

Review

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Review

How can Molecules Induce Hemorrhoids? The Role of Genetics and Epigenetics in Hemorrhoidal Disease

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Abstract

The pathophysiology of hemorrhoids remains elusive; however, recent research has increasingly focused on the role of genetic and epigenetic mechanisms in this condition, offering prospects for targeted treatments. We conducted a review using PubMed, Embase, and Google Scholar, supplemented by citation searching, to summarize current knowledge of the involvement of genetic and epigenetic mechanisms in hemorrhoids. Our review of 250 papers suggests that several genes, including FOXC2, NOX, NOS, and CALM3, may be responsible for predisposing changes leading to the development of hemorrhoids. These genes have been associated with varicose veins, inflammation, and connective tissue alterations. Additionally, epigenetic mechanisms, particularly those mediated by miRNA, have been implicated in the clinical symptoms of hemorrhoids. While epigenetic regulation may influence inflammation, dilated vessels, and connective tissue degeneration, the exact mechanisms involved in these processes remain unclear. Furthermore, certain predisposing factors for hemorrhoids appear to involve both genetic and epigenetic mechanisms. This knowledge contributes to a better understanding of hemorrhoids and holds promise for developing novel therapeutic approaches.

Keywords: hemorrhoids; genetics; epigenetics; gene expression; ncRNA; microRNA; miRNA; inflammation; targeted therapy; molecular therapy

1. Introduction

Around the anus and the lower rectum, there are located anal cushions, which consist of blood vessels and non-vascular components: epithelium (mucosa or anoderm), connective tissue (elastic and collagenous), a layer of muscular tissue (named muscle of Treitz), and an anchoring system which connects them to surrounding tissue [1,2]. Their purpose is to allow the anus to dilate without damage to the tissue and prevent the stool from leaking in case of increased pressure in the abdomen, which they can achieve thanks to rich vascularity that can be filled or drained of blood, depending on the need. In some cases, leading to pathological changes, they can become swollen, inflamed, and displaced, which results in the development of pathological hemorrhoids, in other words, hemorrhoidal disease [1–8].

We can divide the hemorrhoids into two groups: those placed below the dentate line of the anus – internal hemorrhoids, and those placed above that line – external hemorrhoids. In each of those groups, we can differentiate three main anal cushions: left lateral, right anterior, and right posterior, which make up a total of six anal cushions, three internal and three external [9]. Any of those cushions can develop into pathological hemorrhoids. Other types of hemorrhoidal disease are prolapsed hemorrhoids, a subtype of internal hemorrhoids, in which the enlarged veins of the cushion exit the anus together with the tissue; and thrombosed hemorrhoids, a complication that accompanies mainly external hemorrhoids, however, it can occur with internal ones as well. It can develop due to the

formation of blood clots in hemorrhoidal veins and can cause painful swelling of the surrounding tissue [10,11].

Currently, there are three main theories regarding the pathogenesis of hemorrhoids: the varicose vein theory, where hemorrhoids are supposed to originate from abnormally dilated and congested veins of the submucous internal rectal venous plexus [2,8,12–15]; the vascular hyperplasia theory, where the hemorrhoids develop from hyperplasia of the corpus cavernosum recti [2,16]; and the sliding anal lining theory, which implies that hemorrhoids are a result of degradation of the surrounding connective tissue that causes normal anal cushions to displace, possibly because of an increase in the intra-abdominal pressure, caused by constipation and prolonged straining [2,8,12–15]. This process can lead to the obstruction of veins via enclosing them by constricting anal muscles [2], which creates increased venous pressure and results in widening and convoluting the vessels, as well as thrombosis – all of that via inflammatory processes featuring leukocytes and macrophages that secrete cytokines, matrix metalloproteinases (MMPs), and oxygen radicals [17,18].

The exact pathophysiology of hemorrhoids remains elusive, as there are no non-ambiguous, well-proved theories. The role of genetics and epigenetics is currently suspected and studied; that is why it seems important to pose a crucial question about the role of those factors in the development of hemorrhoidal disease, summarize and review current knowledge in this field, in hopes of deepening our knowledge about this condition.

Hemorrhoids are the most commonly occurring proctological disease, and it is estimated that every fourth person suffers from this condition. Because of the scale of the problem, it is a major medical issue – data from the National Center for Health Statistics suggest that approximately 10 million people in the United States suffer from hemorrhoids [7], with annual visit count higher than for colon cancer, irritable bowel syndrome, inflammatory bowel disease, ulcerative colitis, or Crohn's disease [19]. With this many cases, new ways of treatment are constantly in demand [20]. While reviewing gathered studies, we have come across various molecular processes that take part in the development and progression of hemorrhoids. So far, the following mechanisms were reported to occur in hemorrhoidal tissues, which we discuss in detail later in the text: inflammation, changes in vesical pathways, vessel dilation, including that involving an enhanced secretion of NO (nitic oxide), with development of varicose veins, angiogenesis, degeneration of supportive tissue, as well as gene mutations that increased the possibility of development of varicose veins, increased NO secretion or mediated changes in components of connective tissue around the area where hemorrhoids are located. Most, if not all, these mechanisms seem to be a potential base for finding new molecular targeted treatments for hemorrhoids. Targeted therapy based on molecular processes that occur in diseases is not a new concept - numerous works that report on new methods of treatment based on discovered molecular characteristics of a particular disease have been published: in use are cell-free DNA [21], mRNA decay inhibitors [22,23], and anti-cytokines [24]. Some of those methods are based on mechanisms that are similar or corresponding to those uncovered in hemorrhoids – inflammatory bowel disease can be treated with anti-cytokine drugs, targeted at cytokines over expressed in this condition [24], influencing the COX2 and PGE2 expression to After research and some possibly needed modifications, those mechanisms - or similar ones - could be used to treat hemorrhoids as well. However, extensive expertise in the subject is required to develop such a treatment, and in most cases, our current understanding is not sufficient - it seems quintessential to regularly compile current information about known conditions, to accelerate and maximize the potential of treatmentrelated research.

2. Results

2.1. How do Hemorrhoids Develop?

So far, multiple factors have been claimed to be involved in hemorrhoidal development, especially states that cause an increase in the intra-abdominal pressure: prolonged straining during constipation, obesity, pregnancy, and possibly lifting heavy weights [7,8,12,13,15,25–27]. These also

include internal agents such as genetic and immune factors, alongside aging, pelvic floor dysfunction, chronic diarrhoea, cirrhosis with ascites, and environmental agents such as diet, sedentary lifestyle, hygiene, alcohol consumption, diverse sexual behaviours (e.g., anoreceptive intercourse), and prolonged sitting [7,8,12,13,15,25–27].

Those factors are causing stress to tissues, which respond with inflammatory reaction manifested by vein dilation, destruction of extracellular matrix of hemorrhoidal supporting tissue together with anal subepithelial muscle [7], and, in the end, by the promotion of angiogenic and proliferative factors [28,29], which is in line with all three main theories regarding the development of hemorrhoids: the varicose vein theory, the vascular hyperplasia theory, and the sliding anal lining theory. Occurring activities are regulated by, among others, epigenetic mechanisms, such as noncoding RNA (ncRNA) [27,30–33]. They function as a messenger when the stress signal occurs and regulate intracellular pathways to trigger a response to that signal. In case of deficiency in ncRNAs, a response to a particular stress signal is much weakened [11,12]. NcRNA are engaged in regulating the expression by engaging in splicing and translation and are a critical factor in the post-transcriptional regulation of transcriptome expression [33]. To the group of ncRNA belong: long noncoding RNA (lncRNA), microRNA (miRNA), which is particularly important in hemorrhoids, circular RNA, ribosomal RNA (rRNA), transfer RNA (tRNA), and small nuclear RNA (snRNA) [34].

MiRNAs are small, single-stranded, non-coding RNA particles that can regulate gene transcription – they bind to the 3' untranslated region (3'-UTR) of the mRNA molecule transcribed from the target gene, which causes inhibition and induces cleavage of the mRNA by dicer enzymes and silencing the gene expression [35–41]. One molecule of miRNA can target hundreds of genes, and one gene can be targeted by multiple miRNAs, forming a network that can regulate many pathways. The identification of genes crucial in the development of hemorrhoids is a subject of research, and some of these genes remain to be uncovered [42–47].

Below, we discuss currently discovered and documented processes regarding molecular mechanisms occurring in hemorrhoids, with their proven or theorised mechanisms of regulation, in hopes of systematising our knowledge.

2.2. Inflammation

In hemorrhoidal tissue, we can observe very intense inflammation, involving both the dense vascular system and the supportive connective tissue. Inflammation can lead to pathological changes we can observe in hemorrhoids: mucosal ulceration, ischemia, thrombosis, further vessel dilation, and distortion of the smooth muscle layer, together with the surrounding supportive tissue [7,25,26]. This process occurs with the activation of T-lymphocytes, macrophages, neutrophils, monocytes, mast cells, and dendritic cells [48,49], which are responsible for secreting pro- and anti-inflammatory cytokines. The balance, however, shifts very soon to the dominance of pro-inflammatory cytokines, which are highly expressed in hemorrhoids. Among them, there are RANTES (Regulated on Activation, Normal T-cell Expressed and Secreted, CCL-5), TNF-α, and VEGF, which, in addition to proangiogenic function is also increase cell permeability, and as a result, contribute to the inflammation process [49–52], as well as IL-1 β , IL-6, IL-8, IL-17, and IFN- γ – those cytokines were found to be significantly overexpressed in hemorrhoids. IL-10, an anti-inflammatory cytokine, is under-expressed [53] (see Table 1.). A study has shown that some substances help to downregulate the expression of those cytokines in fibroblasts and macrophages of hemorrhoid tissues, which leads to a reduction of inflammation, and, due to VEGF's primary function, to a decrease in vascular density, which is increased in hemorrhoids [48,54].

Table 1. Cytokines presented in the table were identified in hemorrhoidal tissues.

IFN-γ

Cytokines Expressed in Hemorrhoids Pro-inflammatory Cytokines Anti-inflammatory Cytokines RANTES IL-10 TNF-α ... VEGF ... IL-1β ... IL-6 ... IL-8 ... IL-17 ...

In addition to that, genes of CGRP (calcitonin gene-related peptide), substance P (SP), together with TRPV1 (transient receptor potential cation channel, vanilloid receptor 1), which are involved in regulating the expression of cytokines in blood cells [55–57], were found to take part in regulating that expression in serum in the case of hemorrhoids as well [58]. Some substances were proven to inhibit the secretion of pro-inflammatory cytokines in serum via downregulating those genes, which helped to ease hemorrhoid symptoms, suggesting that those genes are up-regulated in hemorrhoids and take part in their development.

Other than those factors, increased levels of COX-2 were detected in hemorrhoidal tissues, and they were secreted by fibroblasts and macrophages [28,53,59]. COX-2 is a molecule involved in the production of prostaglandins, main pain mediators, as well as supporting the inflammation process. It is likely to be the cause of pain in hemorrhoid disease [48,60].

Zhou et al. (2025) have found increased miR-770 levels in hemorrhoid tissues. This miRNA promotes polarization of M Φ 1 macrophages, which results in observed increased infiltration of these macrophages in hemorrhoid-affected tissues. MiR-770 suppresses RYBP, a member of the PRC1 complex – a complex responsible for inhibiting gene expression, and thus weakens the transcriptional repression. A result of this process is upregulation of genes encoding inflammatory genes like nuclear factor- κ B-dependent (NF- κ B), IL-1 β , and TNF- α , further fuelling the inflammation. [61].

In summary, proinflammatory cytokines, especially VEGF, are more expressed in hemorrhoids than in normal cells and play an important part in their pathogenesis, mainly angiogenesis, and maintaining the inflammatory state, which leads to progression of the disease and clinical symptoms.

2.3. The Role of Vesicles

Some studies regarding the role of miRNA in hemorrhoids found that miRNAs were up- or downregulated in hemorrhoids and are possibly targeting genes, based on available databases, involved in various vesicular pathways (see Table 2.) [27,30].

Table 2. MiRNAs differently expressed in hemorrhoids seem to target genes that influence various vesical pathways.

	MiRNAs in vesical pathways in MiRNAs in extracellular ves hemorrhoids pathways in hemorrhoids				
Probable targeted processes *	Endocytosis	Synaptic vesicle pathways	Transcription, protein kinase activity, and ubiquitination	Transcriptional activator activity	
Status	Upregulated	Downregulated	Upregulated	Downregulated	
	miR-375	miR-376b-3p	miR-6741-3p	miR-548t-5p	
	miR-215-5p	miR-34a-5p	miR-6834-3	miR-323b-5p	
	miR-192-5p	miR-152-3p	miR-425	miR-1322	
	miR-143-3p	let-7c-5p	miR-6804-3	miR-3928-5p	
	miR-187-3p	miR-107	miR-744-3	miR-346	
	miR-194-5p	miR-517a-3p	miR-848	miR-4704-5p	
Type of miRNA	miR-145-5p	miR-517b-3p	miR-299-5	miR-1913	
- / F	miR-490-3p	miR-1307-5p	miR-463	miR-876-3p	
	miR-145-3p	miR-190a-5p	miR-317	miR-4460	
		miR-378a-5p	miR-465	miR-892a	
		miR-708-3p			
		miR-450a-5p			
		miR-30e-5p			
		miR-532-5p	••	••	

^{*} These are processes associated with genes that the listed miRNAs possibly target, according to available databases.

According to Song et al. [30], miRNAs upregulated in hemorrhoid tissues were miR-375, miR-215-5p, miR-192-5p, miR-143-3p, miR-187-3p, miR-194-5p, miR-145-5p, miR-490-3p, miR-145-3p, while downregulated were miRNAs in hemorrhoids were: miR-376b-3p, miR-34a-5p, miR-152-3p, let-7c-5p, miR-107, miR-517a-3p, miR-517b-3p, miR-1307-5p, miR-190a-5p, miR-378a-5p, miR-708-3p, miR-450a-5p, miR-450a-5p, miR-30e-5p, miR-532-5p. Two of these, miRNA-133b and miRNA-133a-3p, shared 32 of the possible target genes, and the rest of the miRNAs had independent potential target genes.

Genes possibly targeted by them, for both up- and downregulated miRNAs, are involved mainly in cell composition and protein binding. The upregulated miRNAs' most prominent target, with the most changes in gene expression, is the endocytosis pathway, and the downregulated miRNAs focus the most on genes belonging to the synaptic vesicle pathway. This leads to the higher expression of endocytosis pathway genes and the lower expression of synaptic vesicle pathway genes, which was identifiable in tests and suggests that the development of hemorrhoids may be linked to an imbalance between the expression of the endocytosis and synaptic vesicle cycle pathway genes, generated by changes in levels of miRNAs in hemorrhoidal cells. Those two pathways in hemorrhoidal tissue might be responsible for regulating the infiltration of inflammatory cells, proliferation of vascular endothelial cells, oedema of interstitial cells, or other processes, although that is still a subject for further research [30].

Differences in miRNA expression were found in extracellular vesicles as well [27]. Extracellular vesicles are membranous structures originating from cell membranes [62]. They have a role in cancer progression, metastasis [63], wound healing [64], angiogenesis [65], and immunoregulation [66]. They also function as messengers between cells [67], carrying proteins, lipids, and RNAs [68,69]. Hemorrhoidal extracellular vesicles were found to be carrying different molecules than vesicles derived from healthy tissues, with the most difference being in the content of miRNAs. There were

245 upregulated miRNAs found in hemorrhoidal extracellular vesicles, and within them ten most prominent were: miR-6741-3p, miR-6834-3p, miR-4254, miR-6804-3p, miR-744-3p, miR-8485, miR-299-5p, miR-4636, miR-3175, and miR-4658. Those miRNAs seem to influence the transcription process and target genes involved in protein kinase activity, transcriptional activity, and ubiquitin-protein function, and are most active in proximity to cell junctions. Signalling pathways that are upregulated by them the most are the MAPK (mitogen-activated protein kinases) signalling pathway, axon guidance, and the Ras signalling pathway. They also upregulate AMPK, PI3K-Akt, Hippo, and Wnt signalling pathways and autophagy, though at a lower level than the first three mentioned [27].

The most upregulated miRNA found, miR-6741-3p, is highly likely to be responsible for combining the 3′-UTR of UBQLN1, a gene coding ubiquilin-1, a protein participating in the process of ubiquitination in proteasome-dependent protein degradation, via ubiquitin ligases [70]. An enzyme from this family, HERC3, was established to attenuate nuclear factor-κB-dependent signaling, which mediates inflammatory and immune reactions by inducing its ubiquitination and proteasomal degradation [71]. It means that the upregulation of miR-6741-3p results in lowering the inactivation level of NF-κB and increasing its activity, and consequently, in enhancing local and systemic inflammation, which are prominent in hemorrhoids [27,72].

Some of the upregulated miRNAs in hemorrhoidal extracellular vesicles target the MAPK (mitogen-activated protein kinases) signalling pathway, which is active in physiological and pathological cell proliferation, in carcinogenesis [73] and angiogenesis [74,75], and may enhance inflammation as well [76]. The obtained results suggest that the MAPK pathway may be one of the factors increasing angiogenesis and partially inflammation in hemorrhoids.

Number of downregulated miRNAs found in extracellular vesicles from hemorrhoidal tissues was 202, from which the ten most significant were: miR-548t-5p, miR-323b-5p, miR-1322, miR-3928-5p, miR-346, miR-4704-5p, miR-1913, miR-876-3p, miR-4460, miR-892a. These are the molecules that possibly modulate transcriptional activator activity, also by regulating transcription, and they are the most active around the plasma membrane. Pathways targeted by them are mostly Rap1 signalling pathway, and synthesis, secretion, and action of parathyroid hormone, proteoglycans in cancer, as well as, to a lesser extent, MAPK, cAMP, and Wnt signalling pathways.

The expression pattern of miRNA may vary between proper hemorrhoidal tissues and extracellular vesicles emerging from them, since not always the same miRNAs are present at the same levels between them [27].

2.4. Nitric Oxide and Varicose Veins

Nitric oxide (NO) is a molecule produced in many different cells, and it contributes to vascular dilatation and the development of varicose veins [77]. It was found to be overly present, together with two Nitric Oxide Synthases (NOS): endothelial (eNOS) and neuronal (nNOS) [78] in hemorrhoids, while asymmetric dimethylarginine, a molecule that inhibits NOS, was underexpressed in those tissues [5,8,12–15,32,79,80]. High expression of NOS in hemorrhoids leads to excessive amounts of NO being synthesised, and that causes an increase in blood flow and twisting of veins, which adds to the varicose veins theory of pathogenesis of hemorrhoids.

2.5. Angiogenesis

Hemorrhoids occur with increased angiogenesis, which leads to high vascular density in the pathological tissue, dilatation of blood vessels (which in the end might contribute to the development of varicose veins), and signs of oedema, sometimes with thrombosis [5,8,12–15,32,80]. In some works, it was suggested that thrombosis might be one of many factors inducing angiogenesis (neovascularization) [89,90], possibly via the increase in expression of VEGF [91,92], and that might be the case in hemorrhoids as well [80]. Nuclei of endothelial cells appear enlarged, and vascular endothelial cell markers vWF, CD31, and CD34, as well as endoglin, are expressed much more in hemorrhoids than in normal tissues, which further shows that there is intensified vascular proliferation present [31,80]. Endoglin is a glycoprotein overexpressed in endothelial cells, an

accessory receptor for TGF- β , and a marker for angiogenesis, due to its appearance in different tissues with increased vascular proliferation [93–96]. Prominent levels of VEGF and VEGFR2, proangiogenic factors, were also identified in hemorrhoids, and they intensify the angiogenesis process as well [80,97].

On top of that, signalling pathways responsible for inhibiting angiogenesis were found to be significantly less active in hemorrhoid cells, leading to increased vascular proliferation [31,32].

MiR-143-3p was significantly downregulated in hemorrhoid tissues, especially in severe cases. Its downregulation increases expression of vascular markers, such as CD31, vWf, and VEGFR2, cell proliferation and migration, and enhances apoptosis, and it is a potential key regulator in angiogenesis in hemorrhoid progression and postoperative wound healing [98].

On chromosome 14, there is located a genomic imprinted region – DLK1-DIO3 [43–46]. It contains, among others, microRNAs. Four of those miRNAs, miR-412-5p, miR-422-5p, miR-432-5p, and miR-1185-1-3p, were found to be expressed differently in healthy and hemorrhoidal tissues, and in particular, miR-412-5p and miR-1185-1-3p were found to be significantly underexpressed in hemorrhoidal tissue [32].

MiR-412-5p targets the gene of Exportin1 (Xpo1) (see Figure 1) [32], a nuclear protein in endothelial cells that is responsible for exporting proteins, such as p53, p21, FOXO, PI3K/AKT, Wnt/β-catenin, AP-1, and NF-κB, from the nucleus to the cytoplasm [91,92,99,100]. Under-expression of miR-412-5p leads to overexpression of Xpo1 in hemorrhoidal endothelial cells [32], since miRNAs silence gene expression, and are the reason for augmented translocation of p53 to the cytoplasm. The p53 protein in the nucleus is responsible for regulating the cell cycle by increasing the expression of certain genes. In case of endothelial cells in hemorrhoids, those genes are the SHC genes: they are divided after transcription into three subtypes: $p46^{SHC}$, $p52^{SHC}$, and $p66^{SHC}$ [101–103]. The $p66^{SHC}$ has a role in the Ras signalling pathway [101,102,104,105], inducing apoptosis and aging [101–103,106–110]. Lack of p53 in the nucleus of hemorrhoidal endothelial cells results in a decrease in SHC expression, especially $p66^{SHC}$, blocking the p53-p66 SHC -p16 pathway. The exact connection between that pathway and hemorrhoids is not clear yet, but it appears to inhibit and aggravate the cell cycle control, causing proliferation of endothelial cells and angiogenesis, which is a factor in the formation of pathological hemorrhoids [32].

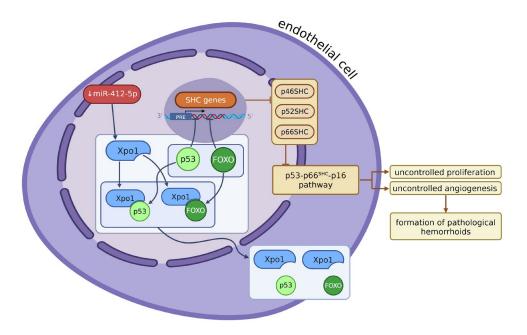


Figure 1. When miR-412-5p is under-expressed, Xpo1 is up-regulated, which results in excessive export of p53 and FOXO from the nucleus. The lack of p53 and FOXO in the nucleus reduces the expression of SHC genes – p46^{SHC}, p52^{SHC}, and p66^{SHC}, which inhibits the p53–p66^{SHC}–p16 pathway. This leads to uncontrolled proliferation and angiogenesis, contributing to the formation of pathological hemorrhoids (*Xpo1 – Exportin-1*, *p53 – tumor*

suppressor protein, FOXO – Forkhead box O transcription factor, SHC – Src homology 2 domain-containing (p46^{SHC}, p52^{SHC}, p66^{SHC}), p16 – cyclin-dependent kinase inhibitor involved in cell cycle arrest). Created in BioRender. Mazurek, M. (2025) https://BioRender.com/c8w1axi.

Another factor contributing to angiogenesis in hemorrhoids is changes in methylation of RNA N-6 methyladenosine (m6ARNA) (see Figure 2). Enzymes from the m6A methyltransferase complex, described also as m6A writers, METTL14 and METTL3, form a heterodimeric complex, with METTL14 acting as a switch for METTL3's activity, and they catalyse the methylation of m6A RNA [33,111–114]. Other components in that complex are auxiliary cofactors such as WTAP, VIRMA, RBM15/15B, ZC3H13, and HAKAI, which help with binding to the target RNA (first three), achieving the correct localization of the whole enzymatic complex (ZC3H1) [33]. For the further fate and function of m6A RNA, the readers are responsible: they improve its stability, regulate splicing, increase its transcriptional and translational activity, and promote carcinogenesis and invasion as well [33,112,114–117].

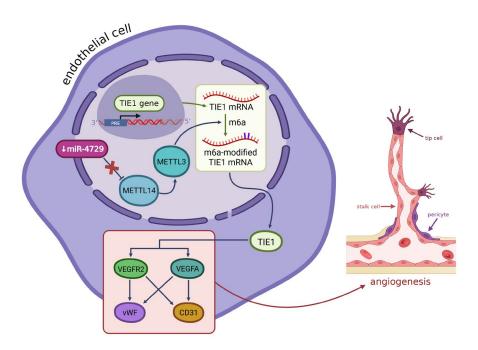


Figure 2. In hemorrhoidal vascular endothelial cells, miR-4729 is significantly down-regulated, leading to over-expression of METTL14, a key m6A RNA methyltransferase. Elevated METTL14 increases m6A methylation via activating METTL3 at the 3' UTR of, enhancing TIE1 mRNA stability and translation. As a result, TIE1 protein is overexpressed and activates the TIE1/VEGFA signaling loop, involving VEGFA, VEGFR2, vWF, and CD31, which promotes endothelial cell proliferation and angiogenesis, prominent in hemorrhoids (*METTL3/14 – methyltransferase-like 3/14, m6A – N6-methyladenosine, TIE1 – tyrosine kinase receptor, VEGFA – vascular endothelial growth factor, VEGFR2 – vascular endothelial growth factor receptor 2, vWF – von Willebrand factor, CD31 – platelet endothelial cell adhesion molecule, tip/stalk cells – specialized endothelial cells involved in new vessel formation). Created in BioRender. Mazurek, M. (2025) https://BioRender.com/fcihnmu.*

Ten miRNAs are predicted to target METTL14 expression, and from these, only one, miR-4729, was significantly low in hemorrhoid tissues. This miRNA, when it is up-regulated, inhibits METTL14 expression in endothelial cells, and, as a result, inhibits m6A RNA methylation as well. It was later observed that in this case, proliferation, as well as overall vascular endothelial cell function, were inhibited. One gene was found to be especially inhibited in cells with miR-4729 overexpression – TIE1. TIE1 is a tyrosine kinase that plays a critical role in angiogenesis and blood vessel stability, as well as tissue remodelling and inflammation; it can be found in endothelial cells [118–123]. This gene is related to VEGFA, VEGFR2, vWF, and CD31 and can induce vWF and CD31 expression by

activating VEGFA/VEGFR2 receptor ligands, which promotes angiogenesis. They form together a signalling pathway called the TIE1/VEGFA signal molecular loop, in addition to the previously known TIE1/TIE2/VEGFR2 signalling pathway. TIE1 was found to be significantly under-expressed in cells with high miR-4729 content, which suggests that this miRNA is a key factor regulating TIE1 expression, via influencing METTL14 expression, and then, as a result, m6A RNA methylation. In hemorrhoids, miR-4729 is under-expressed, which causes an increase in the synthesis of METTL14 and then an intensification in methylation of m6ARNA, especially TIE1 [31], which was found to be present in those cells at very high levels [123]. As a result, we can observe vascular hyperplasia, together with an increased expression of endothelial markers such as CD31, which is distinct in hemorrhoids.

2.6. A Role of Estrogen in Angiogenesis?

In some cases of hemorrhoids in women, we can detect the presence of estrogen nuclear receptors (ER α) in the tissues of the anal canal [81,82]. They bind estrogens, which activate a signalling pathway leading to the downregulation of miR-424-5p. The higher the level of estrogens, the more ER α are present [83]. Low levels of miR-424-5p and elevated levels of ER α cause upregulation of VEGF, and, as a result, angiogenesis, and edema (see Figure 3). The opposite – decrease in expression of VEGF – happens when miR-424-5p is overexpressed. This miRNA's predicted target is the ESR1 gene, whose product regulates the transcription of estrogen-inducible genes [84], such as VEGF [85]. Downregulation of miR-424-5p in hemorrhoids, caused by estrogens activating the ER α , leads to an increase in levels of ESR1 and then, as a result, VEGF, which promotes angiogenesis and edema in hemorrhoids in women. There is also some evidence of the role of estrogens in angiogenesis in other tissues – multiple studies across the years have reported that they are involved in the recovery of arterial endothelium after damage [86], possibly via promoting VEGF expression, as it is another function of estrogens, not only in hemorrhoids, but also in other tissues: uterine and vascular altogether [87,88], suggesting that their influence on hemorrhoids is not a solitary case.

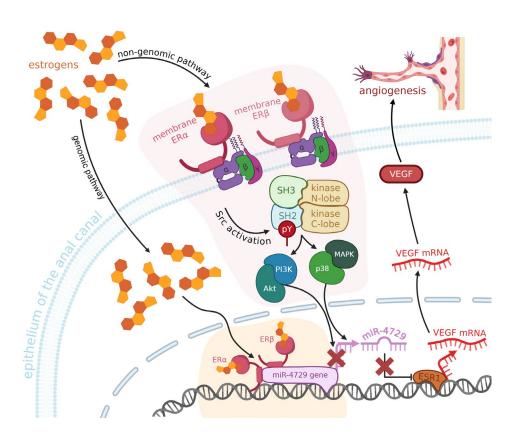


Figure 3. Estrogens activate ER α in the anal canal epithelium of women with hemorrhoids via genomic and nongenomic pathways, leading to Src activation and downstream signaling through PI3K/Akt, MAPK, and p38. This downregulates miR-4729, which results in the overexpression of ESR1 and enhances the VEGF transcription. Increased VEGF promotes angiogenesis and edema in hemorrhoidal tissue ($ER\alpha$ – estrogen receptor alpha, $ER\beta$ – estrogen receptor beta, ESR1 – estrogen receptor 1 gene, VEGF – vascular endothelial growth factor, PI3K – phosphoinositide 3-kinase, MAPK – mitogen-activated protein kinase, miR-4729 – microRNA-4729, SH2/SH3 – Src homology 2/3 domains). Created in BioRender. Mazurek, M. (2025) https://BioRender.com/158e9db.

2.7. Degeneration of Connective Tissue

The stroma of hemorrhoids consists of connective tissue, with collagen and elastic fibres cross-linked with each other, providing tensile strength, elasticity, integrity, and stability to the tissue; a layer of smooth muscle (Treitz's muscle) and blood vessels [2,124].

Abnormalities in collagen structure, especially collagen I and III, participate in the development of hemorrhoids – whether due to its degradation or incorrect structure, which leads to poor mechanical endurance and stability. Conducted studies have shown that patients with hemorrhoids had many more defects in collagen structure than healthy patients, even those advanced in age. The same studies reported that collagen levels and collagen type I/III ratio were significantly reduced in hemorrhoids in comparison to normal anal cushions, with significant predominance of collagen III [125], which results in less cross-linking and poor mechanical endurance, since the mature collagen I provides more tensile strength than the less mature collagen III [126,127]. This suggests that the occurrence of hemorrhoids is associated with early and severe collagen degradation, as well as alterations in collagen type ratio. These changes may result from genetic, metabolic, or environmental factors, potentially leading to the early onset of the disease. However, the precise background of these alterations remains unclear and warrants further study [126,127].

Changes in expression of elastic connective tissue components have been reported as well, in the fibulin family of extracellular matrix proteins. Fibulin-3 and fibulin-5 were found to be underexpressed in hemorrhoids [53,128–132]. Fibulin-5 stabilizes and organizes elastic fibres in extracellular matter and inhibits angiogenesis [133], whereas fibulin-3 maintains the stability of the basal membrane, stabilizes the extracellular matrix [134] and inhibits matrix metalloproteinases (MMPs) – hydrolytic enzymes responsible for the degradation of the extracellular matrix [135]. Low levels of those fibulins may result in damage to elastic fibres, and consequently, to the structure of connective tissue, predisposing to hemorrhoids, since the components of that tissue are linked to one another. Some medicines are successful in increasing their expression [53]. This suggests that some epigenetic mechanism may be regulating that expression, although the specific pathways are yet to be determined.

Levels of various MMPs have been found to be elevated in patients with hemorrhoids [26,27,53,136–138]. In grade I and II of the disease (early stages), those enzymes were MMP-1, MMP-2, and MMP-3; in grade III – MMP-3, MMP-7, MMP-8 and MMP-9; and in grade IV, MMP-2, MMP-8 and MMP-9 [26,139], with very high expression of MMP-9, together with NGAL (*neutrophil gelatinase-associated lipocalin*, *lipocalin*-2) – a marker for neutrophil activation, and consequently for inflammation; NGAL and MMP-9 levels being particularly elevated in thrombosed and prolapsed hemorrhoids [26]. In addition to elastic fibers, these enzymes can target and degrade other components of the extracellular matrix, such as collagen. This process leads to inflammation and severe damage to the supportive tissue of the anal canal, as well as disruption of regenerative processes. Consequently, it contributes to the progression of hemorrhoidal disease, particularly by promoting the development of prolapsed hemorrhoids, as the damaged supportive tissue is no longer able to prevent the prolapse of anal structures [53,137–139]. MMP-9 plays an additional role – it promotes angiogenesis by damaging the basal lamina of endothelium, which stimulates the release of VEGF [140,141]. Prominent levels of those enzymes might be a consequence of under-expression of fibulin-3 in hemorrhoidal tissues, as well as activation of macrophages and lymphocytes, which

secrete MMPs, but that may not be the only mechanism; further studies must be conducted to determine those mechanisms.

2.8. Genes Significant in the Development of Hemorrhoids

Along with the development of our knowledge about molecular biology, especially in the matter of genetics and epigenetics, the significant role of genes and changes associated with them as risk factors for hemorrhoidal disease has been widely considered. Numerous studies have been conducted across the span of years to research the involvement of genetics in the development of hemorrhoids and a possible genetic susceptibility to their occurrence, and we have aimed to gather and summarize them in our paper. The results are displayed in a table below (see Table 3.). The mentioned genes and their mutations seem to be predisposing to hemorrhoids whether by impairing the function and structure of the epithelium and connective tissue, including the smooth muscles, changing the organisation of the extracellular matter (ECM), limiting neuromuscular motility, as well as enhancing the synthesis of some proteins. Those changes can be and were previously associated with gastrointestinal, neuroaffective, and cardiovascular conditions [142].

Table 3. Genes displayed in the table were proposed or reported to contribute to the pathogenesis of hemorrhoids ("-" applies to unknown, unavailable values).

Genes Significant to the Development of Hemorrhoids						
Gene	Produ	Function	Mechanism	Mutations Reported Associated		
	ct		of Action	Conditions		
FOX	FOXC	 development 	_	– 91 C-G – lymphedema		
C2	2	of venous		transversion, in distichiasis [150]		
	(forkh	cardiovascula		the proximal – chronic venous		
	ead	r and		upstream disease		
	box	lymphatic		region of [144,147,151]		
	protei	system [145–		FOXC2 [148] – varicose veins		
	n)	147]		- frameshift - 880'881insT		
	[143,1			mutation of possibly linked to		
	44]			base pair hemorrhoids,		
	11]			insertion at varicose veins,		
				880'881insT in and myocardial		
				the coding infarction [149]		
				region (results		
				in premature		
				'stop' codon at		
				bp 1386) [149]		

NOX	NOX1	_	fluid shear –	generatin		_	_	cardiovascular
1 and	(NAD		stress	g reactive				diseases and
NOS	PH	_	abnormal	oxygen				hypertension
3	oxida		wound	species				[156]
	se)		healing	(ROS),			-	chronic
	NOS3	-	regulation of	which				functional
	(nitric		the cell	damage				constipation
	oxide	-	cofactor	DNA,				[157]
	synth		binding	proteins,			_	inflammatory
	ase)	-	components	and lipids				bowel disease
	/		of the plasma –	ADMA				[153]
			membrane	(asymmet			-	hemorrhoids
			protein	ric				[79,152]
			complex [152]	dimethyla			-	atherosclerosis
		_	maintaining	rginine –				[152]
			the intestinal	NOS				
			crypt	inhibitor)				
			homeostasis	is				
			and	underexp				
			microbiota	ressed in				
			composition	hemorrho				
			[153]	ids [78]				
		_	vasodilatatio					
			n [78,154,155]					
MTH	meth	_	metabolizes	_	_	polymorphism	_	Polymorphisms
FR	ylenet		folate			C677T (alanine		C677T and
	etrah	_	controls			to valine		A1298C were
	ydrof		homocysteine			substitution in		shown to
	olate		levels [158]			the N-terminal		predispose to
	reduc					catalytic		CVD [161]
	tase					domain)	_	polymorphism
					_	polymorphism		677, when
						A1298C		accompanied by
						(alanine to		constipation,
						glutamine substitution in		hemorrhoids,
						the C-terminal		family history of rectal cancer and
						regulatory		was linked to the risk of colorectal
						domain) [159]		
					_	polymorphism 677 [160]		cancer [160]
						077 [100]	_	venous thrombosis, no
								thrombosis, no association with
								thrombosed

MYH 9	heavy - chain of non-muscl e	angiogenesis [163]	_	-	SNP rs735854 [164]	_	hemorrhoidal disease was found [162] mutations lead to thrombocytopeni a and platelet macrocytosis; can be related to bleeding
	myosi n IIA					_	disorders [165] varicose veins and hemorrhoids [164]
F5	coagu lation factor V	cascade [166]	_	-	polymorphism rs6546324 rs6025 – missense mutation (p.Arg534Gln) [167]	- -	endometriosis hemorrhoids [167] venous thrombosis [166]
CYP1 A	aryl hydro carbo n hydro xylase in hepati c and extra hepati c cytoc hrom e P450		_	-	polymorphism CYP1A1*2A (transition of thymidine to cytosine at position 3801 in the 3'UTR) various single allele mutations [168]		mutations are protective for hemorrhoids and peripheral circulatory problems [168]
PON 1	serum parao xonas e 1	_	_	-	Q isoform polymorphism (glutamine at position 192) R isoform polymorphism	_	Q/R isoform polymorphism has a protective effect on chronic constipation[168] leucine/methioni ne substitution is

				has arginine [169,170] - leucine/methio nine substitution at 54. position [171]	associated with a higher risk of hemorrhoids [168]
CAL M3	calmo dulin 3	 signal transduction muscle contraction enzyme regulation pain fever constipation inflammation proliferation [172] 	_		 increased expression in hemorrhoids anemia, leukemia [173]
ANO 1	anoct amin- 1 (volta ge- gated calciu m- activa ted anion chann el)		leads to an increase in the Cl- current and a slowdow n of activation /deactivat ion of the channel - SNP rs2186797 destabiliz es the protein	- SNP rs2186797 - amino acid change p.Phe608Ser [142]	
SPR X	_	located on chromosomeX	- rs3531893 1 may destabiliz e the C-	- missense mutation rs35318931	_

		component of	terminal –	amino acid	Ĺ
		extracellular	domain of	change	
		matter	the amino	p.Ser413Phe	
		(ECM),	acid chain	[142]	
		especially in			
		colon and			
		liver [174]			
ACH	acetyl	 hydrolyzatio 		mutation	– increased
E	cholin	n of		rs4556017	expression in
	estera	acetylcholine			hemorrhoids
	se	at			[142]
		neuromuscul			Hirschsprung's
		ar junctions			disease [175]
SRT	cappe	_	_	_	increased
T	d-				expression in
	RNA				hemorrhoids
	bindi				[142]
	ng				
	protei				
	n				
GSD	gasde	– expressed in		mutation	– increased
MC	rmin	epithelial		rs10956488	expression in
	С	cells			hemorrhoids
					[142]
MYH	muscl	– ECM –	overexpre –	mutation	increased
11	e	organization	ssion	rs6498573	expression in
	myosi	– muscle	linked to		hemorrhoids
	n	contraction	increased		[142]
	heavy		autophag		
	chain		y and		
	11		impairme		
			nt of		
			contractil		
			e		
			signaling,		
			leading to		
			a decrease		
			in protein		
			levels		
			[176]		
ELN	elasti	 component in 	_	_	– increased
	n	the			expression in
		extracellular			hemorrhoids
		matrix			- cutis laxa [142]

COI	- trans					increased
COL	type	_	_	_	_	
5A2	V					expression in
	collag					hemorrhoids
	en					[142]
	(regul				_	Ehler-Danlos
	atory)					syndrome
	,					(hypothesized to
						be linked to
						hemorrhoids)
						[177]
PRD	histon –	regulation of	_	_	-	increased
M	e	gene				expression in
	meth	expression				hemorrhoids
	yltran –	affects				[142]
	sferas	vascular				
	e	smooth				
	-	muscle cells				
		contractility				

2.9. Possible Epigenetic Factors in the Development of Hemorrhoids

There are numerous environmental and lifestyle-dependent factors considered to be connected to the pathogenesis of hemorrhoids. Some of those factors, discussed below, are either known or suspected to cause epigenetic changes in the cells, which can lead to changes that are a direct cause for hemorrhoids (see Figure 4).

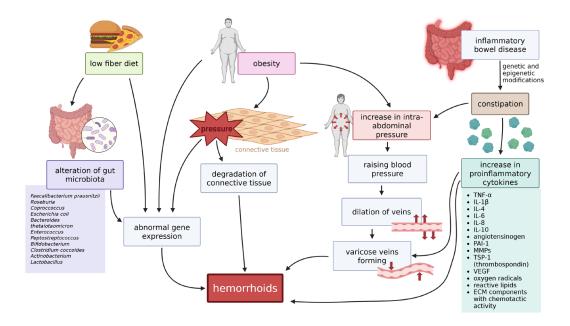


Figure 4. Hemorrhoid development is influenced by epigenetic and lifestyle factors. A low-fiber diet alters gut microbiota, affecting gene expression. Obesity increases intra-abdominal pressure and inflammation via cytokines, while constipation, present in IBS and IBD, raises venous pressure and degrades connective tissue, promoting varicose vein formation ($TNF-\alpha-tumor$ necrosis factor alpha, IL-interleukin, VEGF-vascular endothelial

growth factor, IBS – irritable bowel syndrome, IBD – inflammatory bowel disease). Created in BioRender. Mazurek, M. (2025) https://BioRender.com/rnrh8xd.

2.9.1. Diet and Gut Microbiota

Dietary changes are known to change the composition of gut microbiota. An exemplary, lowfiber diet was reported to induce changes in microbiota [178], as well as it was observed that hemorrhoids occur more often in patients with a deficiency of diet-sourced fiber [7,179]. Although the change of microbiota components is not conditioned by epigenetic mechanisms, it can induce epigenetic modifications in the organism. Diet compounds, together with their bacterial metabolites, can influence gene expression via removing or providing compounds that are substrates for epigenetic modifications [180]. Among bacterial species that influence the levels of such proteins are butyrate-producing species such as Faecalibacterium prausnitzii, Roseburia, and Coprococcus species; species that can produce isothiocyanates, such as Escherichia coli, Bacteroides thetaiotaomicron, Enterococcus, Peptostreptococcus, and Bifidobacterium, or those that metabolize ellagitannins to urolithins - e.g., Clostridium coccoides, Actinobacterium, Lactobacillus, or - again - Bifidobacterium. Those changes were observed to be involved in the pathogenesis of various diseases, such as colon cancer, type 2 diabetes, obesity, and possibly constipation [180-182], with the last two being among risk factors for hemorrhoidal disease. Furthermore, there is a theory that implicates a correlation between the alteration of gut microbiota and the development of hemorrhoids [183], although no research has been conducted to prove that theory yet.

2.9.2. Obesity

Across many different studies, obesity has been named as a factor increasing the probability of developing hemorrhoids [184–187]. It is suspected that the pathogenesis of that process includes the increase in intra-abdominal pressure (that is the case in pregnancies as well) due to enlarged amounts of adipose tissue exerting pressure on veins, especially, which causes them to widen and create varicose veins, present in hemorrhoids [188–190]. Adiposity also escalates the inflammatory process in tissues by stimulating the release of the proinflammatory cytokines – among others adipokines, TNF- α , IL-6, and other interleukins – as well as angiotensinogen, PAI-1 (plasminogen activator inhibitor-1), MMPs, TSP-1 (thrombospondin), VEGF, oxygen radicals, reactive lipids, and ECM components with chemotactic activity [191–193], which accelerates the inflammation [187]. A study conducted by Huang et al. (2023) has highlighted a causal association between hemorrhoids and high body weight [190], and it was in conformity with observational studies on this subject conducted across different populations [187,194–196]. Obesity is known to be conditioned by genetic and epigenetic modifications [197–199], so development of hemorrhoids may also be linked to those changes; however, that connection has not been proved yet.

2.9.3. Constipation

Constipation has been known as one of the crucial factors for hemorrhoids for a long time and is still being recognised in modern research [185,200–202]. It seems to be an effect of chronic stress subjected to anal tissues during defecation, causing them to stretch and degenerate, or increasing intra-abdominal pressure, leading to an impairment of venous circulation, promoting dilatation of veins and development of varicose veins and hemorrhoids [2,7]. There are various causes for constipation, and amongst them is irritable bowel syndrome (IBS) – a disorder of the brain-gut axis, resulting in abdominal pain and alteration of frequency of bowel movements. Recently, there have been published some works hinting at the possible association of IBS with hemorrhoids [142,203–205]. Development of hemorrhoids was observed in multiple cases of IBS across several independent studies. IBS is multifactorial, and it is mediated, among others, by genetic and epigenetic mechanisms [206]. Although a direct connection has not yet been established, hemorrhoids can likely occur because of constipation during genetic and epigenetic modifications in IBS. It is also theorized that

changes in gut microbiota, possibly caused by a low-fiber diet, can participate in inducing constipation [178].

3. Discussion

Constipation has been known as one of the crucial factors for hemorrhoids for a long time and is still being recognised in modern research [185,200–202]. It seems to be an effect of chronic stress subjected to anal tissues during defecation, causing them to stretch and degenerate, or increasing intra-abdominal pressure leading to impairment of venous circulation, promoting dilatation of veins and development of varicose veins and hemorrhoids [2,7]. There are various causes for constipation, and amongst them is irritable bowel syndrome (IBS) – a disorder of the brain-gut axis, resulting in abdominal pain and alteration of frequency of bowel movements. Recently, there have been published some works hinting at the possible association of IBS with hemorrhoids [142,203–205]. Development of hemorrhoids was observed in multiple cases of IBS across several independent studies. IBS is multifactorial, and it is mediated, among others, by genetic and epigenetic mechanisms [206]. Although a direct connection has not yet been established, hemorrhoids can likely occur because of constipation during genetic and epigenetic modifications in IBS. It is also theorized that changes in gut microbiota, possibly caused by a low-fiber diet, can participate in inducing constipation [178].

Table 4. A summary table presenting molecular factors involved in the development of hemorrhoids.

Molecular Components Altered in Hemorrhoids.

State	Upregulated	Downregulated	Mutated or Altered* Genes
	Pro-inflammatory cytokines, especially VEGF	Anti-inflammatory cytokines	FOXC2
	CGRP, SP, and TRPV1	Inhibitory pathways of angiogenesis	MTHFR
	COX-2	Vesical miRNAs modulating synaptic vesicle pathways and transcriptional activator activity	MYH9
	Vesical miRNAs modulating endocytosis, transcription, protein kinase activity, and ubiquitination	deregiliation of the cell cycle	СҮР1А
Molecule	NOS3	miR-4729, leading to overexpression of TIE1 and angiogenesis via METTL14 regulation	PON1
	NOS and NO	miR-424-5p, caused by estrogens, leading to increased expression of VEGF	ANO1
	vWF, CD31, CD34, endoglin	Fibulin-3 and fibulin-5	SPRX*
	VEGF, VEGFR2	Collagen levels, collagen I/III ratio	SRTT*
	MMPs	<u></u>	GSDMC*
	NOX1	··	COL5A2
	CALM3	··	
	ACHE		··
	MYH11	<u></u>	
	ELN PRDM	 	

^{*} The phrase "altered genes" refers to genes that were found to be altered in hemorrhoidal cells, in comparison to normal cells, but the nature of that change is not specified.

As for other factors suspected to influence the development of hemorrhoids, such as a low-fiber diet, obesity, and constipation, it is conceivable that genetic and epigenetic mechanisms may play a

role, albeit indirectly. Dietary changes can trigger epigenetic alterations and modifications in gut microbiota, potentially leading to gut motility issues and predisposing individuals to constipation. Constipation, a long-established primary risk factor for hemorrhoids, is not inherently linked to genetic and epigenetic changes, but certain forms, like irritable bowel syndrome (IBS), may be associated with them. Given the higher incidence of hemorrhoids in patients with IBS, there may be an indirect connection between the two conditions. Obesity is also known to be influenced by epigenetic mechanisms, as excessive adipose tissue exerts pathological pressure on veins, initiating the pathological mechanisms underlying hemorrhoids. While these connections have not been conclusively established through scientific methods and are primarily based on observation or association studies, they represent an area that warrants further research. All those mechanisms are possible targets for the treatment of hemorrhoids, which may help in either relieving the symptoms, stopping the aggravation of the current condition, or even preventing its occurrence in patients who are highly likely to develop hemorrhoids, based on their medical record and risk factors. A deeper understanding of the molecular pathological mechanisms of hemorrhoids will allow us to work on more precise ways of pharmacological treatment before the state of the patient requires surgical intervention.

An evident limitation of our study is the lack of validation in a clinical setting. The studies analysed in our review encompass both clinical and in vitro investigations. We refrain from assessing the clinical relevance of the research included in our review concerning the utility of the discussed genes or their products as therapeutic targets. Instead, we view our study as an impetus for researchers to delve further into the molecular aspects of hemorrhoids, aiming to discover new avenues for targeted and much-needed treatment. However, our study is also constrained by the number of databases reviewed, the keywords searched, and the necessity to limit our search on PubMed and Google Scholar to 200 articles per query, owing to the vast quantity of available records. While we believe our selection of databases is adequate, it remains possible that we did not retrieve and review 100% of the available research on this topic. Additionally, there is limited research on this topic, as the molecular components have often only been investigated in a single original study. Moreover, the validation of these results solely within the research team raises the possibility of inconsistency, which we, as reviewers, lack the means to confirm, representing yet another limitation. To conclusively validate the information gathered in this review, further studies are imperative.

4. Materials and Methods

Our narrative review was conducted following the SANRA (Scale for the Assessment of Narrative Review Articles) checklist [207], as it is the standard for narrative reviews. We aimed for our work to meet all six quality criteria of these guidelines to ensure the highest standards of scientific rigor and reliability (see Figure 5).

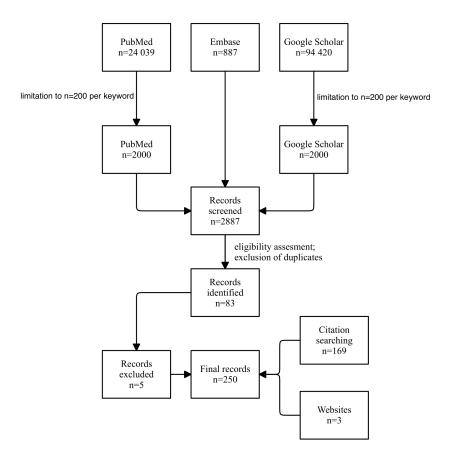


Figure 5. The diagram above demonstrates the process of gathering evidence while performing this review.

For the search, we have used PubMed, Embase, and Google Scholar, as this combination of scientific databases was shown to be sufficient for reviews in peer-reviewed studies [208,209]. We searched for data about genetic and epigenetic factors contributing to the development of hemorrhoids. Search was conducted using a combination of keywords, one combination for one search: ("hemorrhoids") AND ("genetics" OR "epigenetics" OR "genetic factors" OR "epigenetic factors" OR "factors"). Terms were searched as a combination of the word "hemorrhoids" and one word from the second group, e.g., "hemorrhoids genetics". The initial search revealed the following number of records, combined from all keywords: n=24039 for PubMed, n=887 for Embase, and n=94420 for Google Scholar, finding a total of 119 346 records. Based on the initial search, we have decided to limit the number of publications qualified for screening to 200 per search. This limited the number of results to 2887, from which we identified papers that met our criteria.

In the first screening, we have looked for papers that have mentioned hemorrhoids in the title, keywords, or abstract, together with genetics in a broad sense, gene expression, specific epigenetic mechanisms, or changes in mechanisms that are likely to be mediated by epigenetics. We tried to minimize errors by double screening of papers by two independent researchers. Moreover, after identifying papers, to minimize errors, we have utilized first-pass screening, including only titles and keywords, and second-pass screening, including abstracts, full text was read during the second pass if needed.

Based on the criteria mentioned above, we identified, while also excluding the duplicates, 83 articles. Articles included in the study were only original papers about performed studies, meta-analyses, as well as reviews, which suited the topic of our review. At this point, all types of research papers other than meta-analyses, reviews, and original studies were excluded. We performed a secondary review of articles we first identified, which led to the exclusion of five more articles due to

their irrelevance to the topic of this study after reviewing their text, lack of full text in a language understandable to us, or inability to be retrieved. If a paper was deemed irrelevant by one author but relevant by another, it was up for discussion until a unanimous decision was reached. The inclusion criteria stayed the same as during the search for papers.

The next step in our research was citation searching. We have searched previously identified papers and added more articles to our base. Finally, 250 articles were included for data extraction and analysis.

We divided articles from our base into four sub-groups: those concerning only genetics, only epigenetics, possibly epigenetics, and a mixed one, including both genetics and epigenetics. One part of our team was responsible for reviewing articles and writing the text related to the involvement of genetics in hemorrhoids, based on groups: genetics and mixed genetics, and epigenetics, while the other focused solely on epigenetic mechanisms by reviewing articles from groups epigenetics, possibly epigenetics, and mixed genetics and epigenetics.

Author Contributions: Conceptualization, B.P. and M.M.; methodology, B.P., M.M.; data analysis, B.P., O.S.; writing—original draft preparation, B.P., O.S.; writing—review and editing, B.P., O.S., M.M., S.W., Z.D.; figure design, K.D.; supervision, S.W., Z.D.; project administration, B.P., Z.D. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

The following abbreviations are used in this manuscript:

FOXC2 Forkhead Box C2 NOX NADPH Oxidase NOS Nitric Oxide Synthase CALM3 Calmodulin 3 miRNA microRNA mRNA messenger RNA DNA Deoxyribonucleic Acid COX2 Cyclooxygenase-2

RYBP Ring1 and YY1-binding protein
PRC1 Polycomb Repressive Complex 1

NF-κB Nuclear Factor Kappa-light-chain-enhancer of Activated B Cells

PGE2 Prostaglandin E2 ncRNA non-coding RNA **lncRNA** long non-coding RNA rRNA ribosomal RNA tRNA transfer RNA snRNA small nuclear RNA UTR Untranslated Region **MMP** Matrix Metalloproteinase

RANTES Regulated on Activation, Normal T-cell Expressed and Secreted

CCL-5Chemokine (C-C motif) Ligand 5TNF- α Tumor Necrosis Factor AlphaVEGFVascular Endothelial Growth Factor

 $\begin{array}{ccc} IL & & Interleukin \\ IFN-\gamma & & Interferon \ Gamma \end{array}$

CGRP Calcitonin Gene-Related Peptide



SP Substance P

TRPV1 Transient Receptor Potential Vanilloid 1
MAPK Mitogen-Activated Protein Kinase
AMPK AMP-Activated Protein Kinase
PI3K Phosphoinositide 3-Kinase

UBQLN1 Ubiquilin-1

HERC3 HECT and RLD Domain Containing E3 Ubiquitin Protein Ligase 3

ECM Extracellular Matrix vWF von Willebrand Factor CD Cluster of Differentiation

TGF-β Transforming Growth Factor Beta

Xpo1 Exportin 1

PI3K/AKT Phosphoinositide 3-Kinase/Protein Kinase B

AP-1 Activator Protein 1

SHC Src Homology 2 Domain Containing

m6A N6-methyladenosine
METTL14 Methyltransferase Like 14
METTL3 Methyltransferase Like 3

WTAP Wilms Tumor 1 Associated Protein

VIRMA Vir-Like m6A Methyltransferase Associated

RBM15/15B RNA Binding Motif Protein 15/15B ZC3H13 Zinc Finger CCCH-Type Containing 13

TIE1 Tyrosine Kinase with Immunoglobulin Like and EGF Like Domains 1

VEGFA Vascular Endothelial Growth Factor A

 $\begin{array}{lll} \text{ESR1} & \text{Estrogen Receptor 1} \\ \text{ER}\alpha & \text{Estrogen Receptor Alpha} \\ \text{IBS} & \text{Irritable Bowel Syndrome} \end{array}$

PAI-1 Plasminogen Activator Inhibitor-1

TSP-1 Thrombospondin-1

NGAL Neutrophil Gelatinase-Associated Lipocalin

SANRA Scale for the Assessment of Narrative Review Articles

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