ASSOCIATION FOR MOLECULAR PATHOLOGY
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August 7, 2018

Seema Verma, CMS Administrator
Centers for Medicare & Medicaid Services
Department of Health and Human Services
Hubert H. Humphrey Building, Room 445-G
200 Independence Avenue, SW
Washington, DC 20201

Dear Ms. Verma:

RE: 2018 Preliminary Gapfill Payment Determinations for CY2019

Dear Ms. Verma:

On behalf of the Association of Molecular Pathology (AMP), thank you for this opportunity to submit comments on the 2018 preliminary gapfill determinations for CY2019. AMP is an international medical and professional association representing approximately 2,400 physicians, doctoral scientists, and medical technologists who perform or are involved with laboratory testing based on knowledge derived from molecular biology, genetics, and genomics. Membership includes professionals from the government, academic medicine, private and hospital-based clinical laboratories, and the in vitro diagnostics industry.

Many of the codes that are going through the gapfill pricing exercise are not new codes but existing Clinical Laboratory Fee Schedule (CLFS) codes for which the Centers for Medicare and Medicaid Services (CMS) received no (i.e., values of zero) and/or insufficient data to calculate a weighted median private payor rate during the 2017 Protecting Access to Medicare Act (PAMA) pricing process. The PAMA final rule states that "for a CDLT for which CMS receives no applicable information, payment is made based on the crosswalking or gapfilling methods described in 414.508(b)(1) and (2)." However, the pricing process employed by CMS to solicit stakeholder input on these codes provided stakeholders and the Advisory Panel on CDLTs little time to provide meaningful and comprehensive input to CMS. We recommend that in the future the agency include these codes on the agenda for the CLFS public meeting that immediately follows the reporting period. We believe this will allow all interested stakeholders the opportunity to provide meaningful input on the re-pricing of these codes.

Since CMS began utilizing the gapfill process to price services on the CLFS, AMP has expressed concerns about the lack of transparency. It remains difficult to constructively respond to preliminary gapfill values without increased transparency and no discernible rationale as to how the MACs determined preliminary pricing. We hoped that the implementation of PAMA would ultimately improve this process. In the PAMA final rule, CMS noted that although it generally provided its rationale for the basis of payment and for crosswalks, it did "not typically provide explanations of final payment amounts" for gapfilled tests in the past. CMS explained that it

was adding 42 CFR 414.506(d)(3) and (4) to "provide an explanation of gapfilled payment amounts and how we took into account the Panel's recommendations." However, the preliminary gapfill rates posted by CMS do not include explanations. AMP plans to follow-up with CMS on this issue to get a better understanding of how the agency plans to implement this and improve the process.

Based on the limited information released by CMS, we are extremely concerned that the preliminary national limitation amounts (NLAs) do not accurately reflect the value of these procedures. We urge CMS to seriously consider the comments provided by AMP and other stakeholders during the preliminary determination comment period. Undervaluation of these services threatens patient access to care if laboratories can no longer afford to provide these procedures.

Genome CPT codes (81425, 81426, and 81427)

Whole genome sequencing procedures are clinically actionable, most often for patients with severe genetic disorders. These patients have no alternatives: either no existing diagnostic panel is appropriate or the cost of multiple panels exceeds the cost of either whole exome or whole genome sequencing. There is now a significant body of peer-reviewed literature that shows the value of whole genome sequencing in clinical practice. In July 2018, a literature review of exome and genome sequencing was published that examined the role of genome sequencing in clinical care of select patients[1].

AMP appreciates that all MACs recommended a price for each code undergoing gapfill, however we remain very concerned about many of the gapfill values submitted. Under 42 C.F.R 414.508(b)(1), Medicare regulations state that MACs are required to consider the following criteria when establishing gapfill rates:

> *(b) Gapfilling. Gapfilling is used when no comparable existing test is available. (1) In the first year, carrier-specific amounts are established for the new test code using the following sources of information to determine gapfill amounts, if available:*
>
> *(i) Charges for the test and routine discounts to charges;*
>
> *(ii) Resources required to perform the test;*
>
> *(iii) Payment amounts determined by other payers; and*
>
> *(iv) Charges, payment amounts, and resources required for other tests that may be comparable or otherwise relevant.*

The preliminary determinations for genome sequencing (CPT codes 81425, 81426, and 81427) fall significantly below the actual costs to perform these procedures. A recent publication reports that it costs $8,482 per patient to perform a clinical genome sequencing on a patient.[2] Further, in investigating charges for these services, a search of whole genome sequencing services using the Concert Genetics database, laboratories with prices available currently charge prices that range from $7,395 to $7,500[3] for 81425.

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[1] Clark, M. M. (2018). "Meta-analysis of the diagnostic and clinical utility of genome and exome sequencing and chromosomal microarray in children with suspected genetic diseases." Genome Med EPUB.
[2] Farnaes, L., et al. (2018). "Rapid whole-genome sequencing decreases infant morbidity and cost of hospitalization." NPJ Genom Med 3: 10.
[3] https://www.concertgenetics.com/

AMP cannot support pricing of the genome codes at this level and urges CMS not to finalize the preliminary pricing determinations for these codes. Instead, CMS should consider crosswalks for these services based on their relationship to CPT codes currently on the CLFS to set an appropriate price. Due to the PAMA reporting process, comparable codes are now priced on the CLFS, namely the whole exome sequencing codes (81415, 81416, and 81417). Below, AMP offers a method for establishing a relationship between the priced exome codes to the genome codes.

The exome codes are comparable for a number of reasons. Whole genome sequencing and whole exome sequencing are similar in methodology, both in terms of sequencing and informatics pipelines, as well as interpretation requirements. However, genome sequencing procedures require sequencing and interpretation of more DNA content than exome sequencing procedures. Therefore, the exome sequencing procedures codes are comparable to the genome sequencing procedure codes, but the work and resources required for genome sequencing are approximately twice that of the exome sequencing procedure codes. AMP recommends that CMS reconsider the preliminary determinations for the genome sequencing procedure codes and consider a value that is twice the value of the exome sequencing codes.

Comparator Codes (Exome codes 81415, 81416, 81417)

Code	Descriptor	2018 NLA
81415	**Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis**	**$4,780.00**
81416	**Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator exome (eg, parents, siblings) (List separately in addition to code for primary procedure)**	**$12,000.00**
81417	**Exome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained exome sequence (eg, updated knowledge or unrelated condition/syndrome)**	**$320.00**

Recommendations for Insufficiently-priced 2018 Gapfill Genome CPT codes

Code	Descriptor	Preliminary Gapfill Recommendation	Recommendation
81425	**Genome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis**	**$349**	**81415 X 2 = $4780 X 2 = $9560**
81426	**Genome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator genome (eg, parents, siblings) (List separately in addition to code for primary procedure)**	**$349**	**81415 X 2 = $4780 X 2 = $9560**

Code	Descriptor	Preliminary Gapfill Recommendation	Recommendation
81427	**Genome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (eg, updated knowledge or unrelated condition/syndrome)**	**$25**	**81417 X 2 = $640**

If CMS intends on gapfilling these codes, AMP urges the agency and the MACs to evaluate charges, payment amounts, and resources for these services as directed by the regulation cited above. We have provided some preliminary information in these comments, but would welcome the opportunity to work with CMS and the MACs to identify additional information required to develop accurate gapfill amounts.

X-linked Intellectual Disability Codes (81425, 81426, and 81427)

Again, AMP appreciates that all MACs recommended a price for each code undergoing gapfill, however we remain concerned about many of the gapfill values submitted. In accordance with 42 C.F.R 414.508(b)(1), CMS should instead evaluate charges, payment amounts, and resources required for other tests that may be comparable or otherwise relevant.

CPT Code 81470 detects pathogenic variants (*e.g.,* single nucleotide variants, small indels) in genes known to be causative of X-linked intellectual disability (XLID). This procedure is performed by next generation sequencing and bioinformatics analysis followed by professional interpretation. Similar methodologies are employed to comparable code 81432, but a larger number of required genes exist in the XLID panel. Therefore, 81470 is roughly equivalent to twice the resources required for 81432. Further, in investigating charges for these services, a search of XLID panel testing using the Concert Genetics database, laboratories with prices available currently charge prices that range from $1,700 to $3,500[4]. Similarly, CPT code 81471 detects pathogenic deletion and duplication variants in genes known to be causative of XLID. This procedure is performed most commonly using a targeted array for the X chromosome.

AMP urges CMS and the MACs not to finalize the preliminary determinations for these codes. Instead, CMS should consider the relationship of these codes to CPT codes currently on the CLFS. The preliminary gapfill determinations are insufficient when one examines comparable tests and current charges for the tests. Below, AMP offers a method for establishing more accurate pricing for 81470 and 81471 using comparable codes that exist on the CLFS.

Comparator Codes (81432 and 81436)

Code	Descriptor	2018 NLA
81432	**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**	**$838.33**
81436	**Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); duplication/deletion analysis panel, must include analysis of at least 5 genes, including MLH1, MSH2, EPCAM, SMAD4, and STK11**	**$722.10**

[4] https://www.concertgenetics.com/

Recommendations for Insufficiently-priced 2018 Gapfill Genome CPT codes

Code	Descriptor	Preliminary Gapfill Recommendation	Recommendation
81470	**X-linked intellectual disability (XLID) (eg, syndromic and non-syndromic XLID); genomic sequence analysis panel, must include sequencing of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2**	**$914**	**81432 X 2 = $838.33 X 2 = $1676.66**
81471	**X-linked intellectual disability (XLID) (eg, syndromic and non-syndromic XLID); duplication/deletion gene analysis, must include analysis of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2**	**$914**	**81436 X 2 = $722.10 X 2 = $1444.20**

We thank you for the opportunity to submit these comments on the preliminary gapfill recommendations. We believe that the rationale, data, and recommendations provided above will result in more accurate and equitable pricing for these services. We are happy to answer any questions about our recommendations and provide follow up information. Please direct your correspondence to Tara Burke, Director of Public Policy and Advocacy, at tburke@amp.org.

Sincerely,

Samuel K. Caughron, MD
Chair, Economics Affairs Committee
Association for Molecular Pathology