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Article

The Molecular Comorbidity Network of Periodontal Disease

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Abstract: Periodontal disease, a multifactorial inflammatory condition affecting the supporting structures of the teeth, has been increasingly recognized for its association with various systemic diseases. Understanding the molecular comorbidities of periodontal disease is crucial for elucidating shared pathogenic mechanisms and potential therapeutic targets. In this study, we conducted comprehensive literature and biological database mining utilizing tools such as DisGeNET2R, Romin, and Rentrez R libraries to identify diseases sharing associated genes, proteins, or molecular pathways with periodontitis. Our analysis revealed significant molecular overlaps between periodontal disease and several systemic conditions, including cardiovascular diseases, diabetes mellitus, rheumatoid arthritis, and inflammatory bowel diseases. Shared molecular mechanisms implicated in the pathogenesis of these diseases and periodontitis encompassed dysregulation of inflammatory mediators, immune response pathways, oxidative stress pathways, and alterations in the extracellular matrix. Furthermore, network analysis unveiled key hub genes and proteins that play pivotal roles in the crosstalk between periodontal disease and its comorbidities, offering potential targets for therapeutic intervention. Insights gained from this integrative approach shed light on the intricate interplay between periodontal health and systemic well-being, emphasizing the importance of interdisciplinary collaboration in developing personalized treatment strategies for patients with periodontal disease and associated comorbidities.

Keywords: periodontal disease; comorbidities; molecular mechanisms of systemic diseases; genetic associations; biological databases; inflammatory pathways

Introduction

Periodontal disease, a chronic inflammatory condition affecting the supporting structures of the teeth, has long been recognized as a significant public health concern globally. Beyond its impact on oral health, accumulating evidence suggests that periodontal disease is intricately linked to various systemic conditions, thereby emphasizing the need for a deeper understanding of its molecular comorbidities [1]. The recognition of shared pathogenic mechanisms between periodontal disease and systemic diseases holds profound implications for both clinical management and therapeutic interventions.

Periodontal disease is an extremely prevalent condition among adults [2,3], yet not uncommon in children [4,5]. There is a diverse spectrum of inflammatory ailments that affect the periodontium, an overarching term encompassing gingiva, cementum, periodontal ligament, and alveolar bone [6]. Periodontitis typically commences with an uncontrolled inflammatory response triggered by gradual bacterial colonization of tooth surfaces and soft gingival tissues—referred to as Gingivitis [7]. However, it is generally thought that is the host's inflammatory reaction to microbial challenges that primarily instigates the degradation of the periodontium, leading to Periodontitis [8].

In Periodontitis, pathogens incite leukocytes of the innate immune system to release pro-inflammatory mediators like cytokines, which significantly contribute to the progression of chronic periodontitis (CP) [9]. Although infection is a prerequisite for periodontitis, it alone does not suffice for disease advancement. Pathogens instigate the acquired immune system, exacerbating the inflammatory condition's progression and inflicting severe damage on soft and hard periodontal tissues [9]. Individual

susceptibility tied solely to organismal immune and inflammatory responses is deemed crucial, as most signaling pathways and cellular events common to these disorders can be traced back to concurrent molecular origins [6,10].

The Genetic and Molecular Origins of Periodontitis

Genetic factors linked to susceptibility, severity, and progression of periodontitis have identified various gene variants of interest [11,12]. Notably, certain genetic polymorphisms in genes like IL1B, IL1RN, Fc γ RIIIb, VDR, and TLR4 have been associated with aggressive periodontitis susceptibility, while others in IL1B, IL1RN, IL6, IL10, VDR, CD14, TLR4, and MMP-1 are linked to chronic periodontitis [13]. The heritability of periodontal disease susceptibility has been discussed extensively, with studies estimating a heritability of up to 50% after adjusting for behavioral and environmental factors, although no evidence of heritability has been found in gingivitis, a precursor to periodontitis [14]. Genome-wide association studies have provided valuable insights into the genetics of periodontal disease, revealing heritability dependencies and identifying associated loci, with most of them located in non-coding genomic regions that likely modulate gene expression through regulatory interactions [15]. However, pinpointing causal variants remains challenging in GWAS, hindering elucidation of molecular mechanisms crucial for diagnostics and therapeutics. Nevertheless, systematic reviews and meta-analyses have identified significant associations between genetic variants in genes like IL-1A, IL-1B, IL-6, IL-10, MMP-3, and MMP-9 and periodontitis risk [16].

Furthermore, investigations combining periodontal disease with other conditions, such as cardiovascular diseases, have uncovered potential shared genetic backgrounds. Studies have identified genes like ANRIL/CDKN2B-AS1, PLG, and CAMTA1/VAMP3 implicated in both periodontitis and coronary artery disease pathogenesis, shedding light on functional features and accounting for some missing heritability of periodontal disease [17]. Additionally, joint genetic and functional studies have highlighted disrupted immunogenetic blueprints associated with inflammation, revealing a signature of over 65 genes involved in inflammatory processes and their association with cardiovascular diseases [18]. Genes related to bone morphogenetic and developmental processes have also been implicated in periodontal disease. For instance, single nucleotide polymorphisms (SNPs) in BMP2, BMP4, SMAD6, and RUNX2 genes have been significantly associated with persistent apical periodontitis, suggesting epistatic interactions contributing to increased risk [19]. Moreover, larger genetic variants like long runs of homozygosity (LROH) spanning multiple genes have been linked to various stages of periodontitis severity [20].

The complex relationship between microbial infections and hosts, particularly in chronic infections like those underlying periodontal disease, involves intricate molecular mechanisms triggering and sustaining infection-associated inflammation [21]. Genetic immunodeficiencies like leukocyte adhesion deficiency-1 (LAD1) result in severe periodontal inflammation and bone loss, with recent evidence implicating enhanced inflammatory responses mediated by IL-17 [22,23]. Genetic variants in chemokine receptor CXCR2 have also been associated with susceptibility to prolonged periodontal bacteremia leading to chronic periodontitis [24].

Periodontitis and Systemic Health

Historically, the association between oral health and systemic health has been debated, with early observations often dismissed as anecdotal. However, over the past few decades, epidemiological studies have consistently demonstrated compelling associations between periodontal disease and a spectrum of systemic conditions, including cardiovascular diseases, diabetes mellitus, rheumatoid arthritis, and inflammatory bowel diseases. These associations transcend mere coincidence and suggest underlying molecular connections that warrant exploration.

The advent of high-throughput technologies and bioinformatics tools has revolutionized our ability to dissect complex molecular networks underlying disease pathogenesis. In this context, integrative approaches that leverage literature mining and biological databases provide valuable

insights into the shared molecular signatures and pathways between periodontal disease and its comorbidities. By systematically analyzing genetic associations, protein interactions, and pathway crosstalk, researchers can unravel the molecular underpinnings of these complex relationships.

Understanding the molecular comorbidities of periodontal disease holds immense promise for advancing both oral and systemic health. By elucidating shared molecular mechanisms and identifying novel therapeutic targets, this interdisciplinary approach has the potential to transform clinical practice and improve patient outcomes in the management of periodontal disease and its associated comorbidities.

This paper aims to review and synthesize the current knowledge on the molecular comorbidities of periodontal disease, with a particular focus on diseases sharing associated genes, proteins, or molecular mechanisms. By integrating data from diverse sources, including DisGeNET2R, Romin, and Rentrez R libraries, we seek to elucidate the intricate interplay between periodontal health and systemic well-being at the molecular level. Furthermore, we aim to identify potential therapeutic targets and pathways for intervention, thereby paving the way for personalized treatment strategies tailored to individuals with periodontal disease and associated systemic conditions.

Materials and Methods

Molecular Association Analysis

Primary genetic associations with periodontal disease was performed using the R Entrez and R0mim libraries. The R Entrez library (<https://cran.r-project.org/web/packages/rentrez/index.html>), provides a powerful interface for accessing biological data from the National Center for Biotechnology Information (NCBI) through the Entrez Programming Utilities (E-utilities) API. The R0mim library (<https://github.com/davetang/romim>), in turn was used to query the Online Mendelian Inheritance in Man (OMIM) database (<https://www.omim.org/>). Both database tools were used first, to look up for molecular information about periodontal disease, this information allowed to generate customized queries used to gather further information about diseases sharing genes and other biomolecules, as well as functional biological and biochemical pathways with periodontitis.

Molecular Comorbidity and Diseasome Networks

Once preliminary queries were carried out, a systematic *molecular comorbidity network* analysis and a *diseasome* network construction were performed by using the *disgenet2r* package (<https://www.disgenet.org/disgenet2r>). *disgenet2r* is an Application Programming Interface (API) to the *DisGeNET* database (<https://www.disgenet.org/>). *DisGeNET* is a discovery platform containing one of the largest publicly available collections of genes and variants associated to human diseases. *DisGeNET* consolidates information sourced from meticulously curated repositories, GWAS catalogs, animal models, and scholarly publications. The data within *DisGeNET* are uniformly annotated using standardized vocabularies and collaborative ontologies. Furthermore, *DisGeNET* offers various novel metrics aimed at aiding the prioritization of relationships between genotypes and phenotypes. An annotated pipeline to reproduce the workflow to build comorbidity and diseasome networks for periodontitis can be found at github.com/CSBIG/.

Molecular Comorbidity Network Reconstruction

A molecular comorbidity network, defined as a set of diseases that share associated genes, proteins or biomolecular pathways with a given disease was built for periodontitis using the module of *disgenet2r*. Parameters were set to include only *Curated* molecular interactions, i.e., genetic and biomolecular associations supported by direct experimental evidence. Breadsearch score was set to 0.4 (medium-high) and confidence score was set to 1 (maximum confidence based on the available experimental evidence). *PODNet* was used not only to build the comorbidity network but also to generate a heatmap of shared molecules among the different diseases and a *Protein class* heatmap

that displays functional information of the different biomolecules for the different diseases in the comorbidity network.

Diseasome Network Reconstruction

Diseasomes are network-based approaches that allow researchers to explore the complex relationships between diseases, identify common underlying mechanisms, and uncover potential targets for therapeutic intervention. They serve as valuable resources for studying disease etiology, understanding disease comorbidities, and developing strategies for precision medicine and personalized healthcare. Diseasome networks centered in periodontal disease were built using the `disease2disease_by_gene` module of `disgenet2r`. Only *Curated* associations were retained and the maximum number of connected diseases was considered. A disease-disease network centered in Periodontitis and a full diseasome of periodontitis-associated diseases were built. A bar plot visualization depicting number and fraction of shared genes were also generated using the `disease2disease_by_gene` module.

Functional Enrichment Analysis

Functional enrichment analysis, was performed by using the `gProfiler2` tool (<https://cran.r-project.org/web/packages/gprofiler2/index.html>) to mine the *g:Profiler* webserver (<https://biit.cs.ut.ee/gprofiler/gost>). Hypergeometric tests were applied to the list of periodontitis comorbidity network genes. Only annotated genes were considered. Statistical significance was set for all categories with `g:SCS` corrected p-value (equivalent to non-independent FDR tests, i.e., is a form of multiple testing correction that considers that Gene Ontology (GO) categories for instance form a hierarchy and thus are not all independent) less than 0.05. Values less than $1E^{-16}$ were *capped* in the visualizations. `gProfiler` parameters used were as follows: version `e111_eg58_p18_30541362`, query date: 28/3/2024,14:37:37, organism: *hsapiens*.

A general workflow for the methods and analyses performed in this work is presented in Figure 1.

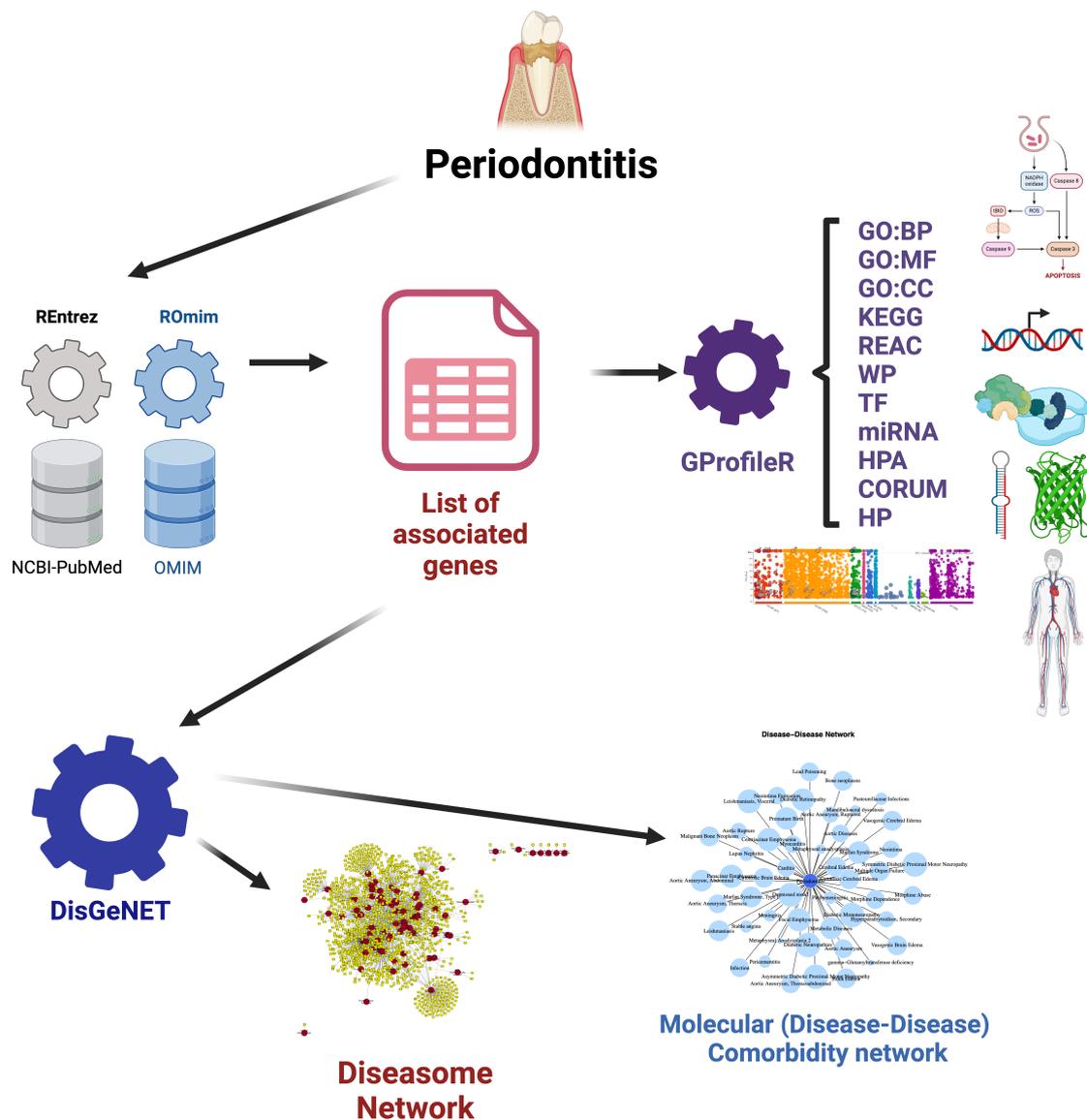


Figure 1. Workflow for the analysis presented. A list of Periodontitis associated genes was curated from a literature (NCBI-Pubmed) and database (OMIM) rigorous search. This list was used to mine high-confidence reported associations for diseases and conditions sharing genetic and molecular hits with periodontitis (DISGENET) to build Comorbidity and Diseasome Networks. The same list was also used to mine (GProfileR) biomolecular, pathway and phenotype databases and to perform statistical tests for functional over-representation.

Results

Molecular Comorbidity Network

The molecular comorbidity network of periodontitis spanned over 2,219 curated gene-disease interactions involving 80 different disease conditions. The top 10 periodontitis comorbidity conditions ordered by the gene PLI index of their leading gene interactions are: *Malignant neoplasm of breast, Breast Carcinoma, Malignant neoplasm of prostate, Atrial fibrillation, Depressive disorder, Obesity, Adenocarcinoma, Diabetes mellitus, non-insulin dependent, Rheumatoid arthritis, Alzheimer's Disease*. Gene PLI (Probability of being Loss-of-function Intolerant) is an estimate of the probability that a gene is intolerant to loss-of-function (LoF) mutations, meaning that these mutations are likely to have a deleterious effect on the function of the gene. The PLI score is derived from large-scale sequencing data, such as data from the

Exome Aggregation Consortium (ExAC), which aggregates exome sequencing data from thousands of individuals. Genes with high PLI scores are less likely to be found in the general population and may be thus more likely to cause severe phenotypic consequences when present.

In DisGeNET, the gene PLI score provides valuable information about the functional importance of a gene and its potential relevance to human diseases. Genes with high PLI scores may be prioritized for further investigation in disease studies, as mutations in these genes are more likely to contribute to disease susceptibility or pathogenesis. For the full annotated list of 2,219 gene-disease interactions covering 80 highly significant comorbidities of periodontitis, please refer to **Supplementary Table 1**.

Periodontitis Centered Disease Network

A periodontitis-centered comorbidity network is presented in Figure 2. It can be noticed that periodontitis comorbidities are quite diverse in nature, ranging from expected oral conditions such as *Pericementitis*, to inflammatory, immune and autoimmune diseases, infections, cardiovascular damage, to neoplasms and psychiatric conditions including substance abuse. When we consider this in addition to the information reported in **Supplementary Table 1**, it calls to attention the *systemic* nature of periodontal disease.

Figure 3 presents a plot depicting the absolute number and relative size of the intersection of the gene sets (Jaccard Index) associated to the different diseases with periodontitis. It can be observed that some diseases share up to 25% of their associated genes with Periodontitis.

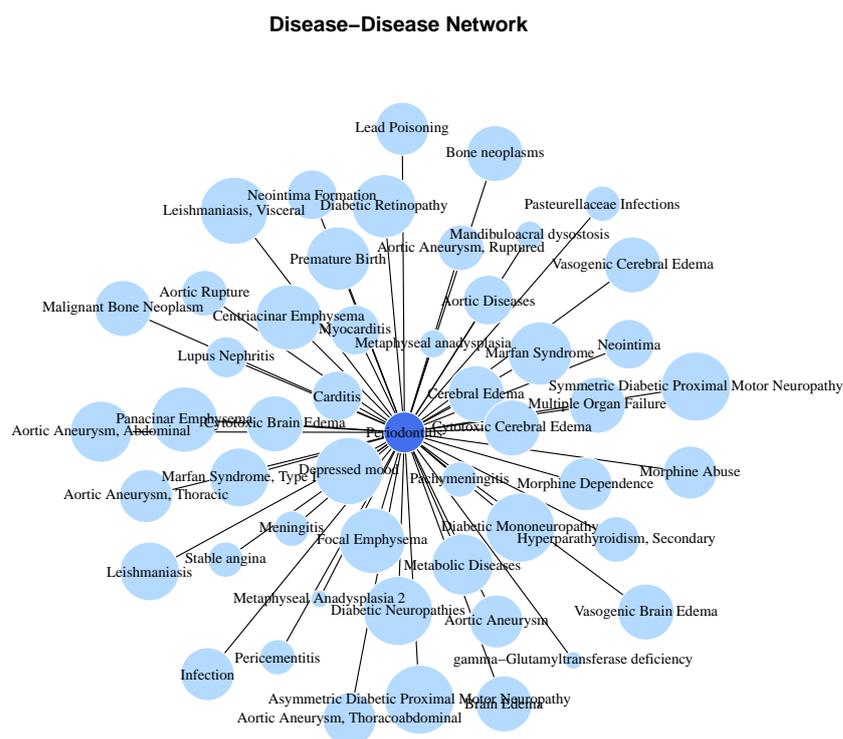


Figure 2. A periodontitis centered molecular comorbidity network. Diseases sharing biomolecular players with Periodontitis are shown. Node sizes correspond to the Jaccard index (relative size of the intersection of the gene sets) with Periodontitis.

Within this intricate network, the Top10 diseases linked to a higher number of genes (in parentheses) are *Malignant neoplasm of breast* (278), *Breast carcinoma* (260), *Malignant neoplasm of prostate* (164), *Diabetes mellitus, Non-Insulin-Dependent* (116), *Atrial fibrillation* (112), *Obesity* (106), *Rheumatoid arthritis* (77), *Depressive disorder* (75), *Alzheimer's disease* (66) and *Asthma* (54). The top10 genes (actually 11 genes because of ties) implicated in the higher number of diseases (also in parentheses) in this diseasome are: *TNF* (24), *IL6* (23), *PTGS2* (14), *IL10* (13), *NOS3* (12), *IL1B* (12), *VEGFA* (11), *BCL2* (11), *STAT3* (11), *LEP* (11) and *TP53* (11). For a comprehensive list please refer to **Supplementary Table 2**.

Analyzing the relative numbers of genes involved in the molecular diseasome network associated with periodontitis reveals interesting patterns and potential insights into disease relationships. Some diseases exhibit a higher number of shared genes with periodontitis compared to others. For example, diseases like *Alzheimer's disease*, *Depressive disorder*, and *Breast carcinoma* show a relatively large number of shared genes with periodontitis, suggesting closer molecular associations or shared genetic underpinnings (**Supplementary Table 2**).

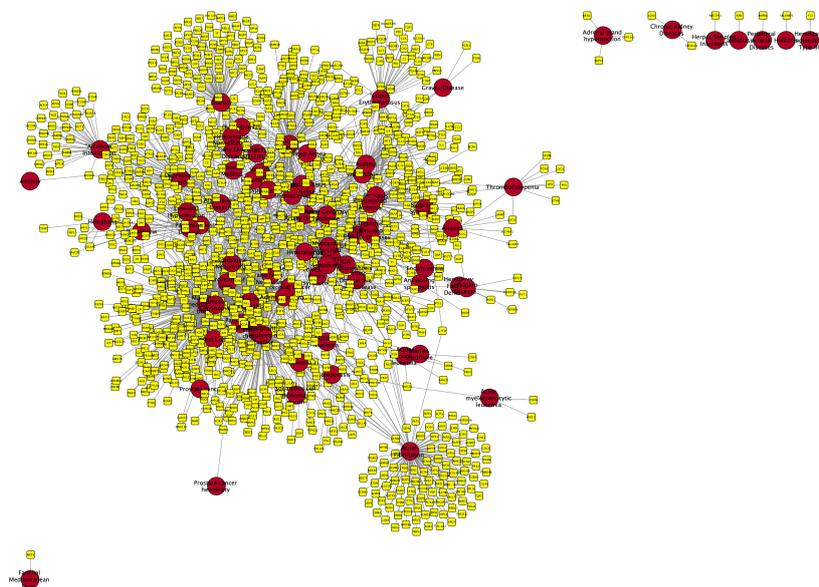


Figure 4. Molecular Diseasome network depicting the interconnections created between periodontitis other diseases sharing common genetic associations. Red nodes correspond to the more significant health conditions associated with periodontitis. Yellow nodes correspond to the genes linked with each condition. This bipartite network consists in 80 disease-nodes, 1,197 gene-nodes and 2,212 genetic associations between them.

Looking at groups of somewhat similar diseases in the list provided in **Supplementary Table 2**, we can observe several clusters based on disease categories or shared pathophysiological mechanisms. We have for instance the following general categories:

1. **Cardiometabolic Diseases:** Diseases like *Acute coronary syndrome*, *Atrial fibrillation*, *Coronary artery disease*, and *Coronary heart disease* are all cardiovascular conditions that share a common underlying feature of vascular dysfunction or cardiac abnormalities. The presence of shared genes between these diseases (say, *Myocardial infarction*, *Atrial fibrillation*, *Cerebrovascular accident*, or *Coronary artery disease*) and periodontitis suggests potential molecular links related to inflammation, endothelial dysfunction, or immune dysregulation, which are known to contribute to both periodontal disease and cardiovascular disorders. Other conditions related to metabolism associated with cardiovascular health and present in the molecular (gene) comorbidity space of periodontitis are: *Diabetes mellitus, non-insulin-dependent*, *Non-alcoholic fatty liver disease* and *Dyslipidemias*, as well as *Essential hypertension* and *Peripheral arterial diseases*.
2. **Inflammatory Disorders and Immunological Diseases:** Conditions such as *Rheumatoid arthritis*, *Crohn's disease*, *Chronic obstructive airway disease*, and *Asthma* are all characterized by chronic inflammation and immune dysregulation. These diseases share overlapping inflammatory pathways with periodontitis, indicating potential common mechanisms contributing to their co-occurrence. The shared genes between these inflammatory disorders and periodontitis suggest that immune-mediated processes may play a critical role in the interplay between oral health and systemic inflammation as exemplified for instance, in *Sjogren's Syndrome*, *Rheumatoid arthritis* and *Lupus erythematosus systemic*, but also in *Psoriasis*, *Glomerulonephritis*, and *Graves disease*.
3. **Cancer:** Several types of cancer are represented in the list, including *Breast cancer*, *Cervical cancer*, *Carcinoma of lung*, and *Adenocarcinoma*. Although cancer types vary in their tissue origins and molecular profiles, they all involve dysregulated cell growth and proliferation. The presence of shared genes between these cancers and periodontitis may reflect shared molecular pathways related to cell cycle regulation, tumor progression, or immune evasion, highlighting potential links between periodontal health and cancer development such is the case of *Breast carcinoma*, *Pancreatic Neoplasm*, and *Cervical cancer*, *Prostate cancer*, as well as *Multiple myeloma*, *Hodgkin disease*, and some types of *Leukemia*.
4. **Neurological and Psychiatric Disorders:** Diseases like *Alzheimer's disease* and *Depressive disorder* represent neurological and psychiatric conditions that have been associated with chronic inflammation and immune activation. The shared genes between these disorders and periodontitis suggest potential bidirectional relationships, where systemic inflammation may contribute to neuroinflammation and cognitive decline, while neurological conditions may influence systemic inflammatory responses and periodontal health.
5. **Other Diseases:** There are other less-general conditions such as *Pneumonia*, *Osteoporosis*, *Amyloidosis*, aside from hormonal diseases like *Polycystic ovary syndrome*, *Adrenal gland hypofunction*, *Hereditary angioedema type III*, as well as *Chronic kidney diseases* and connective tissue diseases like *Marfan syndrome* that also share relevant biomolecular players with Periodontitis.

As we can see, groups of somewhat similar diseases in the list exhibit commonalities in pathophysiological mechanisms, such as inflammation, immune dysregulation, and cell proliferation, which may contribute to their co-association with periodontitis in the molecular disease network. Further context upon this central issue will be presented in the discussion.

More specific information can be derived of the top genes in significance within this disease network that can be found in Figure 6. One can see a number of well known disease-associated genes ranging from DNASEs like DNASE1, tyrosine kinases such as PTPN22, PIK3CA, AKT2, and oncogenes such as BRCA 1, tumor suppressors like PTEN and ATM, all commonly associated with neoplasms; nuclear receptors such as PPARG associated to metabolic diseases, extracellular matrix glycoproteins such as FBN1, often found in inflammatory and collagen related diseases, etc.

Further systemic functional information can be found in the heatmap shown in Figure 7. There one can see a summary of the different biological functions carried out by the set of genes/proteins within the periodontitis diseaseome. A prevalence of Enzymes as well as Signaling and Kinase proteins can be seen associated with most of the different diseases. Still relevant, though less generalized, is the presence of Transporter, Nucleic acid binding and Enzyme modulator proteins.

Other functional categories however, even if not present in most of the diseases are prevalent (as a class) within a given one. Such is the case of Transcription factors and Cellular structure proteins in *Acute coronary syndrome* or G-protein coupled receptors in *Rheumatoid arthritis*, for instance.

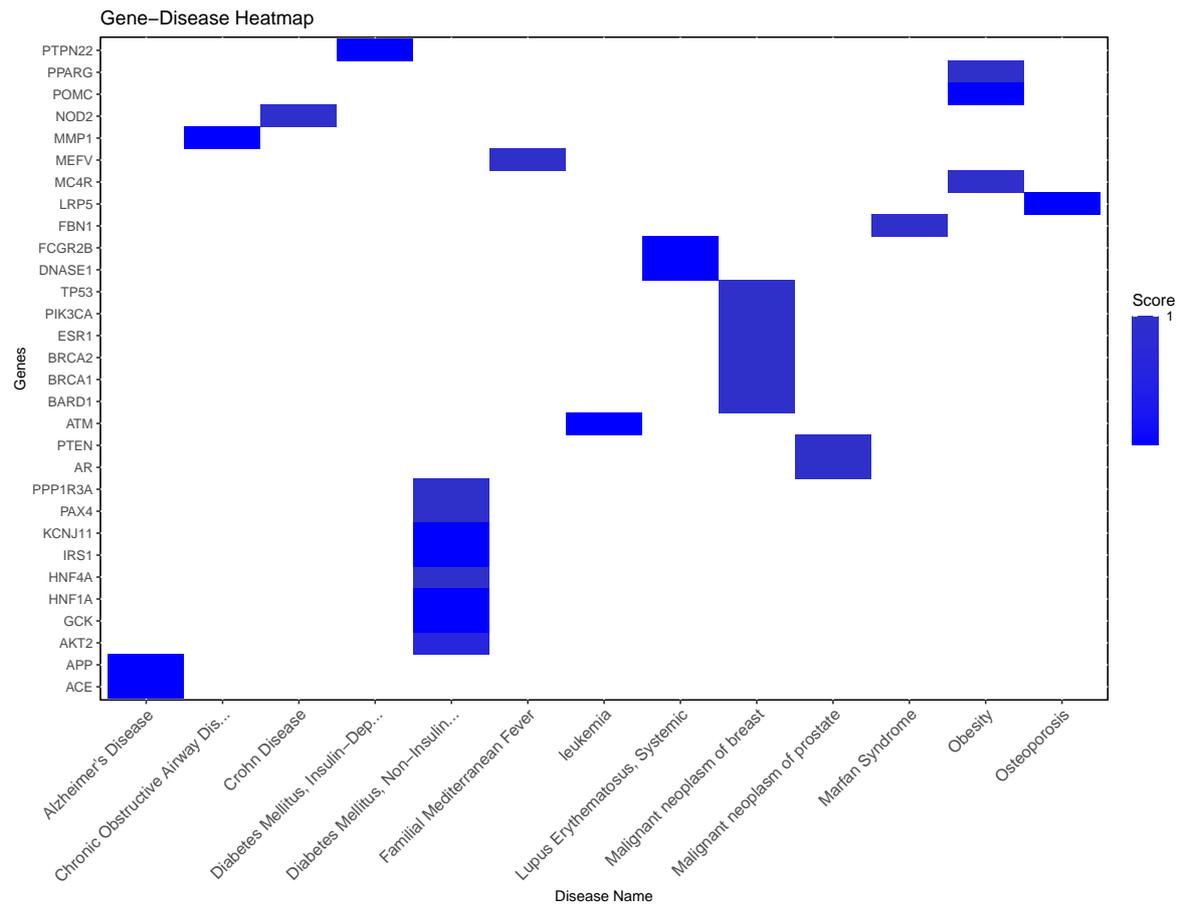


Figure 6. Top significant genes in the gene-disease map projected from the Periodontitis associated diseaseome.

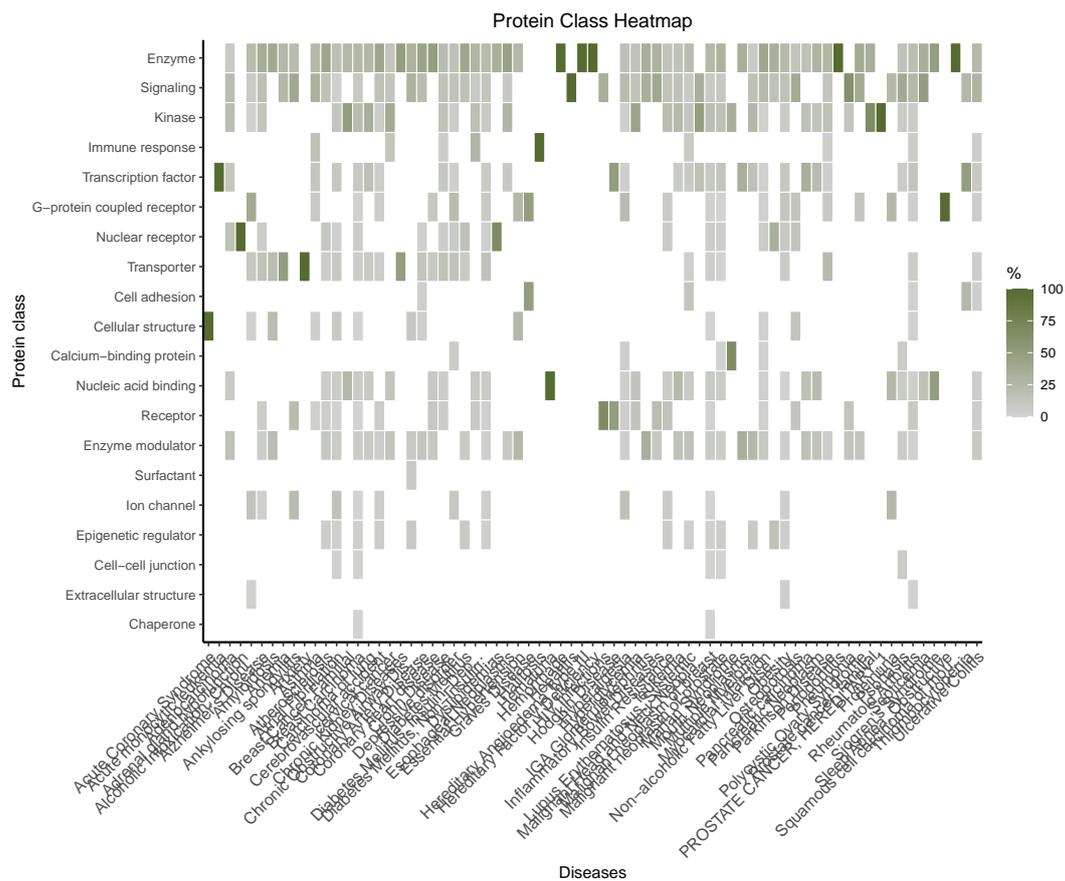


Figure 7. Heatmap of protein classes for the genes in the Periodontitis associated diseasome.

Functional Enrichment of the Diseasome Genes

Biological function enrichment analysis plays a crucial role in understanding the underlying molecular mechanisms and pathways associated with periodontitis within the context of the diseasome. Periodontitis is a multifactorial inflammatory disease influenced by various genetic, environmental, and microbial factors. By conducting enrichment analysis on genes or proteins associated with periodontitis within the broader diseasome network, we have been able to identify common biological functions, pathways, and processes that are dysregulated in both periodontitis and closely-related diseases as mentioned.

One key aspect of biological function enrichment analysis is its ability to uncover shared pathways and molecular signatures among diseases within the diseasome. For instance, enrichment analysis (see Figure 8) revealed enrichment of inflammatory pathways, immune response processes, or extracellular matrix remodeling functions in both periodontitis and other inflammatory diseases such as rheumatoid arthritis or inflammatory bowel disease. This suggests common underlying mechanisms driving inflammation and tissue destruction across different diseases within the diseasome. Understanding these shared pathways not only enhances our knowledge of disease pathogenesis but also offers potential targets for therapeutic intervention that may have broader implications beyond periodontitis alone. Additionally, biological function enrichment analysis can help prioritize genes or proteins for further experimental validation, providing guidance towards key players in the pathophysiology of periodontitis and its interplay with other systemic conditions within the diseasome network.

A glimpse at Figure 8 reveals an outstanding issue. There is a very large number of highly significant biological features enriched in the periodontitis-associated diseasome. There are 221 Gene Ontology (GO) Molecular Function (GO:MF) categories, 2720 GO biological process categories (GO:BP), 176 GO cellular components (GO:CC), 153, 174 and 270 molecular pathways as reported by the KEGG,

Reactome (REAC) and Wikipathways (WP) databases respectively. There are also 18 statistically significant transcription factor binding site signatures, 38 associated microRNAs, 113 hits from the Human Protein Atlas (HPA), 24 mammalian protein complexes from the CORUM database and 506 matching conditions in the Human Phenotype Ontology (HPO), a standardized vocabulary of phenotypic abnormalities encountered in human diseases. The full list of features has been included as **Supplementary Table 3**.

Some outstanding results include strong binding in membrane receptor and immune signaling, enzymatic activity and transcriptional regulation (GO:MF); response to stress, proliferation, cell adhesion and communication, development and regulation of cell death mechanisms (GO:BP); nearly all cellular locations are enriched a fact that, in addition to the just mentioned GO:MFs and GO:BPs, point out to extremely systemic phenomena. From the multiplicity of biochemical pathways in the diverse databases, we can highlight those related to extreme abnormalities in cancer, hormone deregulation, muscle failure, inflammation, senescence and atherosclerosis. Transcription factor (TF) binding motifs (See Figure 8 and **Supplementary Table 3**), belong to the MAZ, GKLF, WT1, MED8, ZNF148, OPATZ, CKROX, SMAD3, EGR-1, and PAX4 TFs. A number of these TFs are indeed master regulators associated to development (e.g., SMAD3, PAX4).

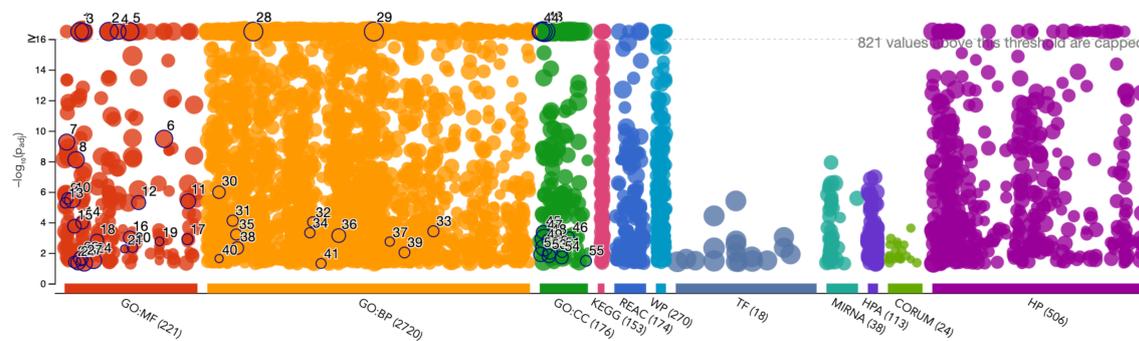


Figure 8. Functional enrichment analysis (over-representation) of genes shared by periodontitis and its comorbidity-related diseases. Notice that g:SCS-corrected p-values less than $1E-16$ are capped.

We can also notice how different regulatory non-coding transcripts, corresponding to 38 miRNAs are associated with the core genes in the periodontitis diseasome. Each one of these regulatory transcripts is able to regulate a large number of gene targets (from a few dozens to close to a hundred) in the periodontitis diseasome (to examine the full list of miRNAs and their gene targets please refer to **Supplementary Table 3**). An additional dimension of complexity is the one formed by active proteins (113) and protein complexes (24) reported as significantly enriched in the periodontitis diseasome. Furthermore, in addition to the 80 diseases directly related to periodontitis by sharing associated genes, there is a staggering set of 506 different health conditions reported significantly enriched in the set of genes in the periodontitis diseasome (see **Supplementary Table 3**).

Discussion

In recent years, numerous research and clinical investigations have documented connections between periodontitis and various systemic inflammatory conditions, including *Arthritis*, *Type 2 diabetes mellitus*, and *Atherosclerosis* [3]. The infectious, molecular, and physiological underpinnings of these relationships have been explored in previous sections. Now, we delve into their implications for the onset and progression of a wide spectrum of diseases, encompassing cardiovascular disease, gastrointestinal and colorectal cancer, diabetes and insulin resistance, *Alzheimer's disease*, respiratory tract infection, adverse pregnancy outcomes, among others [2,25].

Understanding the association between periodontitis and other systemic inflammatory diseases gains significance due to the availability of therapeutic interventions, such as cytokine-based treatment

strategies, with potential benefits for both periodontitis and systemic health [26]. Immune markers linking CP and diabetes, such as glycation dynamics and TNF- α , have been identified as reliable indicators of inflammation in gingival crevicular fluid and serum [27]. The glycemic status has been linked to periodontitis through mechanisms of systemic inflammation [28]. Moreover, interactions between local inflammation and innate immune responses have been observed in bone marrow stem cells co-cultured with macrophages obtained from diabetic periodontitis patients, further emphasizing the interplay between these conditions [29]. Conversely, evidence suggests that periodontal treatment can mitigate systemic inflammation in type 2 diabetes [30].

Recent experimental (mouse) models have demonstrated how periodontitis can induce systemic inflammation, exacerbating atherosclerosis through mechanisms driving endothelial-mesenchymal transitions [31,32]. Similar mechanisms have been discussed in the clinical care of human patients with lacunar infarct [33]. In what follows, we will further analyze different disease categories that share molecular origins with Periodontitis.

Cardiometabolic Diseases

Consistent epidemiological evidence underscores the association between periodontitis and heightened risk for cardiovascular diseases (CVDs) [26,34]. Given the inflammatory nature of vascular diseases like *Atherosclerosis*, where immune reactions mediated by cytokines contribute to pathogenesis, the link with periodontitis is not unexpected [26]. Chronic infections in the vessel wall can incite a pro-inflammatory milieu, driving autoimmunity to vascular cells and initiating *Atherosclerosis* [35]. Consequently, the sustained inflammatory state of periodontitis correlates with increased cardiovascular risk, with bacteremia and systemic inflammation precipitating endothelial lesions and vascular wall inflammation [33]. Moreover, periodontal treatment has been shown to reduce systemic inflammation and endothelial dysfunction, albeit with limited evidence of modifying atherosclerotic vascular disease outcomes [26,30].

Persistent periodontal inflammation exacerbates endothelial dysfunction and vascular inflammation [10,36]. Notably, inflammatory mediators like TNF- α and IL-6 impair nitric oxide production and endothelial function, contributing to atherosclerosis and CVD development [10]. Periodontitis is associated with inflammation, the molecular players common to both types of disease may be indeed related to pathways impacting endothelial function and vascular structure [10]. Severe periodontitis heightens risks for acute myocardial infarction and stroke, with periodontal treatment also significantly reducing their incidence [2,10].

Endocrine and metabolic dysfunction is another molecular and physiological component of the association of Periodontitis and Cardiometabolic diseases. *Non-insulin-dependent Diabetes mellitus* for instance has been associated with periodontal disease for at least two decades [37,38]. This relationship has indeed many components, including the role of inflammation and signaling crosstalk [39,40], immune responses and immune cell infiltrates [41,42], the effects of the microbiome [43–45], as well as epidemiologic and common risk factors [46–48]. *Insulin resistance* has also been considered in these associations [49–51]. *Obesity* is a complex trait that has been related to Periodontitis [52]. Similarly, molecular, epidemiological and lifestyle factors conform this association [53–56].

Several conditions related to metabolic disruption have been discussed regarding their connections with periodontal disease, such is the case of *Dyslipidemias* [57–60], and *Non-alcoholic fatty liver disease* (now renamed Metabolic Dysfunction-Associated Steatotic Liver Disease (MASLD)) [61–64], in the latter case a clearer genomic molecular picture of the associated mechanisms has even been proposed [65]. Heart conditions with molecular links to Periodontitis also include *Atrial fibrillation* [66–68], *Coronary heart disease* [69–73], as well as vascular maladies such as *Essential hypertension* [74–79] and *Peripheral arterial disease* [80–84].

Inflammatory and Immunological Disorders

The comorbidity profile of periodontal disease encompasses various conditions, including autoimmune disorders like *Rheumatoid arthritis* (RA), *Systemic lupus erythematosus* (SLE), and *Inflammatory bowel diseases* (IBD). Disturbances in the delicate balance between innate and adaptive immunity, often triggered by chronic infections, may lead to autoimmune responses. For instance, in RA, patients exhibit increased bacterial loads and dysbiotic oral microbiota similar to those seen in periodontitis, with shared genetic susceptibility factors contributing to both conditions [3,85,86]. The inflammation observed in RA synovitis mirrors the immune response seen in periodontitis, involving a complex network of cytokines and immune cells that contribute to joint damage [87,88]. Additionally, periodontal pathogens like *P. gingivalis* may exacerbate RA progression by increasing mucosal permeability and facilitating immune cell migration to the joints [89]. Similar parallels exist between periodontitis and SLE, where disrupted microbiome composition and upregulated pro-inflammatory cytokines contribute to disease pathogenesis [10,90].

IBDs, such as ulcerative colitis and Crohn's disease, share common inflammatory pathways with periodontitis, potentially arising from dysbiotic intestinal microbiota and genetic predisposition [91,92]. Furthermore, periodontal disease has been linked to hematological conditions like leukemia and thrombocytopenia, where oral manifestations and impaired immune function contribute to disease progression and oral complications [93–96].

Other conditions related to immune and inflammatory changes that share molecular basis with Periodontitis include *Psoriasis* [97–100], *IGA glomerulonephritis* –though in spite of the molecular association, most studies have centered around the microbiological component of this association [101,102], *Graves disease* [103–105] and *Sjogren's syndrome* [106–108], although in this latter case some studies have found inconsistencies and ambiguities between the epidemiological and biomarker findings [109–111].

Cancer

In recent years, numerous research and clinical studies have unveiled connections between periodontitis and several systemic conditions, including cancer [112]. While the precise relationship remains debated, individuals with periodontitis exhibit an elevated risk of fatal cancer, particularly *Lung cancer*, other consistent correlations have been observed for *Oral and esophageal carcinomas* [113–115]. For *Breast cancer*, meta-analyses have confirmed significant associations with periodontitis, albeit the risk diminishes in patients with a history of periodontitis who underwent periodontal treatment [116]. Importantly, it has been stated that periodontitis leading to tooth loss is associated with increased cancer risks [117,118].

Systemic inflammation, a hallmark of periodontitis, is implicated in various phases of cancer development, from initiation to metastasis, reflecting the complex interplay between inflammation, immune responses, and genetic instability [26]. Notably, studies have shown positive correlations with *Pancreatic, Head and neck, and Lung cancers* [2,112]. Periodontal pathogens, particularly *P. gingivalis* and *F. nucleatum*, have been implicated in oral cancer pathogenesis through mechanisms involving direct interaction with oral epithelial cells and modulation of the host immune response [119]. Furthermore, chronic inflammation may influence carcinogenesis and cancer mortality, as observed in *Breast cancer*, where periodontal inflammation promotes the recruitment of *Metastatic breast cancer* cells [120,121].

Other neoplasms sharing some genetic origins with periodontal disease are *Prostate Cancer* (in particular the hereditary forms) [122], however an additional association related to periodontal pathogens has also been discussed [122].

Neurological and Psychiatric Diseases

Periodontitis exhibits intricate connections with neuroinflammation and neurodegenerative diseases, notably *Parkinson's* and *Alzheimer's disease* (AD). Studies have revealed a higher prevalence of periodontitis in patients with *Parkinson's disease*, suggesting a bidirectional relationship between

neurological conditions and periodontitis [2,10,123–125]. Evidence suggests that pro-inflammatory cytokines released from ulcerated periodontal pockets may weaken the blood-brain barrier, facilitating the entry of inflammatory mediators into the brain and triggering neurodegenerative cascades [10,126].

Activated glial cells in the brain produce inflammatory cytokines similar to those implicated in AD, exacerbating neuronal damage caused by β -amyloid plaques and τ aggregates [127]. The presence of periodontal pathogens, such as *P. gingivalis* and *T. denticola*, in peri-postmortem human brains with AD further supports the role of these pathogens in brain inflammation associated with neurodegenerative diseases [2]. Moreover, the association between depression and chronic periodontitis underscores the involvement of systemic inflammatory processes in psychiatric conditions, implicating neuroinflammation in depressive disorders [36,128,129]. Inflammatory dysregulation is also involved in the sensitisation of nociceptive fibres, thus leading to pro-pain processes that may unleash *Hyperalgesia* [130–133].

Respiratory Diseases

Some diseases of the respiratory tract share also molecular and other factors with Periodontitis [134–136]; Such is for instance the case of *Asthma* [137–140], *Pneumonia* [141–143], *Sleep apnea* [144–148] and *Chronic obstructive airway disease* (COAD/COPD) [149–152]. We can notice, however, that most studies in the current literature (with some exceptions such as in COAD/COPD) consider these associations based on epidemiological rather than relying on their molecular and mechanistic origins which gain support in view of our results presented above.

Musculoskeletal and connective tissue diseases

More comprehensive –yet still incomplete– molecular and mechanistic links have been established between Periodontitis and musculoskeletal and connective tissue diseases such as *Osteoporosis* [153–158], *Amyloidosis* [159–162] and *Marfan syndrome* [163–167]. The common axis to these maladies seems to be crosstalk between inflammation and tissue development pathways [168,169] involving in some cases oxidative stress deregulation [170–174].

Hormonal Diseases

Common genetic molecular origins between Periodontitis and conditions related to hormone dysruption have also arise in our analysis. For instance, *Polycystic ovary syndrome* [175–178], *Adrenal gland hypofunction* [179–182] and *Hereditary angioedema type III* [183–186]. Interestingly it seems that a common link between many of the molecular pathways involved is via crosstalk with the complement system [187–191].

Kidney Diseases

Oxidative stress also plays a role in the connections between Periodontitis and *Chronic kidney disease* [192–194], under some circumstance via mechanisms driven by intertwining with glutathione [195], phosphatidylcholine [196] or even vitamin D [197] metabolism. Other mechanisms and risk associations have been found though [198–201].

Some Open-Ended Avenues for Future Inquiry

Interestingly, some diseases in the network are seemingly unrelated to periodontitis from a clinical standpoint, such as *Acute monocytic leukemia*, *Cervical cancer*, and *Alcoholic intoxication*. However, the presence of shared genes between these diseases and periodontitis (See **Supplementary Materials 2**) suggests possible molecular connections or shared pathogenic mechanisms that warrant further investigation. As previously mentioned, the immune dysregulation and chronic inflammation characteristic of periodontitis may intersect with pathways involved in cancer development or hematological disorders, contributing to their co-association in the diseasome network.

The top10 genes (actually 11 genes because of ties) implicated in the higher number of diseases (number of hits in parentheses) in this diseasome are: *TNF* (24), *IL6* (23), *PTGS2* (14), *IL10* (13), *NOS3*

(12), *IL1B* (12), *VEGFA* (11), *BCL2* (11), *STAT3* (11), *LEP* (11) and *TP53* (11). For a comprehensive list please refer to **Supplementary Table 2**. One can see that, unsurprisingly, most of these molecules are associated with immunity and signaling pathways.

The extent to which these genes are able to modulate relevant biological functions from inflammation, hormone function, metabolism, development and differentiation processes, nutrient intake and processing, cell cycle and DNA repair further highlights their relevance in multimorbidity associated with periodontal disease. This, in turn help us to provide a molecular and physiological basis [32,202–205] to the growing body of epidemiological evidence on these associations [206–210]. Thus systematic exploration of the biologically functions of these molecules in the context of such (and other potential) comorbidities seems to be a worth pursuing endeavor.

Conclusions

This study aimed to provide a comprehensive analysis of the molecular comorbidity network of periodontal disease, revealing extensive gene-disease interactions that highlight the systemic nature of periodontitis. By leveraging robust bioinformatics tools and databases, we identified significant overlaps in genetic and molecular pathways between periodontitis and a wide array of systemic conditions. Our findings underscore the importance of inflammatory mediators, immune response pathways, oxidative stress pathways, and extracellular matrix alterations in the shared pathogenesis of these diseases.

Notably, the identification of key hub genes and proteins central to the crosstalk between periodontal disease and its comorbidities offers promising targets for therapeutic intervention. The diseases most strongly linked to periodontitis, including cardiovascular diseases, diabetes mellitus, rheumatoid arthritis, and inflammatory bowel diseases, are characterized by shared molecular mechanisms that may inform the development of personalized treatment strategies.

The visualization of the periodontitis-centered comorbidity network and the associated diseaseome highlights the complexity and interconnectedness of these conditions. The entangled web of interactions emphasizes the need for interdisciplinary collaboration in both research and clinical practice. Our integrative approach not only advances the understanding of the molecular underpinnings of periodontal disease and its comorbidities but also sets the stage for future investigations aimed at unraveling the intricate relationships between oral health and systemic diseases.

In conclusion, this study elucidates the molecular comorbidities of periodontal disease, providing valuable insights into the shared pathogenic mechanisms and potential therapeutic targets. By integrating literature mining and biological database interrogation, we have identified a broad spectrum of diseases sharing significant molecular overlap with periodontitis. This overlap encompasses critical genes, proteins, and biological pathways, highlighting potential shared pathogenic mechanisms. Network analysis revealed a highly interconnected web of diseases associated with periodontitis, (its *diseaseome*). This intricate network underscores the complex interplay between oral and systemic health, emphasizing the influence of periodontal disease on overall well-being. Furthermore, the identification of key hub genes within the network offers promising targets for therapeutic intervention strategies aimed at managing both periodontitis and its associated comorbidities. These findings pave the way for more holistic approaches to patient care, considering the multifaceted interactions between periodontal and systemic health. Future investigations aimed at functionally validating the identified molecular connections and exploring targeted therapeutic strategies hold then significant promise for improving patient outcomes.

Supplementary Materials: The following supporting information can be downloaded at website of this paper posted on [Preprints.org](https://www.preprints.org).

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