

Genetic Testing for Oral Disease

Policy Number: DCP036.05
Effective Date: September 1, 2020

[➔ Instructions for Use](#)

| | |
|---|------|
| Table of Contents | Page |
| Coverage Rationale | 1 |
| Applicable Codes | 1 |
| Description of Services | 1 |
| Clinical Evidence | 2 |
| U.S. Food and Drug Administration | 5 |
| References | 6 |
| Policy History/Revision Information | 7 |
| Instructions for Use | 7 |

| Related Dental Policies |
|-------------------------|
| None |

Coverage Rationale

Collection and Preparation of Genetic Sample Material for Laboratory Analysis and Report

The collection, preparation and testing of genetic sample material is not indicated due to insufficient evidence of efficacy.

Genetic Test for Susceptibility to Diseases – Specimen Analysis

Genetic testing for susceptibility to periodontal diseases and caries is not indicated due to insufficient evidence of efficacy.

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

| CDT Code | Description |
|----------|--|
| D0422 | Collection and preparation of genetic sample material for laboratory analysis and report |
| D0423 | Genetic test for susceptibility to diseases – specimen analysis |

CDT® is a registered trademark of the American Dental Association

Description of Services

Genetic testing is available for a wide array of medical conditions. In dentistry, there is specific genetic testing available for susceptibility to periodontal disease, and the most common HPV infections known to more frequently progress to cancer-HPV16/18. Genetic testing may be a way to identify an individual's risk for the development of periodontal diseases and caries. However, individual patient behaviors, lifestyles, and overall health affect the risk of developing these oral diseases, regardless

of the genetic profile. Regarding caries risk, the majority of the research is focused on enamel formation genes, immune response genes, as well as inherited taste preferences (Vieira 2014).

Clinical Evidence

HPV Related Oral Cancer

Castellsagué et al (2016) conducted a large international study to estimate fractions of head and neck cancers (HNCs) attributable to human papillomavirus (HPV-AFs) using six HPV-related biomarkers of viral detection, transcription, and cellular transformation. Formalin-fixed, paraffin-embedded cancer tissues of the oral cavity (OC), pharynx, and larynx were collected from pathology archives in 29 countries. All samples were subject to histopathological evaluation, DNA quality control, and HPV-DNA detection. Samples containing HPV-DNA were further subject to HPV E6*1 mRNA detection and to p16 (INK4a), pRb, p53, and Cyclin D1 immunohistochemistry. Final estimates of HPV-AFs were based on HPV-DNA, HPV E6*1 mRNA, and/or p16 (INK4a) results. A total of 3680 samples yielded valid results: 1374 pharyngeal, 1264 OC, and 1042 laryngeal cancers. HPV-AF estimates based on positivity for HPV-DNA, and for either HPV E6*1 mRNA or p16 (INK4a), were 22.4%, 4.4%, and 3.5% for cancers of the oropharynx, OC, and larynx, respectively, and 18.5%, 3.0%, and 1.5% when requiring simultaneous positivity for all three markers. HPV16 was largely the most common type. Estimates of HPV-AF in the oropharynx were highest in South America, Central and Eastern Europe, and Northern Europe, and lowest in Southern Europe. Women showed higher HPV-AFs than men for cancers of the oropharynx in Europe and for the larynx in Central-South America. HPV contribution to HNCs is substantial but highly heterogeneous by cancer site, region, and sex. This study, the largest exploring HPV attribution in HNCs, confirms the important role of HPVs in oropharyngeal cancer and drastically downplays the previously reported involvement of HPVs in the other HNCs.

D'Souza et al. (2016) conducted a study to explore whether HPV-related biomarkers predict oropharyngeal squamous cell cancer (OPSCC) survival similarly across different global regions, and to explore their prognostic utility among non-oropharyngeal (non-OP) head and neck cancers. Data from 1362 head and neck SCC (HNSCC) diagnosed 2002-2011 was used from epidemiologic studies in: Brazil (GENCAPO study), U.S. (CHANCE study), and Europe (ARCAGE study). Tumors were centrally tested for p16INK4a and HPV16 DNA. Risk of mortality was examined using Cox proportional hazard models. The data showed there were 517 OPSCC and 845 non-OP HNSCC. Cases were primarily male (81%), ever smokers (91%), with median age of 58 years and median follow-up of 3.1 years. The results showed that among OPSCC, the risk of mortality was significantly lower among 184 HPV-related compared to 333 HPV-unrelated cases. Mortality was reduced among HPV-related OPSCC cases from the U.S., Europe, and Brazil, and after adjustment, remained significantly reduced. Among non-OP HNSCC, neither p16, HPV16 DNA, nor p16+/HPV16+ was a significantly predictor of mortality. When interaction was tested, the effect of HPV16/p16 was significantly different in OPSCC than non-OP HNSCC. The authors concluded that HPV-related OPSCCs had similar survival benefits across these three regions. Prognostic utility of HPV among non-OP HNSCC is limited so tumor HPV/p16 testing should not be routinely done among non-OP HNSCC.

Chai et al (2016) Human papilloma virus-16 (HPV-16) infection is a major risk factor for a subset of head and neck squamous cell carcinoma (HNSCC), in particular oropharyngeal squamous cell carcinoma (OPSCC). Current techniques for assessing the HPV-16 status in HNSCC include the detection of HPV-16 DNA and p16 (INK4a) expression in tumor tissues. When tumors originate from hidden anatomical sites, this method can be challenging. A non-invasive and cost-effective alternative to biopsy is therefore desirable for HPV-16 detection especially within a community setting to screen at-risk individuals. The present study compared detection of HPV-16 DNA and RNA in salivary oral rinses with tumor p16 (INK4a) status, in 82 HNSCC patients using end-point and quantitative polymerase chain reaction (PCR). Of 42 patients with p16 (INK4a)-positive tumours, 39 (sensitivity=92.9%, PPV=100% and NPV=93%) had oral rinse samples with detectable HPV-16 DNA, using end-point and quantitative PCR. No HPV-16 DNA was detected in oral rinse samples from 40 patients with p16 (INK4a) negative tumours, yielding a test specificity of 100%. For patients with p16 (INK4a) positive tumours, HPV-16 mRNA was detected using end-point reverse transcription PCR (RT-PCR) in 24/40 (sensitivity=60%, PPV=100% and NPV=71%), and using quantitative RT-PCR in 22/40 (sensitivity=55%, PPV=100% and NPV=69%). No HPV-16 mRNA was detected in oral rinse samples from the p16 (INK4a)-negative patients, yielding a specificity of 100%. The authors demonstrated through this study, that the detection of HPV-16 DNA in salivary oral rinse is indicative of HPV status in HNSCC patients and can potentially be used as a diagnostic tool in addition to the current methods.

Rettig et al (2015) conducted a prospective cohort study to determine whether HPV DNA detection in oral rinses after treatment for HPV-OPC is associated with recurrence and survival. Although HPV-OPC has favorable prognosis, 10% to 25% of HPV-

OPCs recur. Detection of human papillomavirus (HPV) DNA in oral rinses is associated with HPV-OPC, but its potential as a prognostic biomarker is unclear. Patients with incident HPV-OPC diagnosed from 2009 to 2013 at 4 academic tertiary referral cancer centers in the United States. Oral rinse samples were collected at diagnosis and after treatment (9, 12, 18, and 24 months after diagnosis), and evaluated for HPV DNA. Among an initial cohort of 157 participants with incident HPV-OPC treated with curative intent, 124 had 1 or more posttreatment oral rinses available and were included in this study. Disease-free survival (DFS) and overall survival (OS) were estimated by the Kaplan-Meier method, and the association of HPV DNA detection in oral rinses with survival was evaluated using Cox regression analysis. Oral HPV type 16 (HPV16) DNA was common at diagnosis (67 of 124 participants [54%]). In contrast, oral HPV16 DNA was detected in only 6 participants after treatment (5%), including 5 with HPV16 DNA also detected at diagnosis (persistent oral HPV16 DNA). Two-year DFS and OS were 92% (95% CI, 94%-100%) and 98% (95% CI, 93%-99%). Persistent oral HPV16 DNA was associated with worse DFS (hazard ratio, 29.7 [95% CI, 9.0-98.2]) and OS (hazard ratio, 23.5 [95% CI, 4.7-116.9]). All 5 participants with persistent oral HPV16 DNA developed recurrent disease, 3 with local disease involvement. In contrast, just 9 of 119 participants (8%) without persistent oral HPV16 DNA developed recurrent disease, only 1 (11%) with local disease involvement. Median (range) time from earliest posttreatment oral HPV16 DNA detection to recurrence was 7.0 (3.7-10.9) months. Human papillomavirus type 16 DNA in oral rinses is common at diagnosis but rare after treatment for HPV-OPC. The authors concluded that although infrequent, persistent HPV16 DNA in posttreatment oral rinses is associated with poor prognosis and is a potential tool for long-term tumor surveillance, perhaps more so for local recurrence.

Periodontal Disease

In a 2019 literature review, Toy et al. sought to clarify the possible role of genetic polymorphisms in periodontal diseases. The authors searched PubMed for studies published from 1997 to June 2018 and obtained data from original studies, meta analyses, and systematic reviews. They included only case-control studies with large study populations. Several genes with a possible relationship to periodontal disease were analyzed, and the authors concluded that gene polymorphisms may cause phenotypic differences in inflammatory response, which is important in the individual's sensitivity to disease, in the progression of disease, or in the response to treatment. The incidence of genetic polymorphisms may differ according to ethnicity, so a potential association between a genetic polymorphism and disease for a population may not be valid for others.

de Coo et al. (2018) conducted a systematic review to evaluate the various genotyping tools and study strategies employed to define genetic susceptibility to periodontitis. Following data base searches, 25 studies satisfied the established inclusion criteria and were processed for data extraction. The review revealed marked heterogeneity between studies, caused in part by the lack of a universally accepted definition for periodontitis phenotypes and by the variety of genotyping tools available. The most commonly used technique was genotyping candidate genes. The authors concluded that the few rigorous studies that have been published on genetic susceptibility to periodontitis are subject to severe methodological bias due to their design and the genotyping tools employed. Despite their limitations, candidate gene studies continue to be the predominant methodological approach, rather than genome-wide association studies. Further studies must be designed using a universally accepted, validated diagnostic criterion for periodontitis, analyzing multiple genes and polymorphisms in combination with rare variants. There is need for much more comprehensive studies including thousands of individuals to identify the effects of polymorphisms accurately with regard to statistical power. The findings demonstrate a possible association between the FccRIIIB, IL1B, VDR, IL1RN, and TLR4 polymorphisms and aggressive periodontitis; and between the TLR4, IL6, IL1B, MMP1, IL10, VDR, CD14, and IL1RN polymorphisms and chronic periodontitis susceptibility in specific populations.

Diehl et al (2015) conducted a reanalysis of a large scale study that proposed to show that the PST and PerioPredict genetic tests that are based on polymorphisms in interleukin 1 (IL-1) genes identify a subset of patients who experience fewer tooth extractions if provided with 2 annual preventive visits (see reference directly below, Giannobile et al). Economic analyses indicate rationing preventive care to only "high-risk" genotypes, smokers, patients with diabetes, or combinations of these risk factors would reduce the cost of dental care by \$4.8 billion annually in the United States. The data presented in the original study that claimed clinical utility for the PST and PerioPredict tests were obtained for reanalysis using logistic regression to assess whether the PST genetic test, smoking, diabetes, or number of preventive visits were risk factors for tooth extraction during a span of 16 years. Data in the original article on risk factors for tooth extraction and patient stratification were insufficient to perform an independent reanalysis. Specifically, patients who have diabetes and/or were smokers—2 well established risk factors for tooth loss—were pooled together within "high-risk groups" that also included patients who were classified as "high risk" based solely on their PST genotype test. Consequently, it was not possible to evaluate whether the PST genetic test itself had any effect on the clinical outcomes independent of smoking and/or diabetes. Consistency of risk classification by the PST (version 1) and PerioPredict (version 2) genetic tests was evaluated in different ethnic groups from the 1000 Genomes database. Multivariate analyses revealed association of tooth extraction with diabetes ($P < .0001$), smoking ($P <$

.0001), and number of preventive visits ($P = .004$), but no support for the PST genetic test ($P = .96$) nor indication that the benefit of 2 preventive visits was affected by this genetic test ($P = .58$). Classification of risk was highly inconsistent between the PST (version 1) and PerioPredict (version 2) genetic tests. The authors concluded that this reanalysis indicates two annual preventive visits were supported as beneficial for all patients, and there was no evidence that the IL-1 PST genetic test has any effect on tooth extraction risk or influences the benefits of 2 annual preventive visits. Neither IL-1 PST nor PerioPredict genetic tests are useful for rationing preventive dental care. Further research is needed to identify genetic biomarkers with robust clinical validity and clinical utility to effectively personalize the practice of dentistry.

Giannobile et al (2013) Prevention reduces tooth loss, but little evidence supports biannual preventive care for all adults. The authors used risk-based approaches to test tooth loss association with 1 vs. 2 annual preventive visits in high-risk (HiR) and low-risk (LoR) patients. Insurance claims for 16 years for 5,117 adults were evaluated retrospectively for tooth extraction events. Patients were classified as HiR for progressive periodontitis if they had ≥ 1 of the risk factors (RFs) smoking, diabetes, interleukin-1 genotype; or as LoR if no RFs. LoR event rates were 13.8% and 16.4% for 2 or 1 annual preventive visits (absolute risk reduction, 2.6%; 95%CI, 0.5% to 5.8%; $p = .092$). HiR event rates were 16.9% and 22.1% for 2 and 1 preventive visits (absolute risk reduction, 5.2%; 95%CI, 1.8% to 8.4%; $p = .002$). Increasing RFs increased events ($p < .001$). Oral health care costs were not increased by any single RF, regardless of prevention frequency ($p > .41$), but multiple RFs increased costs vs. no ($p < .001$) or 1 RF ($p = .001$). For LoR individuals, the association between preventive dental visits and tooth loss was not significantly different whether the frequency was once or twice annually. A personalized medicine approach combining gene biomarkers with conventional risk factors to stratify populations may be useful in resource allocation for preventive dentistry (ClinicalTrials.gov, NCT01584479). (Participants in this involved several employees of Interleukin Genetics).

Yücel et al (2013). The immune mechanisms and genetic variations that regulate genetic expression, production and biological activity of IL-1beta, are thought to play an important role in the pathogenesis of periodontal disease. The aims of his controlled study were to analyze interleukin (IL)-1beta (+3954) genotype and allele frequency in both chronic and aggressive periodontitis patients, and also to investigate whether this polymorphism is associated with gingival crevicular fluid (GCF) IL-1beta levels, periodontal disease severity and clinical parameters in subjects of Turkish origin. A total of 147 individuals were enrolled in the study including 56 aggressive periodontitis (AP), 44 chronic periodontitis (CP) patients and 47 healthy controls (C). Single nucleotide polymorphism at IL-1beta (+3954) is analyzed by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). GCF samples were analyzed for IL-1beta, using enzyme linked immunosorbent assay (ELISA). The distributions of genotypes and allele frequencies for IL-1beta (+3954) were similar among the groups, in spite of a trend toward a higher frequency of allele 2 in the patient groups. The genotype distribution and allele frequencies were also not different after stratification of subjects according to the clinical attachment level (CAL < 4 mm and CAL > 4 mm). No differences were found between the GCF IL-1beta levels of the different genotypes. Allele 2 was associated with increased bleeding on probing (BOP) sites in chronic periodontitis patients. The results of this study do not support that genetic polymorphism in the IL-1beta (+3954) could be identified as susceptibility or severity factor in aggressive periodontitis, in the present population. The association of allele 2 frequency and higher percentage of BOP sites in chronic periodontitis suggest that IL-1beta (+3954) potentially play a significant but not major role in the clinical outcome.

Karimbux et al (2012) conducted a systematic review and meta-analysis in an attempt to clarify whether IL-1 gene variants were associated with well-defined clinical phenotypes of chronic periodontitis (CP) in white patients. Study inclusion criteria focused on the analytic framework originally proposed for the IL-1 genetic effect in which overexpression of inflammatory mediators is hypothesized to result in more severe periodontitis in response to a bacterial challenge. Interleukin-1 (IL-1) gene polymorphisms have been associated with increased levels of inflammatory mediators and several inflammatory diseases. Periodontitis is a bacterially induced chronic inflammatory disease that destroys the connective tissues and bone that support the teeth, affects substantial numbers of adults, and has been implicated as a contributing factor in systemic diseases. IL-1 gene polymorphisms, most prominently IL1A (-889), IL1A (+4845), and IL1B (+3954), have been associated with CP in whites. Since the first report, ≥ 125 studies have examined IL-1 gene variation in relation to periodontal disease. These studies have produced mixed findings in diverse periodontal phenotypes and in different ethnic groups. One previous meta-analysis has been published on this topic and supported an association between IL-1 genes and periodontitis, but considerable doubt remains about the patient populations in which the association may be of clinical relevance. Twenty-seven studies were included in the qualitative analysis. Nineteen studies yielded significant associations between carriage of the minor IL-1 alleles and periodontitis. The meta-analysis, based on 13 qualifying studies, found significant effects for the two individual gene variations (IL1A odds ratio [OR] = 1.48; IL1B OR = 1.54) and for a composite genotype that combines minor alleles at each locus (OR = 1.51). Statistically significant heterogeneity was found that could not be explained, but there was no indication of publication bias. The authors concluded that this this review and meta-analysis shows that IL1A and IL1B genetic variations are significant contributors to CP

in whites. (Participants in this systematic review and meta-analysis involved several employees of Interleukin Genetics. Additionally, Interleukin Genetics provided an unrestricted grant to fund this review).

Professional Societies

American Dental Association (ADA) Council on Scientific Affairs

Genetics and Oral Health

Predictive tests for dental caries or for periodontal disease do not currently exist. Since these are both complex diseases with multiple gene and environmental risk factors, quantifying risk will require multifaceted assessment. Similar to the situation with cardiovascular disease, environmental factors affect one's risk, regardless of genetic profile, and no gene to date has been identified that has as large an impact on periodontal disease as do environmental influences, such as smoking or diabetes (ADA 2017. Updated June 2019).

National Cancer Care Network (NCCN)

Tumor human papillomavirus (HPV) testing by p16 immunohistochemistry (IHC) is required for the work up of cancers of the oropharynx (base of tongue, tonsil, posterior pharyngeal wall, and soft palate). A small proportion of tumors at non-oropharyngeal sites are HPV related, however routine testing for these sites is not recommended.

National Cancer Institute (NCI)

Based on case-controlled and cohort studies, (including one conducted using data collected prospectively (nested case-control study) the NCI has concluded the following:

- Factors with adequate evidence of an increased risk of oropharyngeal cancer human papillomavirus (HPV) infection:
 - Based on solid evidence, HPV 16 infection causes oropharyngeal cancer. HPV 16 is a sufficient but not necessary cause. Other high-risk HPV subtypes, including HPV 18, have been found in a small percentage of oropharyngeal cancers.
 - Tobacco and alcohol use does not appear to be associated with increased risk among people with evidence of HPV 16 L1 seropositivity or oral HPV 16 infection.
 - Oral infection with HPV 16 confers about a 15-fold increase in risk relative to individuals without oral HPV 16 infection.

United States Preventive Services Task Force (USPSTF)

Summary

Oral and oropharyngeal cancer have different causes. Oral cavity cancer is predominantly caused by tobacco and alcohol use. Oropharyngeal cancer, another subset of neck and head cancer, includes human papillomavirus (HPV) as an important risk factor. The incidence and mortality rate of oral cancer has been decreasing in the United States presumably because of reduced tobacco and alcohol use. However, HPV-related oropharyngeal cancer is increasing in incidence. If HPV continues to become a more clinically significant risk factor for oropharyngeal cancer, the benefits of screening for HPV and selection of populations for oral cancer screening based on HPV status will need to be assessed. As the epidemiology evolves, the most effective screening examination will need to be determined. The epidemiology of HPV-related oropharyngeal cancer is evolving and could have important implications for identifying high-risk populations that might benefit from screening.

The USPSTF concludes that the evidence is insufficient to determine the balance of benefits and harms of screening for oral cancer in asymptomatic adults by primary care providers. Although there is interest in screening for oral HPV infection, medical and dental organizations do not recommend it. Currently, no screening test for oral HPV infection has been approved by the U.S. Food and Drug Administration (FDA). Evaluating the accuracy of tests that detect oral HPV infection is a potentially promising area of research.

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

Products for genetic testing for oral disease include, but are not limited to the following:

- MyPeriodID® (OralDNA Labs)
- OraRisk® HPV

- Complete genotyping (Oral DNA Labs)

Laboratories that perform genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at: <https://www.cms.gov/clia/>. (Accessed June 4, 2020)

Information regarding regulation of Laboratory Developed Tests may be found here:

<https://www.fda.gov/MedicalDevices/ProductsandMedicalProcedures/InVitroDiagnostics/LaboratoryDevelopedTests/default.htm>. (Accessed June 4, 2020)

References

American Dental Association (ADA) CDT Codebook 2020

American Dental Association Center for Scientific Information, ADA Science Institute. Oral Health Topics. Genetics and Oral Health September 2017. Updated June 25, 2019. <https://www.ada.org/en/member-center/oral-health-topics/genetics-and-oral-health>.

Castellsagué X, Alemany L, Quer M, et al. HPV Involvement in Head and Neck Cancers: Comprehensive Assessment of Biomarkers in 3680 Patients. *J Natl Cancer Inst.* 2016 Jan 28; 108.

Chai RC, Lim Y, Frazer IH, et al. A pilot study to compare the detection of HPV-16 biomarkers in salivary oral rinses with tumour p16 (INK4a) expression in head and neck squamous cell carcinoma patients. *BMC Cancer.* 2016 Mar 3; 16:178.

de Coo A, Quintela I, Blanco J, et al. Assessment of genotyping tools applied in genetic susceptibility studies of periodontal disease: A systematic review. *Arch Oral Biol.* 2018 Aug; 92:38-50.

de Lima CL, Acevedo AC, Grisli DC, et al. Host-derived salivary biomarkers in diagnosing periodontal disease: systematic review and meta-analysis. *J Clin Periodontol* 2016; 43(6): 492-502.

D'Souza G, Anantharaman D, Gheit T, et al. Effect of HPV on head and neck cancer patient survival, by region and tumor site: A comparison of 1362 cases across three continents. *Oral Oncol.* 2016 Nov; 62:20-27.

Diehl SR, Kuo F et al. Interleukin 1 genetic tests provide no support for reduction of preventive dental care. *J Am Dent Assoc.* 2015 Mar; 146(3):164-173.

Giannobile WV, Braun TM, Caplis AK, et al. Patient stratification for preventive care in dentistry. *J Dent Res.* 2013 Aug; 92(8):694-701.

Karimbux NY, Saraiya VM, Elangovan S, et al. Interleukin-1 gene polymorphisms and chronic periodontitis in adult whites: a systematic review and meta-analysis. *J Periodontol.* 2012 Nov; 83(11):1407-19.

National Cancer Care Network (NCCN) Guidelines Version 2.2019. Cancer of the Oropharynx. June 28, 2019.

Toy VE, Uslu MO. Do genetic polymorphisms affect susceptibility to periodontal disease? A literature review. *Niger J Clin Pract.* 2019 Apr; 22(4):445-453.

National Cancer Institute: Oral Cavity and Oropharyngeal Cancer Prevention. Updated 2/4/2016.

Rettig EM, Wentz A, Posner MR, et al. Prognostic Implication of Persistent Human Papillomavirus Type 16 DNA.

Detection in Oral Rinses for Human Papillomavirus-Related Oropharyngeal Carcinoma. *JAMA Oncol.* 2015 Oct; 1(7):907-15.

United States Preventive Services Task Force. Final Recommendation Statement Oral Cancer: Screening. November 2013.

Vieira AR, Modesto A, Marazita ML. Caries: review of human genetics research. *Caries Res.* 2014;48(5):491-506.

Yücel OO, Berker E, Mescil L, et al. Association of interleukin-1 beta (+3954) gene polymorphism and gingival crevicular fluid levels in patients with aggressive and chronic periodontitis. *Genet Couns.* 2013; 24(1):21-35.

Policy History/Revision Information

| Date | Summary of Changes |
|------------|--|
| 03/15/2021 | <ul style="list-style-type: none">Updated dental entity brand logo |
| 01/01/2021 | Template Update <ul style="list-style-type: none">Reformatted policy; transferred content to new template |
| 09/01/2020 | Supporting Information <ul style="list-style-type: none">Updated <i>References</i> section to reflect the most current informationArchived previous policy version DCP036.04 |

Instructions for Use

This Dental Clinical Policy provides assistance in interpreting UnitedHealthcare standard dental benefit plans. When deciding coverage, the member specific benefit plan document must be referenced as the terms of the member specific benefit plan may differ from the standard dental plan. In the event of a conflict, the member specific benefit plan document governs. Before using this policy, please check the member specific benefit plan document and any applicable federal or state mandates. UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Dental Clinical Policy is provided for informational purposes. It does not constitute medical advice.