Aligning Genetic Panel Utilization with Clinical Practice Guidelines Through Education

Jerm Day–Storms, PhD, MA¹, Amy Zitiello, DO, MPH, FAAP¹ Paige Xu, MPH¹, Erin Kren, PhD¹, Tatiana Souslova, PhD, MSc, DABCC¹

¹Avalon Healthcare Solutions

Background

• Next Generation Sequencing (NGS) panel tests can provide clinically actionable data.
• Contrary to AMA guidelines, many labs have continued to either stack or unbundle individual test codes, which may result is increased reimbursement at the expense of patients and payers rather than use an AMA-issued procedure code for the gene panel test.

Study Objective

• The objective of this study is to gauge how education and quality assurance (QA) processes affect correct implementation of clinical practice coding guidelines.

Methods

• Administrative prior authorization data were collected from Avalon Healthcare Solutions network providers over an 18-month period (1/1/2018 – 8/30/2019).
• Data were further restricted to a single network provider conducting gene panel testing to demonstrate the course of change in sequencing ordering over time from education and QA processes.
• Descriptive statistics were conducted for the single network provider, and service utilization was tracked over the 18-month period by procedure code.
• Cost analysis was conducted to evaluate impact.

Results

• Among the total cohort, 6559 service units were ordered. Of the total service units, 4248 (64.8%) were paid, and 2311 (35.2%) were denied. In total, 1893 (28.9%) units of procedure code 81211 and 1937 (29.5%) units of procedure code 81213, 1937 (29.5%) units of procedure code 81432, 1137 (17.3%) units of procedure code 81433, and 446 (6.8%) units of procedure code 81612 were performed (Figures 1 and 2).

Figure 1: Aggregate Data. The total units submitted containing CPT codes included within the purview of the study. The values indicate the total number.

Figure 2: Normalized Aggregate Data. Average units for the duration CPT code was active within study time frame.

• Utilization by approved units before and after the retirement of codes 81211 and 81213 is comparable. A decrease in utilization of code 81162 occurs over the course of education with a subsequent increase in the uses of codes 81432 and 81433 (Figure 3).

Figure 3: Impact of Education on Claims History. Approved [Left] and denied [Right] claims submitted during the course of the study. The vertical red bar on each graph indicates the date when the CPT® codes 81211 & 81213 were retired by the AMA (2019).

• Denials are due primarily to lack of medical necessity (86.8%), and thereby not from inappropriate filing or administrative reasons. Decreases in denials due to lack of medical necessity are seen (Figure 4).

Figure 4: Impact of Education on Denials Due to Lack of Medical Necessity. Count of claims denied due to lack of medical necessity over study period. Vertical red bar indicates the date when the CPT® codes 81211 & 81213 were retired by the AMA (2019).

• Finally, cost analysis based on 2018 CMS national average pricing on the most common co-ordered unbundled genetic tests compared to appropriate NGS panel codes show a substantial cost differential (Figure 5).

Figure 5: Financial Impact of Unbundling Codes. Comparison of financial cost between unbundling codes and appropriate NGS panel codes based on the 2018 CMS Procedure Cost Per Unit. [Code 81479 was not included due to variable reimbursement rates.]

Conclusion

• Education and QA processes can positively redirect providers and laboratories to follow AMA coding practice guidelines while providing patients with clinically appropriate genetic testing without increasing coverage denials due to inappropriate filing or other administrative reasons.
• Trends in decrease denials can be attributed to education and QA measures, ensuring correct coding and medical necessity as described by medical policy.

References


AMA CPT® Codes

<table>
<thead>
<tr>
<th>Code</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>81162</td>
<td>BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (ie, deletion of large gene rearrangements)</td>
</tr>
<tr>
<td>81211</td>
<td>BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and common duplication/deletion variants in BRCA1 (ie, exon 13 del 3.635kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb)</td>
</tr>
<tr>
<td>81213</td>
<td>Uncommon duplication/deletion variants</td>
</tr>
<tr>
<td>81432</td>
<td>Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); genomic sequence analysis panel, must include sequencing of at least 10 genes, always including BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, and TP53</td>
</tr>
<tr>
<td>81433</td>
<td>Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); duplication/deletion analysis panel, must include analyses for BRCA1, BRCA2, MLH1, MSH2, and STK11</td>
</tr>
</tbody>
</table>

Key Features:

1. Test Identification: Analyte-specific evaluation of molecular panel and unlisted codes
2. Panel Evaluation: Promotes appropriate use of lab-specific molecular panels (elimination of unsuitable code stacking and/or excessive panels)
3. Decision Detail: Accessibility & Easy to understand