Genetic Testing for Tamoxifen Treatment

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Current Effective Date: 09/20/2017

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Based on review of available data, the Company considers genotyping to determine cytochrome p450 2D6 (CYP2D6) variants for the purpose of managing treatment with tamoxifen for women at high risk for or with breast cancer to be investigational.*

Background/Overview

TAMOXIFEN METABOLISM
Tamoxifen undergoes extensive primary and secondary metabolism, and plasma concentrations of tamoxifen and its metabolites vary widely. The metabolite 4-hydroxytamoxifen (4-OH tamoxifen) has demonstrated a 100-fold greater affinity for the estrogen receptor and 30- to 100-fold greater potency in suppressing estrogen-dependent cell proliferation in vitro compared with the parent drug (summarized in Goetz et al [2008]). Another metabolite, 4-hydroxy-N-desmethyl tamoxifen (endoxifen), has properties and potency identical to 4-OH tamoxifen. Because 4-OH tamoxifen represents less than 20% of the product of tamoxifen primary metabolism and because steady-state plasma endoxifen concentrations are on average 5- to 10-fold higher than 4-OH tamoxifen plasma levels, it has been assumed that endoxifen is the major active metabolite of tamoxifen.

The metabolism of tamoxifen into 4-OH tamoxifen is catalyzed by multiple enzymes. However, endoxifen is formed predominantly by CYP2D6. Plasma concentrations of endoxifen exhibit high interindividual variability, as described in breast cancer patients. Because CYP2D6 enzyme activity is known to vary across individuals, variants in the CYP2D6 gene are of great interest for understanding tamoxifen metabolism variability and variation in levels of circulating active metabolites. Moreover, known variability in endoxifen levels has been hypothesized to result in variable response to tamoxifen treatment.

Alternatively and more recently, it has been estimated that, at doses used for adjuvant treatment, which are intended to saturate the estrogen receptor, more than 99% of estrogen receptors are bound by low-affinity tamoxifen and both low- and high-affinity metabolites. Lash et al (2009) modeled the effect of CYP2D6-variant alleles on estrogen receptor binding by tamoxifen and metabolites, and found a negligible effect. As they noted, however, modeling cannot account for many metabolic complexities, and mechanistic data would be needed to show how a decrease in high-affinity metabolites associated with CYP2D6 variants reduces the protection against recurrence conferred by tamoxifen therapy.

Metabolic Enzyme Genotypes
The CYP2D6 gene exhibits a high degree of polymorphism, with more than 75 allelic variants identified. Although the most prevalent CYP2D6*/1 and *2 alleles (both termed “wild-type” for this evidence review)
produce an enzyme with normal activity, there are several variant alleles that result in enzymes with no activity or reduced activity. Because individuals have two CYP2D6 alleles, various combinations of the possible alleles result in a spectrum of CYP2D6 function; they have been categorized as extensive metabolizers (EMs ["normal"]), intermediate metabolizers (IMs), and poor metabolizers (PMs). An additional, rare category of ultrarapid metabolizers is defined by possession of 3 or more functional alleles due to gene duplication.

The prevalence of CYP2D6 PMs is approximately 7% to 10% in whites of Northern European descent, 1.9% to 7.3% in blacks, and 1% or less in most Asian populations studied. The PM phenotype in whites is largely accounted for by CYP2D6*3 and *4 nonfunctional variants, and in black and Asian populations, by the *5 nonfunctional variant. Some PMs may have 1 nonfunctional allele and 1 reduced-function allele. Among reduced function variants, CYP2D6*17, *10, and *8 are the most important in blacks, Asians, and whites, respectively. Few studies have investigated the frequency of CYP2D6-variant alleles or PMs in the Hispanic population.

Other enzymes metabolize tamoxifen into the active metabolite, 4-OH tamoxifen. Polymorphisms in the genes for these enzymes could have an effect on overall tamoxifen efficacy. Research on the effect of variant alleles for these enzymes is in earlier stages.

**Endocrine Therapy Regimens**

Tamoxifen has several labelled indications:

- chemoprevention of invasive breast cancer in high-risk women without current disease or with ductal carcinoma in situ;
- adjuvant treatment of primary breast cancer; and
- treatment of metastatic disease.

In women with breast cancer, endocrine receptor–positive disease predicts a likely benefit from tamoxifen treatment.

Tamoxifen is currently the most commonly prescribed adjuvant treatment to prevent recurrence of the endocrine receptor–positive breast cancer in pre- or perimenopausal women. The pharmacogenomic evaluation could direct consideration of ovarian ablation or suppression in those found to be CYP2D6 PMs. In pre- or perimenopausal women with hormone receptor–positive tumors, ovarian ablation is more effective treatment than no adjuvant therapy, but may be accompanied by acute and chronic adverse effects (eg, hot flushes, sweats, sleep disturbance). Similarly, functional ovarian suppression with gonadotropin-releasing factor analogues in pre- or perimenopausal women with hormone receptor–positive tumors confers benefits comparable with chemotherapy. National Comprehensive Cancer Network (NCCN) guidelines indicate that ovarian ablation or suppression are options in combination with endocrine therapy for premenopausal women who have invasive or recurrent disease and are recommended for premenopausal women with systemic disease.
For postmenopausal women with osteoporosis or at high-risk for invasive breast cancer, raloxifene is an alternative treatment for invasive cancer risk reduction. Efficacy equals that of tamoxifen, and risk of endometrial hyperplasia is markedly reduced. Currently, raloxifene is not indicated for treatment of invasive breast cancer; reduction of breast cancer recurrence risk; or noninvasive breast cancer risk reduction.

The pharmacogenomics of tamoxifen have been most often studied in postmenopausal women who have endocrine receptor–positive tumors and require endocrine therapy to prevent recurrence. For this population, the NCCNs 2017 guidelines for the management of breast cancer includes a number of statements related to the use of adjuvant tamoxifen (among other endocrine therapies), which are summarized in Table 1.

### Table 1. 2017 NCCN Guidelines for Adjuvant Endocrine Therapy for Postmenopausal Women With Breast Cancer

<table>
<thead>
<tr>
<th>Recommendation</th>
<th>COR</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Premenopausal at Diagnosis</strong></td>
<td></td>
</tr>
<tr>
<td>Tamoxifen for 5 years (with or without ovarian suppression), followed by AI for 5 years if postmenopausal</td>
<td>1</td>
</tr>
<tr>
<td>Tamoxifen for 5 years	extsuperscript{a} (with or without ovarian suppression)	extsuperscript{b} followed by consideration for tamoxifen for 5 years	extsuperscript{c} if postmenopausal</td>
<td>2A</td>
</tr>
<tr>
<td>Tamoxifen for 5 years	extsuperscript{a} (with or without ovarian suppression)	extsuperscript{b} followed by consideration for tamoxifen for 5 y OR no further therapy if still premenopausal</td>
<td>2A</td>
</tr>
<tr>
<td><strong>Postmenopausal at diagnosis</strong></td>
<td></td>
</tr>
<tr>
<td>AI for 2-3 years followed by tamoxifen for a total of 5 years of endocrine therapy</td>
<td>1</td>
</tr>
<tr>
<td>Tamoxifen for 2-3 years followed by AI for a total of 5 years of endocrine therapy</td>
<td>1</td>
</tr>
<tr>
<td>Tamoxifen for 2-3 years followed by up to 5 years of an AI	extsuperscript{c}</td>
<td>2A overall</td>
</tr>
<tr>
<td>Tamoxifen for 2-3 years followed by 1 of 3 AIs to complete 5 years of endocrine therapy</td>
<td>2B</td>
</tr>
<tr>
<td>Tamoxifen for 4.5-6 years followed by AI for 5 years</td>
<td>1</td>
</tr>
<tr>
<td>Tamoxifen for 4.5-6 years followed by consideration for tamoxifen for 5 more years</td>
<td>2A</td>
</tr>
<tr>
<td>In women with a contraindication to AIs, or who decline or are intolerant of AIs, consideration for tamoxifen for 5 years of tamoxifen for up to 10 years</td>
<td>1</td>
</tr>
</tbody>
</table>

AI: aromatase inhibitor; COR: category of recommendation.

\textsuperscript{a} COR 1.
\textsuperscript{b} COR 2A.
\textsuperscript{c} COR 2B.

### PHARMACOLOGIC INHIBITORS OF METABOLIC ENZYMES

CYP\textsubscript{2D6} activity may be affected not only by genotype but also by coadministered drugs that block or induce CYP\textsubscript{2D6} function. Studies of selective serotonin reuptake inhibitors in particular have shown that fluoxetine and paroxetine, but not sertraline, fluvoxamine, or venlafaxine, are potent CYP\textsubscript{2D6} inhibitors. Some individuals treated with fluoxetine or paroxetine changed from extensive metabolizer phenotype to PM. The degree of inhibition may depend on selective serotonin reuptake inhibitors dose.
Thus, CYP2D6 inhibitor use must be considered in assigning CYP2D6 functional status, and potent CYP2D6 inhibitors may need to be avoided when tamoxifen is administered.

**FDA or Other Governmental Regulatory Approval**

U.S. Food and Drug Administration (FDA)
The AmpliChip CYP450 Test (Model 04381866190; Roche) was cleared for marketing by the U.S. FDA through the 510(k) process (K042259) and can be used to identify CYP2D6 genotype.

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments. CYP2D6 genotyping assays are also available under the auspices of Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by Clinical Laboratory Improvement Amendments for high-complexity testing. To date, the U.S. FDA has chosen not to require any regulatory review of this test

Centers for Medicare and Medicaid Services (CMS)
There is no national coverage determination. In the absence of a national coverage determination, coverage decisions are left to the discretion of local Medicare carriers.

**Rationale/Source**

Validation of the clinical use of any genetic test focuses on 3 main principles: (1) analytic validity, which refers to the technical accuracy of a test in detecting a variant that is present or in excluding a variant that is absent; (2) clinical validity, which refers to the diagnostic performance of a test (sensitivity, specificity, positive and negative predictive values) in detecting clinical disease; and (3) clinical utility (ie, how the results of a diagnostic test will be used to change management of the patient and whether these changes in management lead to clinically important improvements in health outcomes). The following is a summary of the key literature.

**CYP2D6 GENOTYPING FOR TAMOXIFEN TREATMENT**

**Clinical Context and Test Purpose**
The purpose of testing for CYP2D6 genotype is to tailor drug selection based on a patient’s gene composition for drug metabolism. In theory, this should lead to early selection and optimal dosing of the most effective drugs (eg, aromatase inhibitor) or strategy (eg, ovarian ablation in premenopausal women), while minimizing treatment failures or toxicities.

The questions addressed in this evidence review are: (1) Is there evidence that testing for CYP2D6 genotype has clinical validity?; and (2) Does CYP2D6 genotyping change patient management in a way that potentially improves outcomes as a result of testing?

The following PICOTS were used to select literature to inform this review.
Patients
The relevant population of interest is patients receiving or being considered for tamoxifen therapy:
- Treatment of breast cancer in the adjuvant setting to prevent recurrence (alone or preceding aromatase inhibitor therapy) or for metastatic disease.
- Prevention of breast cancer in high-risk women or women with ductal carcinoma in situ; and absence of contraindications to aromatase inhibitors (for treatment) or raloxifene (for disease prevention).

Interventions
Table 2. Commercially Available Genetic Tests for CYP2D6

<table>
<thead>
<tr>
<th>Manufacturer</th>
<th>Test Name</th>
<th>Total No. of Genes Tested</th>
</tr>
</thead>
<tbody>
<tr>
<td>OneOme</td>
<td>OneOme RightMed</td>
<td>22 (including CYP2D6)</td>
</tr>
<tr>
<td>Roche</td>
<td>AmpliChip</td>
<td>2 (including CYP2D6)</td>
</tr>
</tbody>
</table>

Comparators
The comparator of interest is standard clinical management without genetic testing.

Outcomes
The general outcomes of interest are overall survival (OS), disease-specific survival, test accuracy, test validity, medication use and treatment-related morbidity. Specific outcomes are listed in Table 3.

Table 3. Outcomes of Interest for Individuals With or at High Risk for Breast Cancer

<table>
<thead>
<tr>
<th>Outcomes</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medication use</td>
<td>Change to alternative treatment (aromatase inhibitor or ovarian ablation in premenopausal women)</td>
</tr>
<tr>
<td>Treatment-related morbidity</td>
<td>Reduction in adverse events</td>
</tr>
</tbody>
</table>

The potential beneficial outcomes of primary interest would be reduction in rate of recurrence and improvement in disease-free survival or OS.

The potential harmful outcomes are those resulting from a false test result. False-positive or false-negative test results can lead to the initiation of unnecessary treatment and adverse effects from that treatment or undertreatment.

Timing
Genetic testing may be used for treatment selection before initiating or during therapy.

Setting
Patients requiring treatment for prevention or treatment for breast cancer are managed by an oncologist and are likely to be tested in an outpatient setting. Referral for genetic counseling is important for the explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.
Analytic Validity
The Roche AmpliChip CYP450 Test for detecting variants in CYP2D6 has been fully validated for analytic validity; a summary of results submitted for clearance to the U.S. FDA is provided in the agency’s decision summary.

Although comparable information on the analytic validity of laboratory-developed tests usually is not available, in an experienced laboratory and with validation of in-house results compared with either sequencing or AmpliChip, accurate and reliable performance should be achievable, as demonstrated by Heller et al (2006).

Section Summary: Analytic Validity
Evidence for the analytic validity of AmpliChip CYP450 Test is provided in the FDA’s decision summary. Comparable information on the analytic validity of laboratory-developed tests usually is not available.

Clinical Validity
Four studies have evaluated the CYP2D6 genotype as a prognostic marker in patients not treated with tamoxifen to ensure that a prognostic association would not confound the effect of genotype on tamoxifen outcomes. Although there were limitations in study quality or reporting, none of the studies found that outcomes varied by CYP2D6 genotype in untreated patients.

Indirect Association Between Genotype and Clinical Outcomes
Sixteen prospective cohort studies of adjuvant tamoxifen treatment have provided consistent evidence that CYP2D6 nonfunctional variant alleles are associated with significantly reduced plasma endoxifen levels. However, endoxifen levels overlap across all genotypes, suggesting that CYP2D6 genetic variability does not explain all variation in endoxifen levels; in a 2013 study of 224 Asian women, 10% of the variance in endoxifen levels was explained by CYP2D6 genotype. Seven of 8 studies reported significant associations between low CYP2D6 function and reduced plasma 4-OH tamoxifen levels. Coadministration of potent CYP2D6 inhibitors to CYP2D6 homozygous wild-type patients EMs was associated with endoxifen levels near those of patients who are PMs, suggesting that use of CYP2D6 inhibitors should be taken into account when assigning metabolizer status in clinical studies.

Three studies have reported on the relation between CYP2D6 genotype and active tamoxifen metabolites and between genotype and clinical outcomes in the same patient population. Two studies enrolled breast cancer patients from Asian populations, focusing almost exclusively on the reduced (but not absent) function CYP2D6*10 variants. Both studies reported reduced endoxifen and/or 4-OH tamoxifen concentrations in conjunction with 1 or 2 variant alleles and also reported decreasing disease-free survival (DFS) or recurrence-free survival. Both studies were small and had design flaws likely resulting in selection bias. A third study assessing 306 premenopausal white patients reported that the association between serum endoxifen levels and distant relapse-free survival was inconclusive. In 2011, Madlensky et al reported on the association between tamoxifen metabolite levels and breast cancer outcomes in 1370 samples from the Women’s Healthy Eating and Living study. The Women’s Healthy Eating and Living enrolled 3088 women with early-stage breast cancer who were diagnosed from 1991 to early 2000 and had
received tamoxifen. Endoxifen and 4-OH tamoxifen levels were strongly associated with CYP2D6 phenotype but did not have a linear association with breast cancer outcomes. A threshold effect was identified with endoxifen, such that patients with endoxifen levels greater than 6 ng/mL had a 30% lower risk of additional breast cancer events (hazard ratio [HR], 0.70; 95% confidence interval [CI], 0.52 to 0.94). Notably, 24% of PM patients had endoxifen levels above this threshold.

Four prospective studies published in 2011, 2012, and 2014 assessed the impact of an increased tamoxifen dose for patients who were already taking tamoxifen. These patients were genotyped as IMs or PMs (and not administered CYP2D6 inhibitors). Tamoxifen metabolite levels were measured at baseline and after 2 to 4 months and compared with levels from those EM patients who had no tamoxifen dose change. In general, tamoxifen metabolite concentrations increased with increasing dose; IM patient levels reached those of EM patients, and PM patient levels remained somewhat lower. However, these results were not related to breast cancer outcomes. Moreover, metabolite levels were highly variable across individuals, and, in 1 study, low plasma endoxifen concentrations were found in all CYP2D6 genotypes. Thus, CYP2D6 may only account for part of the variability in endoxifen levels, suggesting that the influence of other gene variants on tamoxifen treatment outcomes has been reported.

**Direct Association Between Genotype and Clinical Outcomes**

An ideal study assessing a direct association between genotype and outcomes would compare tamoxifen-treated women with those not receiving tamoxifen, stratified by CYP2D6 genotype to assess whether PMs derive less benefit from tamoxifen than EMs. One group conducted such a study retrospectively, on archived samples from a randomized controlled trial of tamoxifen treatment. Paradoxically, in this trial, Wegman et al (2005) found that EMs treated with tamoxifen received no statistically significant clinical benefit compared with EMs not treated with tamoxifen and that carriers of a CYP2D6*4 nonfunctional variant allele obtained significant benefit from tamoxifen treatment. There were several limitations to this study.

A 2013 Technology Evaluation Center (TEC) Assessment identified 24 other studies evaluating the association between CYP2D6 genotype and clinical outcomes in women treated with tamoxifen.

- Nine small studies (N range, 21-282 patients) in Asian populations focused on the CYP2D6*10 reduced function allele, and 5 reported significant results for the association between CYP2D6 genotype and outcomes of tamoxifen treatment. However, some of these studies may have been influenced in unpredictable ways by different biases (eg, by selecting among survivors at a time distant from diagnosis and surgery to draw whole blood for CYP2D6 genotyping [survivor selection bias]). Two studies that reported no association might have had less potential for bias. One larger study (N=716) of Korean patients with breast cancer who received adjuvant tamoxifen therapy (most with adjuvant chemotherapy) found no significant CYP2D6 genotype–associated difference in recurrence-free survival, regardless of treatment or prognostic subgroup.

- Thirteen studies evaluated samples from primarily white patients administered tamoxifen for adjuvant treatment of invasive breast cancer and 1 study for metastatic breast cancer. Of the 5
largest studies, 4 reported no significant association for time to recurrence. Two of the negative studies were retrospective analyses of clinical trial samples, and a third was a case-control study nested in a population-based cancer registry. All 3 were designed to minimize the potential for bias; their size (N range, 588-991 patients) permitted comparison of homozygous nonfunctional \textit{CYP2D6} genotypes with fully functional wild-type genotypes (i.e., the most extreme comparison and most likely to reveal a true association). The largest of the 5 studies (N = 1345 patients) reported significant results; however, this study combined samples from different sources, some of which had already been analyzed for this hypothesis. Additionally, it is unclear from the report whether nearly half of the samples were obtained from patients who had survived and were available at a time distant from their diagnosis and surgery, a type of selection bias that can unpredictably affect results. The remaining 8 small studies reported a variety of significant and nonsignificant results; no pattern of bias, genotyping or group scheme, or accounting for \textit{CYP2D6} inhibitor use (among possibilities) explained the differences in results. The heterogeneity of results across all studies and clear results of no genotype–tamoxifen treatment outcome in 3 large studies with the least apparent potential for bias strongly would suggest a lack of support for clinical validity in postmenopausal patients treated with adjuvant tamoxifen for breast cancer.

- Two nested, matched, case-control studies examined patients originally enrolled in chemoprevention trials using tamoxifen. In neither the larger (591 cases, 1126 controls) nor the smaller study (47 cases, 135 controls) was \textit{CYP2D6} genotype associated with the risk of developing breast cancer. A 2013 matched case-control study from the Women’s Environment Cancer and Radiation Epidemiology study sample reported no association between \textit{CYP2D6} variants and risk for contralateral breast cancer in tamoxifen-treated women (139 cases, 338 controls). The Women’s Environment Cancer and Radiation Epidemiology participants (998 cases [women with contralateral breast cancer], 2112 controls [women without contralateral breast cancer]) were women from 4 U.S. cancer registries and 1 Danish registry who were diagnosed with localized invasive breast cancer before age 55.

Published literature on the association between \textit{CYP2D6} genotype and tamoxifen therapy effectiveness for treatment of nonmetastatic breast cancer has yielded inconsistent results. A 2012 review tried to identify factors that may have led to discrepant findings. The authors selected 6 factors to compare across 11 negative and 6 positive studies; they identified 3 factors that could account for contradictory results: tamoxifen combination therapy (defined as any additional therapy, including radiotherapy); genotyping comprehensiveness (how many and which alleles were tested); and \textit{CYP2D6} inhibitor coadministration. Studies that enrolled patients on tamoxifen monotherapy, genotyped \textit{CYP2D6} more comprehensively, and accounted for \textit{CYP2D6} inhibitor coadministration were more likely to have positive findings. To elucidate the impact of germline genotype misclassification in studies where deoxyribonucleic acid (DNA) was genotyped from tumor-infiltrated tissues, Ahern et al (2017) systematically reviewed 6 studies on the concordance between genotypes obtained from paired nonneoplastic and breast tumor-infiltrated tissues, all of which showed excellent \textit{CYP2D6} genotype agreement but found no clinically important association between \textit{CYP2D6} genotype and breast cancer survival in tamoxifen-treated women.
Other studies also have reported discrepant results. Two large studies (2013, 2014) from Scandinavia (total N=1365 patients) reported no association between \textit{CYP2D6} genotype and disease recurrence in tamoxifen-treated women with early breast cancer. In contrast, a 2013 German study of 94 women with advanced breast cancer reported significantly shorter progression-free survival and OS in patients without any fully functional \textit{CYP2D6} allele (IM/IM, IM/PM, PM/PM) compared with those who had at least 1 functional allele (EM/EM, EM/IM, EM/PM) (HR for disease progression or death, 2.19; 95% CI, 1.15 to 4.18; \textit{p}=0.017; HR for death from any cause, 2.79; 95% CI, 1.12 to 6.99; \textit{p}=0.028). Martins et al (2014) found no association between \textit{CYP2D6} genotype and DFS in 58 Brazilian women with locally invasive breast cancer, although the study was likely underpowered to detect a difference (only 1 patient was classified PM). Some authors have suggested that \textit{CYP2D6} genotyping may be clinically relevant in premenopausal women, but not for postmenopausal women, and others support its clinical relevance for postmenopausal women.

Several 2013 and 2014 meta-analyses have published inconsistent results. None included studies on the concomitant use of \textit{CYP2D6}-inhibiting drugs in their analyses. These analyses may be considered exploratory because of varying inclusion criteria, outcome definitions, and comparisons of interest across reviews. Relevant meta-analyses are discussed next.

In 2014 the International Tamoxifen Pharmacogenomics Consortium pooled retrospective data from 12 participating sites. Results from 1996 postmenopausal women with estrogen receptor–positive breast cancer who were prescribed tamoxifen 20 mg daily for 5 years (40% of the total sample) reported a significant association between \textit{CYP2D6} PM status and both reduced invasive DFS (HR for invasive disease or death, 1.25; 95% CI, 1.06 to 1.47; \textit{p}=0.009) and reduced breast cancer–free interval (HR for recurrence, 1.27; 95% CI, 1.01 to 1.61; \textit{p}=0.041), presumably compared with EMs (the comparison group was not explicitly defined). Statistical heterogeneity was nonsignificant (Cochran \textit{Q}, \textit{p}>0.05) for both outcomes. For analyses using less stringent inclusion criteria (eg, pre- and postmenopausal women combined), associations between \textit{CYP2D6} metabolizer status and survival outcomes were not statistically significant. A critique of this meta-analysis is that adjustments for multiple comparisons were not performed; the reported associations may not have been statistically significant adjustments for multiple comparisons had been reported. Additionally, the prespecified end point of OS was not reported in the published article.

Lum et al (2013) conducted a systematic review and meta-analysis to January 2012 and pooled results from 22 retrospective studies (total N=4936 patients). For the outcome of all-cause mortality, the relative risk (RR) for \textit{CYP2D6} PMs or IMs compared with EMs or ultrarapid metabolizers was not statistically significant (RR=1.11; 95% CI, 0.94 to 1.31; \textit{p}=0.237). Statistical heterogeneity was low (\textit{I}^2=20%). When outcomes were expanded to include progression-free survival (RR=1.27; 95% CI, 1.11 to 1.45; \textit{p}<0.001) and recurrence (RR=1.19; 95% CI, 1.07 to 1.33; \textit{p}=0.002), RRs were statistically significant, but statistical heterogeneity was moderate to substantial (\textit{I}^2=56% and 53%, respectively).

Zeng et al (2013) conducted a meta-analysis to February 2013 and pooled 20 retrospective studies (total N=11,701 patients). Among several comparisons (PM vs EM, IM vs EM, PM/IM vs EM, PM vs IM/EM), the association between \textit{CYP2D6} metabolizer status and both DFS and OS was statistically significant only for the comparison of any variant allele versus wild-type EM (HR for DFS=1.37; 95% CI, 1.12 to 1.69; \textit{p}=0.002;
HR for OS=1.24; 95% CI, 1.03 to 1.50; p=0.021). Statistical heterogeneity was substantial for the analysis of DFS ($I^2=67\%$) but minimal for OS ($I^2=0\%$). There was evidence of publication bias for the DFS outcome. Jung and Lim (2014) pooled results from 10 retrospective studies (total N=5183 patients) and found an increased risk of recurrence among carriers of $CYP2D6$ variant alleles compared with wild-type EMs (pooled HR=1.64; 95% CI, 1.07 to 2.79). However, this result is questionable because of the inclusion of 4 small studies (N range, 18-282 patients) with unstable risk estimates (HRs >3 with large CIs).

**Section Summary: Clinical Validity**

Multiple studies have evaluated the association between $CYP2D6$ genotype and the consequences of altered metabolism of tamoxifen on clinical outcomes. Results have been conflicting. However, most of the earlier studies were retrospective and evaluated small numbers of patients. In an attempt to settle this issue, investigators assessed archived samples from a large randomized controlled trial but results did not demonstrate the expected associations. Subsequent meta-analyses have also shown inconsistent results. The inconsistencies may be due to differences across studies in the types of additional therapies patients received, how many and which $CYP2D6$ alleles were tested, tissue type examined (tumor or germline DNA), and coadministration of $CYP2D6$ inhibitors.

**Clinical Utility**

**Direct Evidence**

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. The strongest direct evidence comes from randomized controlled trials.

No direct evidence of clinical utility was identified. Ruddy et al (2013) implemented a tamoxifen adjustment algorithm for 99 patients treated at a cancer treatment institute. Recommendations to modify tamoxifen therapy were made for 18 (18%) patients, all of whom had low endoxifen levels (<6 ng/mL), and 2 of whom also were identified as $CYP2D6$ PMs. Survival outcomes were not reported.

In a 2016 study, Hertz et al increased tamoxifen doses from 20 to 40 mg per day based on genotype. Endoxifen concentrations in IM patients were similar to those of EM patients, but endoxifen levels in PM patients were not. The dose escalation did not increase toxicity or reduce the quality of life, raising the possibility that more effective doses of tamoxifen might be given. A beneficial effect on survival with this increase in tamoxifen dose would be needed to demonstrate clinical utility.

**Chain of Evidence**

It is not possible to construct a chain of evidence for clinical utility due to the lack of clinical validity.

**Section Summary: Clinical Utility**

Multiple studies have evaluated the association between $CYP2D6$ genotype and resulting altered tamoxifen metabolism on clinical outcomes, and have reported conflicting results. However, most of the earlier studies were retrospective and evaluated small numbers of patients. In an attempt to settle this issue, investigators conducted multiple reanalyses of large, prospective randomized controlled trials and meta-analyses. They too reported conflicting results. It is thought the inconsistencies in the literature may be due to differences
across studies in the types of additional therapies patients received, how many and which CYP2D6 alleles were tested, tissue type examined (tumor or germline DNA), and coadministration of CYP2D6 inhibitors.

No direct evidence of clinical utility was identified. One prospective cohort study implemented a tamoxifen adjustment algorithm but did not report outcomes. In another prospective cohort study of CYP2D6 genotype-guided tamoxifen dose escalation, dose escalation in PM or IM patients increased the endoxifen concentrations but not toxicity. However, the study did not attempt to delineate whether increased endoxifen levels were associated with greater efficacy. A beneficial effect on survival with the increase in tamoxifen dose would be needed to demonstrate clinical utility. It is not possible to construct a chain of evidence for clinical utility due to the lack of clinical validity.

**SUMMARY OF EVIDENCE**

For individuals who are treated with tamoxifen for breast cancer or high risk of breast cancer who receive testing for CYP2D6 metabolizer status by CYP2D6 genotyping, the evidence includes multiple retrospective studies, post hoc analysis of randomized controlled trials, and meta-analysis. Relevant outcomes include OS, disease-specific survival, test accuracy and validity, medication use, and treatment-related morbidity. Published data on the association between CYP2D6 genotype and tamoxifen treatment outcomes have yielded inconsistent results. Some inconsistencies in the literature may be due to differences across studies in the types of additional therapies patients received, how many and which CYP2D6 alleles were tested, tissue type examined (tumor or germline DNA), and coadministration with CYP2D6 inhibitors. The largest, most well-designed studies do not support a significant association. At present, the clinical utility of CYP2D6 testing is also poorly defined. An interventional study of CYP2D6-specific tamoxifen dosing found that personalized dosing was associated with changes in endoxifen level, but it has not been demonstrated that endoxifen level is associated with improved outcomes. It is not known whether clinical management guided by CYP2D6 genotyping improves patient outcomes such as appropriate selection of a treatment strategy that would reduce the rate of recurrence, improve disease-free survival or OS, or reduce adverse events. The evidence is insufficient to determine the effects of the technology on health outcomes.

**References**


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43. Cross and Blue Shield Association Technology Evaluation Center (TEC). CYP2D6 Pharmacogenomics of Tamoxifen Treatment. TEC Assessments 2013;Volume 28;Tab 8. PMID

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Genetic Testing for Tamoxifen Treatment

Policy # 00269
Original Effective Date: 09/15/2010
Current Effective Date: 09/20/2017


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09/09/2010 Medical Policy Committee review
09/01/2011 Medical Policy Committee review
09/14/2011 Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
09/06/2012 Medical Policy Committee review
09/19/2012 Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
01/23/2013 Coding updated
09/05/2013 Medical Policy Committee review
09/18/2013 Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
09/04/2014 Medical Policy Committee review
09/03/2015 Medical Policy Committee review
09/08/2016 Medical Policy Committee review
09/21/2016 Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
01/01/2017 Coding update: Removing ICD-9 Diagnosis Codes
09/07/2017 Medical Policy Committee review
09/20/2017 Medical Policy Implementation Committee approval. Policy revised with updated genetics nomenclature; coverage eligibility otherwise unchanged.

Next Scheduled Review Date: 09/2018

Coding
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Codes used to identify services associated with this policy may include (but may not be limited to) the following:

<table>
<thead>
<tr>
<th>Code Type</th>
<th>Code</th>
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<tbody>
<tr>
<td>CPT</td>
<td>81226</td>
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<td>Code added eff 8/1/17: 0015U</td>
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<tr>
<td>HCPCS</td>
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<tr>
<td></td>
<td>C50.911-C50.919</td>
</tr>
</tbody>
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*Investigational – A medical treatment, procedure, drug, device, or biological product is Investigational if the effectiveness has not been clearly tested and it has not been incorporated into standard medical practice. Any determination we make that a medical treatment, procedure, drug, device, or biological product is Investigational will be based on a consideration of the following:

A. Whether the medical treatment, procedure, drug, device, or biological product can be lawfully marketed without approval of the U.S. Food and Drug Administration (FDA) and whether such approval has been granted at the time the medical treatment, procedure, drug, device, or biological product is sought to be furnished; or

B. Whether the medical treatment, procedure, drug, device, or biological product requires further studies or clinical trials to determine its maximum tolerated dose, toxicity, safety, effectiveness, or effectiveness as compared with the standard means of treatment or diagnosis, must improve health outcomes, according to the consensus of opinion among experts as shown by reliable evidence, including:

1. Consultation with the Blue Cross and Blue Shield Association technology assessment program (TEC) or other nonaffiliated technology evaluation center(s);

2. Credible scientific evidence published in peer-reviewed medical literature generally recognized by the relevant medical community; or

3. Reference to federal regulations.

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