36, *41, *57, *61, *63, *68, *83, *xN)

Codes that do not meet medical necessity criteria:

81227	CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9) (eg, drug metabolism), gene analysis, common variants (e.g, *2, *3, *5, *6)
81230	CYP3A4 (cytochrome P450 family 3 subfamily A member 4) (eg, drug metabolism), gene analysis, common variant(s) (eg, *2, *22)
81231	CYP3A5 (cytochrome P450 family 3 subfamily A member 5) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *5, *6, *7)
81291	MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis, common variants (eg, 677T, 1298C)
81328	SLCO1B1 (solute carrier organic anion transporter family, member 1B1) (eg, adverse drug reaction), gene analysis, common variant(s) (eg, *5)
81346	TYMS (thymidylate synthetase) (eg, 5-fluorouracil/5-FU drug metabolism), gene analysis, common variant(s) (eg, tandem repeat variant)
81350	UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg, drug metabolism, hereditary unconjugated hyperbilirubinemia [Gilbert syndrome]) gene analysis, common variants (eg, *28, *36, *37)
81355	VKORC1 (vitamin K epoxide reductase complex, subunit 1) (eg, warfarin metabolism), gene analysis, common variant(s) (eg, -1639G>A, c.173+1000C>T)
0029U	Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis (ie, CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 and rs12777823)
0030U	Drug metabolism (warfarin drug response), targeted sequence analysis (ie, CYP2C9, CYP4F2, VKORC1, rs12777823)
0031U	CYP1A2 (cytochrome P450 family 1, subfamily A, member 2) (eg, drug metabolism) gene analysis, common variants (ie, *1F, *1K, *6, *7)
0032U	COMT (catechol-O-methyltransferase) (drug metabolism) gene analysis, c.472G>A (rs4680) variant

0033U	HTR2A (5-hydroxytryptamine receptor 2A), HTR2C (5-hydroxytryptamine receptor 2C) (eg, citalopram metabolism) gene analysis, common variants (ie, HTR2A rs7997012 [c.614-2211T>C], HTR2C rs3813929 [c.- 759C>T] and rs1414334 [c.551-3008C>G])
0071U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, full gene sequence (List separately in addition to code for primary procedure) (Use 0071U in conjunction with 0070U)
0072U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D6-2D7 hybrid gene) (List separately in addition to code for primary procedure) (Use 0072U in conjunction with 0070U)
0073U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D7-2D6 hybrid gene) (List separately in addition to code for primary procedure) (Use 0073U in conjunction with 0070U)
0074U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, non-duplicated gene when duplication/multiplication is trans) (List separately in addition to code for primary procedure) (Use 0074U in conjunction with 0070U)
0075U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 5’ gene duplication/multiplication) (List separately in addition to code for primary procedure) (Use 0075U in conjunction with 0070U)
0076U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 3’ gene duplication/ multiplication) (List separately in addition to code for primary procedure) (Use 0076U in conjunction with 0070U)
0078U	Pain management (opioid-use disorder) genotyping panel, 16 common variants (ie, ABCB1, COMT, DAT1, DBH, DOR, DRD1, DRD2, DRD4, GABA, GAL, HTR2A, HTTLPR, MTHFR, MUOR, OPRK1, OPRM1), buccal swab or other germline tissue sample, algorithm reported as positive or negative risk of opioid-use disorder

Background

Pharmacogenomic Testing

Pharmacogenomic testing is utilized as a tool in the field of precision medicine. Precision medicine can guide optimal health care decisions by identifying individual variability to direct approaches for prevention, diagnosis, and treatment of disease (Collins and Varums 2015). As this approach to clinical practice has grown, so has the availability of pharmacogenomic testing in the clinical realm.

The CYP450 gene superfamily is composed of many isoenzymes that are involved in the metabolism of about 75% of commonly prescribed drugs. Many of the clinically available pharmacogenomic tests include genes related to the CYP450 superfamily. CYP2C19, CYP2D6 and CYP2C9 enzymes metabolize approximately 15%, 20-25%, and 10% of all currently used drugs, respectively, that are most often prescribed as treatments for oncologic, psychiatric, neurologic, or cardiovascular conditions (Drozda et al. 2014). These genes are highly polymorphic, and certain genotypes have been classified by their effect on metabolism (poor, intermediate, normal or ultrarapid) of specific drugs. While the speed of metabolism can affect optimal dosing strategy for a drug, it is also important to note that genetic variability accounts for only a portion of the individual differences in drug response, and there are many other variables in the pharmacokinetics and pharmacodynamics of medications (Solomon, Cates and Li 2019; Pasternak et al. 2017).

Single Gene Pharmacogenetic Assays

There are many challenges in gathering sufficient evidence to support the clinical utility of pharmacogenetic testing, including the complex interactions between different genetic variants and the large number of confounding factors in medication response across individuals. In addition, there is a high degree of variability in study design, methods, and measured outcomes in the published literature, making comparisons difficult (Fabbri et al. 2018; Zeier et al. 2018; Jarvis et al. 2019). Other limitations of published studies include conflicts of interest among the researchers and lack of blinding for participants and providers (Zeier et al. 2018; Bousman and Dunlop 2018). While genotype-guided drug choice or dosing has been shown to increase efficacy and limit side effects for certain medications, the clinical utility of most pharmacogenetic testing has not yet been established.

As a result, the US Food and Drug Administration (FDA) includes pharmacogenetic testing recommendations with the labeling of many drugs, but the overall number that have genetic testing requirements on the FDA label is relatively small. Many drug/gene pairs for which testing is mentioned on the FDA label are based on evidence from laboratory studies, case reports, or observational studies rather than randomized controlled trials or large subgroup analyses (Chin et al. 2017). Additional recommendations or guidelines are often needed to help clinicians assess the clinical utility of pharmacogenetic testing. In many cases, there is limited evidence that pharmacogenetic testing results in better clinical outcomes (Dong et al. 2018; Nurnberger et al. 2018). In addition, there is significant variability in the specific alleles that are evaluated by different clinical tests. This complicates result interpretation, especially in ethnically diverse populations. It is important to interpret results of pharmacogenetic testing with these limitations in mind (Pratt et al. 2018; Pratt et al. 2019).

The Clinical Pharmacogenetics Implementation Consortium (CPIC) have established guidelines to assist clinicians in guiding drug therapy and dosage based on existing pharmacogenetic results. CPIC guidelines are developed in a standard format after rigorous review and grading of the literature and extensive peer review. They are meant to provide guidance for the use of existing genetic test results, but do not provide recommendations about whether to order specific genetic tests (Caudle et al. 2014).

Multi-Gene Pharmacogenomic Assays

While targeted gene testing for variants in some genes has been proposed to predict patient-specific drug metabolism of specific drugs, there still exists a lack of robust evidence to support the clinical utility of panel testing for multiple genes. There are a number of clinically available combined pharmacogenomic panel tests designed to evaluate variants within multiple genes to provide guidance for prescribing and dosing various medications which may ultimately aid in addressing the recognized

need to alleviate prolonging or complicating the clinical course of a patient's condition due to side effects or lack of response from a trial-and-error approach to medication choice. These panel tests are even marketed as "decision support tools" (Bousman and Dunlop 2018). While pharmacogenomic tests are a promising candidate to address this need, as evidenced by many retrospective reviews, there is a lack of large and adequately powered randomized controlled studies that address whether the use of pharmacogenomic panels in prescribing medications improves outcomes in various conditions (Drozda et al. 2014; Zeier et al. 2018; Lin and Chun 2019). Another hurdle, as evidenced by the systematic review of available studies by Fabbri et al. (2019), is the lack of best practice guidelines for developing clinical evidence. This deficit ultimately impacts the quality of available studies.

Evidence to support pharmacogenomic-guided antidepressant treatment is generally low strength because randomized controlled trials are few and underpowered, and variability in study designs make direct comparisons difficult (Perterson et al. 2017; Rosenblat and McIntyre 2017; Solomon, Cates and Li 2018). While published results from a recent large patient-blinded randomized controlled trial, the Genomics Used to Improve DEpression Decisions (GUIDED) trial, revealed that patients reached secondary outcomes of improvements in response (26.0% versus 19.9%, p=0.036) and remission (15.3% versus 10.1%, p=0.007) rates compared to patients with treatment as usual; the study failed to meet the primary outcome of statistically significant symptom improvement (27.2% versus 24.4%, p=0.107) in patients with treatment guided by pharmacogenomic testing (Greden et al. 2019). This study adds more data to the literature purporting a promising future for pharmacogenomic-directed treatment, but it also underscores the need for additional evidence to support it beyond paired cytochrome gene testing. In addition, it highlights the conundrum of available market-place genetic tests' rate of evolution outpacing evidence of clinical utility in the newest iteration, i.e. the current pharmacogenomic panel available on the market is larger than the panel studied in the GUIDED trial.

The majority of professional society guidelines related to pharmacogenomic testing address specific drug-gene interactions rather than multi-gene panels (Beckett et al. 2018). Although individual biomarkers may have clinical utility in certain circumstances, clinicians will often choose larger panels due to the increasing availability in the market (Moyer et al. 2017), without sufficient evidence that panel testing of multiple genes has any benefit over single-gene testing or standard trial-and-error methods (Zeier et al. 2018).

Among clinically available pharmacogenomic panel tests, interpretation of results and final medication recommendations vary substantially and even contradict each other, highlighting the need for standardized guidelines before panel-based pharmacogenomic testing becomes a routine part of clinical practice (Bousman and Dunlop 2018; Bousman et al. 2018). In 2018, the FDA issued a consumer warning against the use of many pharmacogenetic tests, indicating that there is limited scientific and clinical evidence to support the claims of clinical utility that are advertised by these laboratories (FDA 2018).

Thrombophilia Testing

Thrombophilia describes a state of hypercoagulability that leads to an increased risk of thrombotic events. Venous thromboembolism (VTE) is a common, complex disease associated with both environmental and genetic risk factors. Risk factors for VTE include advancing age, travel, surgery, organ transplantation, central venous catheter use, injury, family history of VTE, and certain genetic polymorphisms leading to excessive clotting. In women, pregnancy, hormonal contraceptive use, selective estrogen receptor modulators (SERMs), and hormone replacement therapy (HRT) are additional risk factors for VTE (Montagnana et al. 2017; Pruthi 2017).

It has been suggested that genetic testing for inherited thrombophilias may allow for prophylactic treatment of individuals at risk for VTE or enhance the prediction of recurrence risk for patients who have already had a VTE. However, the clinical utility of such genetic testing is controversial. An increased risk for VTE has been associated with pathogenic or likely pathogenic (P/LP) variants in several genes including; F5, F2, PROC, PROS1 and SERPINC1 as well as others.

While standard of care for work up of VTE or DVT is to perform protein activity and antigen studies, Factor V and Prothrombin studies are easiest to perform as molecular genotyping given that these conditions are almost always caused by a common variant. There have been conflicting recommendations as to how to approach genetic testing for thrombophilias. ACMG and ACOG have recommended testing for F2 and F5 in certain scenarios, while the Evaluation of Genomic Applications and Prevention Working Group (EGAPP) found insufficient evidence to perform this testing for any indication. The presence of an inherited thrombophilia variant itself does not always require prophylactic treatment with anticoagulants, and other risk factors should be considered when assessing a patient's individual risk of VTE and the need for anticoagulation therapy (ACOG 2018; Carroll and Piazza 2018; Ashraf et al. 2019). The population for which F2/F5 genetic testing results have direct implications for treatment is pregnant women with a previous history of VTE associated with a transient risk factor (e.g., surgery, trauma). These women would typically not be treated with antepartum anticoagulant prophylaxis unless they were found to have a genotype associated with a high risk of VTE recurrence (FVL homozygosity, F2 G20210A homozygosity, or compound heterozygosity for FVL and F2 G20210A). Genetic testing for these patients is indicated. There may also be a benefit to screening pregnant women with a family history of known thrombophilia, as those women found to have a high risk genotype would be offered antenatal prophylactic anticoagulant therapy even in the absence of a personal history of VTE.

Because standard of care for evaluation of thrombophilias includes protein assays for common anticoagulants and single-site P/LP variant studies, large NGS panels are not considered medically necessary. Genetic panel testing for thrombophilia also frequently includes additional genes with limited evidence of association and unclear management implications, such as PAI-1 and MTHFR (Carroll and Piazza 2018; Franchini et al. 2016).

Factor V Leiden

The Factor V Leiden (FVL) variant (1691G>A; R506Q) in the F5 gene is the most common known inherited risk factor for thrombosis. This P/LP variant leads to reduced inactivation of clotting factor V by activated protein C (ie. APC resistance), which causes increased thrombin generation. Heterozygous carriers of the FVL variant have an approximately 3-fold to 8-fold increased risk of VTE compared to non-carriers (Kujovich 2018). However, the absolute risk of VTE in heterozygotes remains low, with only ~5% of carriers developing a VTE by age 65 (Rodeghiero and Tosetto 1999; Heit et al. 2005). Homozygous carriers of the FVL variant have a much higher increased risk of VTE, approximately 9-fold to 80-fold (Rosendaal 2009, EGAPP 2011; Carroll and Piazza 2018). This increased risk corresponds to an absolute incidence of 15 VTE events/1,000 persons/year (Juul et al. 2004).

The prevalence of FVL P/LP variants varies according to population. Approximately 3-8% of the general US and European population carry a heterozygous FVL P/LP variant, while it is rarely identified in individuals from Asian and African populations (Kujovich 2018). Homozygosity of the FVL P/LP variants is seen in approximately 1/5,000 individuals in the general US and European population (Kujovich 2018).

Prothrombin (F2)

The second most common inherited risk factor for VTE is the 20210G>A (G20210A) variant in the F2 gene. This activating P/LP variant leads to higher circulating levels of prothrombin, which results in an increased risk for clot formation. Heterozygous carriers of the F2 variant have a 2-fold to 4-fold increased risk of VTE compared to non-carriers (Rosendaal and Reitsma 2009; Kujovich 2014). However, the absolute risk of a VTE in heterozygotes again remains quite low: 0.19%/year to 0.41%/year in asymptomatic carriers (Lijfering et al. 2009; Kujovich 2014).

The prevalence of F2 heterozygosity varies by population. Approximately 2-3% of the general US and European population are carriers of the F2 variant, while individuals from African and Asian populations have a much lower prevalence (Kujovich 2014). F2 homozygotes are very rare, approximately 1/10,000 in the general US and European population, and the increased risk associated with this genotype is not well-defined, but may be up to 7 times higher than that of the general population (Kujovich 2014; Carroll and Piazza 2018). Patients with compound heterozygosity for Factor V Leiden and prothrombin mutations may have up to a 20-fold increased risk for VTE. Neither of these mutations exhibit a strongly increased risk for VTE recurrence (Carroll and Piazza 2018).

Professional Society Guidelines

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Thrombophilias

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Revision History

Medical Advisory Board Review:

v1.2020 11/04/2019: Reviewed

v2.2019 05/23/2019: No Criteria Changes

v1.2019 11/07/2018: Reviewed

v1.2018 03/31/2018: Reviewed

Clinical Steering Committee Review:

v1.2020 10/11/2019: Approved

v2.2019 04/03/2019: Approved

v1.2019 10/03/2018: Approved

v1.2018 02/28/2018: Approved

v1.2017 01/25/2017: Approved

Revisions:

Version	Date	Editor	Description
v1.2020	09/11/2019	Carrie Langbo, MS, CGC	Semi-annual review. Criteria was expanded to allow thrombophilia testing in pregnant women with a history of any type of VTE. Revised terminology for pharmacogenomic and pharmacogenetic testing. Updated professional society guidelines, background and references.
v2.2019	04/03/2019	Ann Schmidt, MS, CGC	Semi-annual review. No criteria changes. Updated professional society guidelines and references.
v1.2019	10/03/2018	Kate Charyk, MS, CGC	Semi-annual review. Professional society guidelines and references updated. Renumbered to 2019. Reformatted CPT code list. PMID added.
v1.2018	03/31/2018	Heather Dorsey, MS, CGC	Semi-annual review. Expanded F2/F5 criteria to allow additional management changes for unprovoked VTE and estrogen changes with significant family history. Disclaimer sentence added to scope. Professional society guidelines and references updated. Renumbered to 2018.
v1.2017	11/1/2017	Gwen Fraley, MS, CGC	Quarterly review. No criteria changes. Updated references.

v1.2017	09/15/2017	Megan Czarniecki, MS, CGC	Formatted references to NLM style. Moved methodological considerations to appropriate use criteria and background. Updated associated CPT codes. Approved by Policy Lead.
v1.2017	07/03/2017	Heather Dorsey, MS, CGC	Quarterly review. No criteria changes. Updated references.
v1.2017	04/18/2017	Megan Czarniecki, MS, CGC	Quarterly review. No criteria changes. Updated references.
v1.2017	01/23/2017	Cheryl Thomas, MS, CGC	Quarterly review. No criteria changes. Updated references. Renumbered for 2017.
v1.2016	10/05/2016	Gwen Fraley, MS, CGC	Combined Thrombophilias and Pharmacogenetic testing into same guidelines. Updated references.
v1.2015	10/08/2015	Marie Schuetzle, MS, CGC	Original version

Original Effective Date: 10/08/2015

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