Microarray-based Gene Expression Analysis for Prostate Cancer Management

Policy # 00403
Original Effective Date: 02/19/2014
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Applies to all products administered or underwritten by Blue Cross and Blue Shield of Louisiana and its subsidiary, HMO Louisiana, Inc. (collectively referred to as the “Company”), unless otherwise provided in the applicable contract. Medical technology is constantly evolving, and we reserve the right to review and update Medical Policy periodically.

Note: Gene-Based Tests for Screening, Detection, and/or Management of Prostate Cancer is addressed separately in medical policy 00272.

Services Are Considered Investigational
Coverage is not available for investigational medical treatments or procedures, drugs, devices or biological products.

Based on review of available data, the Company considers gene expression analysis to guide management of prostate cancer in all situations to be investigational.*

Background/Overview
Gene expression profile analysis has been proposed as a means to risk-stratify patients with low-risk prostate cancer, diagnosed by needle biopsy, to guide treatment decisions.

Prostate cancer is the second most common cancer diagnosed among men in the U.S. According to the National Cancer Institute (NCI), nearly 240,000 new cases are expected to be diagnosed in the U.S. in 2013, and associated with around 30,000 deaths. Autopsy studies in the pre-prostate-specific antigen (PSA) screening era have identified incidental cancerous foci in 30% of men 50 years of age, with incidence reaching 75% at age 80 years. However, NCI Surveillance Epidemiology and End Results data show age-adjusted cancer-specific mortality rates for men with prostate cancer have declined from 40 per 100,000 in 1992 to 22 per 100,000 in 2010. This decline has been attributed to a combination of earlier detection via PSA screening and improved therapies.

Localized prostate cancers may appear very similar clinically at diagnosis. However, they often exhibit diverse risk of progression that may not be captured by accepted clinical risk categories (e.g., D’Amico criteria) or prognostic tools that are based on clinical findings, including PSA titers, Gleason grade, or tumor stage. In studies of conservative management, the risk of localized disease progression based on prostate cancer-specific survival rates at 10 years may range from 15% to 20% to perhaps 27% at 20-year follow-up. Among elderly men (70 years or more) with this type of low-risk disease, comorbidities typically supervene as a cause of death; these men will die with prostate cancer present, rather than from the cancer. Other very similar-appearing low-risk tumors may progress unexpectedly rapidly, quickly disseminating and becoming incurable.

The divergent behavior of localized prostate cancers creates uncertainty whether or not to treat immediately. A patient may choose definitive treatment upfront. Surgery (radical prostatectomy), external-beam radiation therapy (EBRT), brachytherapy, high-intensity-focused ultrasound, systemic chemotherapy, hormonal therapy, cryosurgery, or combinations are used to treat patients with prostate cancer. Complications associated with those treatments most commonly reported (radical prostatectomy, EBRT)
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and with the greatest variability were incontinence (0-73%) and other genitourinary toxicities (irritative and obstructive symptoms); hematuria (typically 5% or less); gastrointestinal and bowel toxicity, including nausea and loose stools (25-50%); proctopathy, including rectal pain and bleeding (10-39%); and erectile dysfunction, including impotence (50-90%).

American Urological Association (AUA) Guidelines suggest patients with low- and intermediate-risk disease have the option of “active surveillance”, taking into account patient age, patient preferences, and health conditions related to urinary, sexual, and bowel function. With this approach the patient will forgo immediate therapy and continue regular monitoring until signs or symptoms of disease progression are evident, at which point curative treatment is instituted.

Given the unpredictable behavior of early prostate cancer, additional prognostic methods to biologically stratify this disease are under investigation. These include microarray-based gene expression profiling, which refers to analysis of mRNA expression levels of many genes simultaneously in a tumor specimen. Two microarray-based gene expression profiling tests are now offered, intended to biologically stratify prostate cancers: Prolaris™ (Myriad Genetics, Salt Lake City, UT) and Oncotype Dx® Prostate Cancer Assay (Genomic Health, Redwood City, CA). Both use archived tumor specimens as the mRNA source, reverse transcriptase polymerase chain reaction amplification, and the TaqMan low-density array platform (Applied Biosystems, Foster City, CA). Prolaris is used to quantify expression levels of 31 cell cycle progression (CCP) genes and 15 housekeeper genes to generate a CCP score. Oncotype Dx Prostate is used to quantify expression levels of 12 cancer-related and 5 reference genes to generate a Genomic Prostate Score (GPS). In the final analysis, the CCP score or GPS are combined in proprietary algorithms with clinical risk criteria (PSA, Gleason grade, tumor stage) to generate new risk categories (ie, reclassification) intended to reflect biological indolence or aggressiveness of individual lesions, and thus inform management decisions.

FDA or Other Governmental Regulatory Approval
U.S. Food and Drug Administration (FDA)
Neither Prolaris nor Oncotype Dx Prostate Cancer Assay is cleared for marketing by the FDA. Each is available under the auspices of the Clinical Laboratory Improvement Act (CLIA). Clinical laboratories may develop and validate tests in-house (laboratory-developed tests [LDTs]) and market them as a laboratory service; LDTs must meet the general regulatory standards of the CLIA. Laboratories that offer LDTs must be licensed by CLIA for high-complexity testing.

Centers for Medicare and Medicaid Services (CMS)
The Prolaris test will be denied as not reasonable and necessary regardless of the diagnosis billed (http://www.findacode.com/medicare/policies-guidelines/display-medicare-info.php?type=ARTICLE&type_id=52156)

No national coverage determination for the Oncotype Dx Prostate test was identified.
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Rationale/Source
This policy is based on a 2013 Technology Evaluation Centers (TEC) Assessment with a literature review through June 2013. Full-length publications were sought that described the analytic validity, clinical validity, and clinical utility of either Prolaris or Oncotype Dx Prostate gene expression profiling. We reviewed evidence on the use of either test to predict the aggressiveness (or indolence) of newly diagnosed (by needle biopsy), localized prostate cancer.

Analytic Validity (the technical accuracy of the test in detecting a mutation that is present or in excluding a mutation that is absent)

Published data on the analytic validity of Prolaris or OncotypeDx Prostate was not identified. Information is available on the performance of the TaqMan array platform (Applied Biosystems, Foster City, CA) used in Prolaris and Oncotype Dx Prostate through the MicroArray Quality Control (MAQC) project. In the MAQC project, initiated and led by FDA scientists, expression data on 4 titration pools from 2 distinct reference ribonucleic acid (RNA) samples were generated at multiple test sites on 7 microarray-based and 3 alternative technology platforms, including TaqMan. According to the investigators, the results provide a framework to assess the potential of array technologies as a tool to provide reliable gene expression data for clinical and regulatory purposes. The results showed very similar performance across platforms, with a median coefficient of variation of 5% to 15% for the quantitative signal and 80% to 95% concordance for the qualitative detection call between sample replicates.

Clinical Validity (the diagnostic performance of the test [sensitivity, specificity, positive and negative predictive values] in detecting clinical disease)

Prolaris
One full-length, peer-reviewed article reports results of a validation study of Prolaris to determine its prognostic value for prostate cancer death in a conservatively managed needle biopsy cohort. Cuzick et al. did not state whether this study adheres to the PROBE (prospective-specimen-collection, retrospective-blinded evaluation) criteria suggested by Pepe and colleagues for an adequate biomarker validation study. They note that the cell cycle expression data were read blind to all other data, which conforms to the criteria; however, patients were identified retrospectively from tumor registries, and there were no case-control subjects, which does not conform.

Patients were identified from 6 cancer registries in Great Britain and were included if they had clinically localized prostate cancer that was diagnosed by needle biopsy between 1990 through 1996; were younger than 76 years at diagnosis; had a baseline PSA measurement; and were conservatively managed. Potentially eligible patients who underwent radical prostatectomy, died, or showed evidence of metastatic disease within 6 months of diagnosis were excluded. Those who received hormone therapy prior to diagnostic biopsy also were excluded. The original biopsy specimens were retrieved and centrally reviewed by a panel of expert urological pathologists to confirm the diagnosis and, where necessary, to reassign Gleason scores by use of a contemporary and consistent interpretation of the Gleason scoring system.
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Tumor cells were microdissected from needle biopsy blocks, the amount determined by the length of the cancer available in the core and to enable preservation of any remaining cancer tissue for tissue microarray studies. A CCP score, consisting of expression levels of 31 predefined CCP genes and 15 housekeeper genes, was generated using TaqMan low-density arrays. The values of each of the 31 CCP genes were normalized by subtraction of the average of up to 15 nonfailed housekeeper genes for that replicate.

Of 776 patients diagnosed by needle biopsy and for which a section was available to review histology, needle biopsies were retrieved for 527 (68%), 442 (84%) of which had adequate material to assay. Among the 442, a proportion, 349 (79%), produced a CCP score and had complete baseline and follow-up information. The median potential follow-up time was 11.8 years, during which a total 90 deaths from prostate cancer occurred within 2799 person-years of actual follow-up. The main assessment of the study was a univariate analysis of the association between death from prostate cancer and the CCP score. A further predefined assessment of the added prognostic information after adjustment for the baseline variables was also undertaken. The primary end point was time to death from prostate cancer. A number of covariates were evaluated: centrally reviewed Gleason primary grade and score; baseline PSA value; clinical stage; extent of disease (percent of positive cores); age at diagnosis; Ki-67 immunohistochemistry; and initial treatment. The results are shown in Table 1.

Table 1. Univariate and Multivariate Analysis for Death From Prostate Cancer in the Cuzick 2012 Validation Study

<table>
<thead>
<tr>
<th>Variable</th>
<th>N</th>
<th>Univariate Hazard Ratio (95% CI)</th>
<th>Multivariate Hazard Ratio (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1-unit increase in CCP score</td>
<td>349</td>
<td>2.02 (1.62 to 2.53)</td>
<td>1.65 (1.31 to 2.09)</td>
</tr>
<tr>
<td>Gleason score</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt; 7</td>
<td>106</td>
<td>0.46 (0.25 to 0.86)</td>
<td>0.61 (0.32 to 1.16)</td>
</tr>
<tr>
<td>7</td>
<td>152</td>
<td>Referent</td>
<td>Referent</td>
</tr>
<tr>
<td>&gt; 7</td>
<td>91</td>
<td>2.70 (1.72 to 4.23)</td>
<td>1.90 (1.18 to 3.07)</td>
</tr>
<tr>
<td>log (1+PSA)/(ng/mL)</td>
<td>349</td>
<td>1.70 (1.31 to 2.20)</td>
<td>1.37 (1.05 to 1.79)</td>
</tr>
<tr>
<td>Proportion of positive cores</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt; 50%</td>
<td>69</td>
<td>0.50 (0.22 to 1.12)</td>
<td></td>
</tr>
<tr>
<td>50 to &lt; 100%</td>
<td>106</td>
<td>Referent</td>
<td></td>
</tr>
<tr>
<td>100%</td>
<td>160</td>
<td>1.66 (1.01 to 2.73)</td>
<td></td>
</tr>
<tr>
<td>Age at diagnosis (y)</td>
<td>349</td>
<td>1.00 (0.96 to 1.04)</td>
<td></td>
</tr>
<tr>
<td>Clinical stage</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1</td>
<td>38</td>
<td>0.75 (0.32 to 1.75)</td>
<td></td>
</tr>
<tr>
<td>T2</td>
<td>106</td>
<td>Referent</td>
<td></td>
</tr>
<tr>
<td>T3</td>
<td>43</td>
<td>1.74 (0.90 to 3.38)</td>
<td></td>
</tr>
<tr>
<td>Hormone use</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>200</td>
<td>Referent</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>149</td>
<td>1.97 (1.30 to 2.98)</td>
<td></td>
</tr>
</tbody>
</table>

CI: confidence interval.
The median CCP score was 1.03 (IQ range, 0.41-1.74). The primary univariate analysis suggests that a 1-unit increase in CCP score was associated with a 2-fold increase in the risk of dying from prostate cancer. In preplanned multivariate analyses, extent of disease, age, clinical stage, and use of hormones had no statistically significant effect on risk; only the Gleason score and PSA remained in the final model. Further exploratory multivariate modeling to produce a combined score, including CCP, Gleason score, and PSA level, suggested a strong, predominant nonlinear influence of the CCP score in predicting the risk of death from prostate cancer ($p = 0.008$). Cuzick and colleagues suggest this combined score provides additional discriminatory information to help identify low-risk patients who could be safely managed by active surveillance. For example, among patients with a Gleason score of 6, for whom uncertainty exists as to the appropriate management approach, the predicted 10-year prostate cancer death rate ranged from 5.1% to 20.9% based on Gleason score and PSA; the range when assessed against the combined CCP, Gleason, and PSA score was 3.5% to 41%. They caution, however, that because death rates were rare in this group, larger cohorts are required to fully assess the value of the CCP combined score.

Kaplan-Meier analyses of 10-year risk of prostate cancer death stratified by CCP score groupings are shown in Table 2. Cuzick et al. reported no significance tests for the estimates. Nor did they explain the apparent substantial difference in mortality rates among patients in the $0 \leq CCP \leq 2$ grouping (range, 19.3-21.1%) and those in the $2 < CCP \leq 3$ and $> 3$ groupings (range, 48.2-74.9%). The difference may simply reflect clinical criteria, for example, proportions of lower compared with higher Gleason grade cancers, respectively.

<table>
<thead>
<tr>
<th>CCP Score Group</th>
<th>N</th>
<th>10-Year Death Rate (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$CCP \leq 0$</td>
<td>36</td>
<td>19.3</td>
</tr>
<tr>
<td>$0 &lt; CCP \leq 1$</td>
<td>133</td>
<td>19.8</td>
</tr>
<tr>
<td>$1 &lt; CCP \leq 2$</td>
<td>114</td>
<td>21.1</td>
</tr>
<tr>
<td>$2 &lt; CCP \leq 3$</td>
<td>50</td>
<td>48.2</td>
</tr>
<tr>
<td>$&gt; 3$</td>
<td>16</td>
<td>74.9</td>
</tr>
</tbody>
</table>

Oncotype Dx Prostate

No full-length publications on the clinical validity of Oncotype Dx Prostate were identified. The Genomic Health website presents information on gene panel development studies and a clinical validation study that was performed to evaluate this test in specimens obtained by needle biopsy in a cohort of men in the U.S. The latter study was presented at the 2013 annual meeting of the AUA, but slides are not available (abstract 2131 at http://www.aua2013.org/abstracts/archive/abstracts_POD35.cfm). According to the website, the developer of the test and their collaborators from the University of California San Francisco (UCSF) evaluated the Oncotype Dx prostate test on needle biopsy tissue from patients who could have been candidates for active surveillance but underwent radical prostatectomy, then correlated the biopsy results to their radical prostatectomy specimens. This information is insufficient to assess the clinical validity of this test.
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Clinical Utility (how the results of the 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)

No published data on the clinical utility of Prolaris or Oncotype Dx Prostate were identified. At present, no conclusions can be reached on this topic.

Section Summary
The analytic validity of gene expression analysis for prostate cancer management is indirectly suggested by results from the MAQC project, but remains to be specifically established.

No peer-reviewed, published evidence on the clinical validity of Prolaris comprised a retrospective cohort (n = 349) culled from 6 cancer registries in Great Britain. In the primary univariate analysis, a 1-unit increase in CCP score was associated with a 2.02-fold (95% CI, 1.62 to 2.53, p = 8.6 \times 10^{-10}) increase in the hazard of death from prostate cancer at 10-year follow-up. Multivariate analyses showed only the CCP score (hazard ratio [HR] for a 1-unit increase in CCP score = 1.65; 95% CI, 1.31 to 2.09; p = 2.6 \times 10^{-5}), Gleason score < 7 (HR = 0.61; 95% CI, 0.32 to 1.16; p = 5.0 \times 10^{-4}) and PSA titer (HR = 1.37; 95% CI, 1.05 to 1.79; p = 0.017) were statistically associated with prostate cancer-specific mortality at 10 years. The investigators assert the CCP score alone was more prognostic than either PSA titer or Gleason score for tumor-specific mortality at 10-year follow-up. Although the patients may be similar to those of a modern U.S. cohort, comparability is unclear from the single publication that is available. Furthermore, the study is limited by the use of archived biopsy specimens, with attendant issues of reproducibility and test reliability.

No peer-reviewed, published evidence on the clinical validity of Oncotype Dx Prostate was identified. No evidence is available on the clinical utility of either test for any clinical end point.

Ongoing Clinical Trials
No active clinical trials were identified in a search of the Clinicatrials.gov website as of October 14, 2013.

Summary
Two gene expression analysis tests—Prolaris and Oncotype Dx Prostate—are commercially available. The test results are intended to be used in combination with accepted clinical criteria (Gleason score, PSA, clinical stage) to stratify biopsy-diagnosed localized prostate cancer according to biological aggressiveness, and direct initial patient management. Direct evidence is insufficient to establish the analytic validity, clinical validity, or clinical utility of either test. Therefore, gene expression analysis for prostate cancer management is considered investigational.

References
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25. Blue Cross Blue Shield Association Technology Evaluation Center (TEC). Microarray-based Gene Expression Analysis for Prostate Cancer Management. TEC Assessments 2014; Volume 28, Tab TBA.


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<td>CPT</td>
<td>81599</td>
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<tr>
<td>HCPCS</td>
<td>No codes</td>
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<tr>
<td>ICD-9 Diagnosis</td>
<td>All relative diagnoses</td>
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<tr>
<td>ICD-9 Procedure</td>
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Policy History

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02/06/2014 Medical Policy Committee review
02/19/2014 Medical Policy Implementation Committee approval. New policy.
Next Scheduled Review Date: 02/2015

*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
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3. reference to federal regulations.

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