

The role of heredity in pterygium development

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Abstract

• **Several risk factors, which include heredity, ultra-violet (UV) light and chronic inflammation, contribute to pterygium development. However, there is no report integrating these factors in the pathogenesis of pterygium. The aim of this review is to describe the connection between heredity, UV, and inflammation in pterygium development. Existing reports indicate that sunlight exposure is the main factor in pterygium occurrence by inducing growth factor production or chronic inflammation or DNA damage. Heredity may be a factor. Our studies on factors in pterygium occurrence and recurrence identify that heredity is crucial for pterygium to develop, and that sunlight is only a trigger, and that chronic inflammation promotes pterygium enlargement. We propose that genetic factors may interfere with the control of fibrovascular proliferation while UV light or (sunlight) most likely only triggers pterygium development by inducing growth factors which promote vibrant fibrovascular proliferation in predisposed individuals. It also just triggers inflammation and collagenolysis, which may be promoters of the enlargement of the fibrovascular mass. Pterygium probably occurs in the presence of exuberant collagen production and profuse neovascularisation.**

• **KEYWORDS:** pterygium; fibrovascular proliferation; heredity; sunlight; inflammation; growth factors

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INTRODUCTION

Pterygium, which is a wing-shaped fibrovascular growth of the conjunctiva across the limbus onto the cornea^[1,2], is divided into the head that invades the anterior cornea, the neck that includes the superficial limbus, and the body that overlies the sclera^[3]. The cap, which is the first sign of pterygium^[4,5] is the halo in front of the pterygium head. It is deep to the epithelium^[6]. Pterygium can impair vision and it can be cosmetically unacceptable^[7]. Recurrent pterygium after surgery may be more aggressive than the primary growth^[8]. Despite the problems related to pterygium^[7,8] prevention of its occurrence and its recurrence after surgery have not been successful because the pathogenesis of pterygium is not clear.

This review describes the ocular surface anatomy relevant to pterygium, and it discusses the literature related to the current theories on pterygium pathogenesis, and it outlines the modes of genetic inheritance. It summarizes our recent studies on factors in pterygium occurrence and post-surgical recurrence and it concludes by proposing a model of pterygium development.

Ocular Surface Anatomy Relevant to Pterygium The bulbar conjunctiva is loosely attached to the underlying Tenon's fascia before the surgical limbus, thereafter the conjunctiva and Tenon's fascia, fused, adhere to the episclera^[9]. The superficial episcleral plexus is found in the surgical limbus^[10]. From the limbus, centrally, the tissues are compact^[11]. Fibroblasts and blood vessels as well as inflammatory cells are located in the conjunctival stroma, which is at the same plane as the limbal stroma and Bowman's membrane of the cornea^[3,6,12,13,16].

Current Theories on Pterygium Pathogenesis Inflammation^[14] and fibrovascular proliferation^[15-18] may be factors in pterygium occurrence. DNA damage^[19-21] has been reported to initiate pterygium development. Hereditary predisposition^[8,22-24] may be the underlying factor for pterygium occurrence. Ultra violet (UV) light has been shown to induce proinflammatory cytokines, chronic inflammatory cells, and growth factors^[16,17,25,26]. It also may damage DNA in predisposed individuals^[21,23,24,27]. However, integration of factors associated with pterygium occurrence has not been reported.

Sunlight Exposure All individuals may be exposed to UV light, which generates reactive oxygen species (ROS) from the ocular surface^[28]. Excessive exposure is widely believed

to be the reason for pterygium to occur [29,30]. However, some studies have shown that pterygium may be infrequent in individuals highly exposed or, a low exposure may be frequent in pterygium patients [5,31-34]. Excessive sunlight exposure perhaps is also related to pterygium recurrence after surgery[35].

Excessive exposure to sunlight has been correlated with collagen degeneration although collagen degeneration has been discredited as a mechanism of pterygium pathogenesis[4]. Collagen degeneration may be present in primary pterygia but, some primary pterygia may not show collagen degeneration histologically [36,37]. This degeneration is not manifested in recurrent pterygia, suggesting short durations of exposure to UV light[4,38]. It seems that the level of sunlight exposure may not be important for pterygium to occur or to recur.

Inflammation It has been shown that UV light induces pro-inflammatory cytokines in pterygia, however, the degree of induction varied in pterygia exposed to the same level of UV light, suggesting that the level of exposure to sunlight may not be important for inflammation to be severe [25,39]. It might be that the severity of inflammation is genetically controlled. Some individuals may be deficient of T-lymphokine activated killer cell-originated protein kinase (TOPK) and its deficiency appears to increase sunlight induced inflammation[40].

Reactive oxygen species phosphorylate cell membrane lipids, which manifests as increased products of lipid metabolism [41,42]. These lipid products include prostaglandin E-2 (PGE-2), which has been reported in pterygia [18]. Oxidized phospholipids stimulate production of cyclooxygenase-2 (COX-2) enzyme and interleukin-8 (IL-8), which are pro-inflammatory [43,44]. Inflammatory cells are present in all pterygium samples, which indicates inflammation[5,14,15,45,46].

Inflammation has been proposed to be the final step in the formation of pterygia, however, that inflammation was thought to be a type of hypersensitivity because the leukocytes were mainly located in the epithelium [5]. It is not clear whether hypersensitivity is crucial for pterygium to be formed. Although inflammatory cells are present in pterygia older studies [5,14] did not indicate whether the inflammatory cell infiltration was related to the severity of inflammation or to the size of pterygium or to the level of exposure to sunlight. It is not clear how inflammation may be the final step in pterygium formation.

Inflammation activates transforming growth factor-beta (TGF- β) thereby stimulating the fibroblasts to synthesize collagen [47-50]. Transforming growth factor-beta also inhibits MMPs[51,52]. Collagen is deposited randomly (fibrosis), which causes tissues to become opaque[53]. Inhibition of MMPs tends to decrease collagenolysis, however, collagen degeneration

characterizes pterygium[12,15,36]. Collagen degeneration is a sign of prolonged collagenolysis, which may be caused by ROS[41,54]. Although one previous study failed to detect MMPs in pterygium fibroblasts several studies have reported MMP expression, which seems to suggest that collagen degeneration in pterygia is due to MMPs [3,20,55,56]. As all pterygia have inflammatory cell infiltrations it may be that MMPs are not expressed in pterygium fibroblasts despite limbal stem cell damage, but, this needs to be corroborated. Inflammation also induces angiogenic growth factors[18,55,57,58]. Moreover, TGF- β up-regulates vascular endothelial growth factor (VEGF), which in a frame-work of fibronectin stimulates neovascularisation as collagen synthesis proceeds[53,59,60].

Fibrovascular proliferation Ultraviolet light, even of a short duration may induce growth factors such as basic fibroblast growth factor (bFGF), TGF- β , platelet derived growth factor (PDGF), VEGF, connective tissue growth factor (CTGF) and heparin binding epidermal growth factor-like epidermal growth factor (HB-EGF)[15-17]. Oxidative stress induces those growth factors in the fibroblasts, endothelial cells and inflammatory cells in the stroma. It also induces those growth factors in the conjunctival epithelium [15-18,61]. Growth factors promote vibrant proliferation of fibroblasts in pterygia but in controls, the same level of growth factor proteins causes sluggish mitosis [62,63]. This seems to suggest that vibrant fibroblast mitosis is unlikely to be due to overexpression of these proteins in pterygia. It may be due to an abnormal phenotype of pterygium fibroblasts that causes fibroblasts to respond energetically to growth factors [4,62]. Fibroblast abnormality might arise from sunlight damage, which causes these to over-express MMPs [20,56]. However, acquired fibroblast damage fails to explain why pterygium occurs in patients whose fibroblasts do not express MMPs[55].

Heparin binding epidermal growth factor-like epidermal growth factor, a fibrogenic growth factor may be available for at least 48h in pterygia after exposure to UV light has stopped[17,63]. Fibrogenic growth factors such as PDGF are not over-expressed in controls [15,62]. The expression of bFGF in some controls may be the same as in cases, which suggests that over-expression of angiogenic growth factors is not the reason for vibrant fibroblast mitosis or for pterygium to occur [15,62]. Rather, the up-regulation of fibrogenic growth factors is most likely to be the reason for fibroblast proliferation and for pterygium to occur [15,62,63]. Nevertheless, angiogenic growth factors such as bFGF and VEGF are up-regulated in pterygia mainly *via* ROS [15,16,18,64]. Reactive oxygen species in addition directly stimulate capillary growth[65]. Bevacizumab, which is anti-VEGF fails to abolish pterygium recurrence after surgery[66]. Since pterygia occur in the presence of fibrogenic growth factors failure of bevacizumab to abolish post-surgical pterygium recurrence

may be due to its lack of inhibition of fibrogenic growth factors [15]. This seems to suggest that pterygium occurs because fibrogenic growth factors are not inhibited, however, there is no literature that lack of inhibition of fibrogenic growth factors occurs in pterygium.

A fibrogenic growth factor binds to its receptor at the fibroblast cell membrane to form a complex which is internalised to form specific endocytic vesicles [67]. Receptor-regulated sma (small) and mad (mothers against decapentaplegic) proteins abbreviated smad, *via* a series of steps including smad1 and 5 activate the receptor thereby translocating the growth factor to the nucleus [67-70]. A signal for the transcription of genes for fibroblast mitosis is initiated [71]. After adequate signals a different type of specific endocytic vesicles is formed [67]. Inhibitory smad proteins (smad7) in these vesicles terminate the signal for genetic transcription [72,73]. Inhibitory smad proteins stimulate smad ubiquitin regulatory factor-1 (smurf-1), which may compete with smurf-2 to deactivate growth factor receptors [74,75]. The action of smad7 is independent of smurf proteins [72]. Inhibitory smads and smurf proteins are genetically determined [76,77]. Growth factors generate ROS at the cell membrane and TGF- β inhibits antioxidant enzymes [78].

DNA damage Ultraviolet light may damage DNA [20,21,27] irrespective of the dose of radiation, race, or age of the individual [21,27,79]. DNA damage might cause localised limbal stem cell deficiency probably due to migration of both the reserve stem cells and transient amplifying cells [56]. Damaged cells perhaps migrate in all directions [80] assisted by MMPs, which may degrade collagen and fragment Bowman's membrane [20,56]. Pterygium occurs maybe as a result of corneal conjunctivalisation [56]. Migration might be promoted by inflammation whereby epithelial mesenchymal transition occurs to the cells which migrate to the stroma in individuals predisposed to a deficiency of discs large factor-5 (Dlg-5) [81-83]. This may cause a fibrotic mass [80]. The wing-like shape of pterygium may be calculated as due to more epithelial cell loss centrally than at the limbus [84]. However, this theory fails to explain pterygium shape peripheral to the limbus. The theory of DNA damage fails to explain why pterygium develops in those having no evidence of DNA damage [27,85]. Moreover, some pterygium patients do not have predisposition to DNA damage [23,24].

Hereditary predisposition Hereditary predisposition to pterygium development has been acknowledged, but, it has been underemphasized [22,86-89]. The mode of inheritance has been reported to be autosomal dominant based on a study of one [87,88] or two families [86] however, a large sample is necessary to increase credibility [90] since alleles may or may not be transmitted. Autosomal recessive mode might also be possible however, because the original report in French is difficult to find it is difficult to ascertain whether pterygium

patients were compared with unaffected individuals or, how many pedigrees or patients were considered [87]. Multifactorial mode is likely but, it was determined using self-reported family histories which were not tested for independence of association with pterygium occurrence [89]. Knowledge of the mode of inheritance facilitates determination of the possible mechanism of pterygium development [91,92].

Modes of Inheritance These may be Mendelian or non Mendelian. Mendelian inheritance may be autosomal dominant, autosomal recessive or sex linked. Non Mendelian inheritance may be multifactorial or mitochondrial. Mendelian and multifactorial modes of inheritance involve genes that are located in the nucleus.

The phenotype in autosomal dominant inheritance is determined by a single defective allele, which is dominant [91,93]. According to Mendelian principles, whether one or both parents are affected the offspring have a 50% chance of being affected as individuals who are homozygous defective are so severely affected that they perish before birth or early in life [91]. Incomplete penetrance sometimes occurs thereby causing a skipped generation [90].

Inheritance in autosomal recessive mode occurs due to two ineffective alleles, which are recessive [40,94]. It may be homozygous recessive [40] or double heterozygous whereby two heterozygous recessive genes that code for the same phenotype are located in different loci [94]. The risk of the offspring becoming affected is 100% if both parents are homozygous recessive while it is 50% if one parent is homozygous and the partner is heterozygous recessive and it is 25% if both parents are heterozygous [40]. There is no risk of having an affected offspring if one parent has normal paired alleles [40]. According to Mendelian principles [91,93] if both parents are double heterozygotes the unaffected to the affected ratio of the offspring is 5:11.

Mendelian principles require that sex linked conditions are always recessive [95] because males lack one pair of alleles in the Y chromosome, which causes inheritance of a defective dominant allele in the Y chromosome to be lethal [91]. Males may become affected when they inherit a recessive allele from an affected or heterozygous mother and the affected fathers may transmit their recessive gene only to their daughters who may become affected only if the mother is homozygous or heterozygous recessive [95].

In multifactorial inheritance genes may interact with environment [96], or, two or more genes coding for different proteins and in different loci may modify one another's effect [97,98] to produce a phenotype. Genes are not defective [91,93] however, genes have to be activated before transcription to messenger RNA, after which protein synthesis may occur [67,71,99]. One active allele is sufficient for the gene to be effective [97], which allows a protein to be synthesized [40]. The risk of transmission to subsequent offspring, which can be predicted

using Mendelian principles^[91,93] depends on the genotypes of the mating partners. Affected individuals tend to cluster in families^[100].

The polygenic model specifies that the more inactive (determinant) alleles interacting the severer the phenotype^[92] and the higher the risk of transmission to subsequent generations^[100]. The threshold model requires that the contributions by genes and environment reach a threshold that leads to phenotype whereby sometimes, genes are the main contributor and other times, the environment is the main contributor to the threshold^[96].

Recent Studies on Factors in Pterygium Occurrence

These were undertaken in Mankweng Hospital, a tertiary referral centre in Limpopo Province of South Africa, which is mainly rural and it is bisected by the tropic of Capricorn (23.5° south of the Equator). The Province is sunny and dry^[101] and it is inhabited mainly by the Pedi, Tsonga, Venda, and Tswana. These groups of Bantu people have been reported to practice first degree cousin marriage^[102], in which reproduction may promote the occurrence of hereditary conditions^[103]. The population of Limpopo in 2009 when these studies begun was estimated at 5227200, of which 2436400 (46.6%) was 20-64y old, and 87% of the population was rural^[104]. The methods and results of these studies have been reported^[105-108].

The pterygium cases and control patients whose conjunctivas were investigated by immunohistochemistry were selected from the Eye Clinic, and the unaffected individuals matched with pterygium cases were selected from the refraction Clinic. Two hundred and thirty cases and 150 controls matched for age and sex with the first 150 cases, as well as seven unmatched controls whose eyes had been irreparably injured were interviewed and their eyes examined. Data from 150 case-control pairs were analyzed as pre-calculated to give a 20% difference in family history at a power of 80%, assuming a base rate of 10% in controls and *P*-value of 5%. Of the 300 participants whose data were analyzed the age range was 22-65y, modal range was 40-49y; the females were 3.5 times more frequent than males^[106]. Pterygium surgery was done on 200 cases, which had indications for surgery. The indications included corneal astigmatism, pterygium obstructing or threatening to obstruct the visual axis, frequent pterygium inflammation, and disfigurement by pterygium^[108]. Interviews were conducted, a full eye examination done, and the pterygia in patients having indications for surgery were excised. The 59 pterygium specimens and 7 control nasal conjunctivas were investigated by immunohistochemistry^[107]. The control specimens were obtained from males who were aged 23-51y old. Follow-up family visits were conducted on selected cases and controls^[106]. Because alleles may or may not be transmitted a large sample that is necessary for the calculation of a credible mode of

inheritance was obtained by combining the relatives of cases and controls into 2 separate families^[90,108]. There were 382 combined relatives of pterygium probands and 394, of unaffected probands; their age range was 10-86y, and 275 of 382 relatives of cases (71.9%) were ≥40y old compared with 284 of 394 relatives of controls (72%)^[106]. The ratio between the unaffected and pterygium-affected relatives in the combined families of cases was calculated, which was used to determine the likely mode of inheritance based on Mendelian principles^[40,91,93,94]. As that ratio was not Mendelian the equivalent ratio was computed and estimated because decimals of individuals do not exist. The estimated ratio predicted the likely genotypes of a mating couple whose offspring are expected to be in the proportion of the estimated ratio. Mendelian principles^[93,94] were applied to that mating to depict genotypes of the offspring. One pedigree was used to demonstrate the likely mode of inheritance^[87,88].

Heredity is fundamental for pterygium to occur Family history, which implicates heredity^[22,89] was associated with pterygium occurrence^[105,106] independent of the use of traditional eye medication and of the unstable tear film^[106]. Having diagnosed pterygium-affected relatives, which implicates heredity^[8,86-88] was associated with pterygium occurrence hence confirming familial occurrence of pterygium^[106]. Pterygium patients with the unaffected individuals had similar exposure to sunlight, which suggests that familial occurrence was due to heredity rather than environment^[106].

Traditional eye medication was the only environmental factor associated with pterygium however, the controls also had used this medication in a similar way, obtained from the same practitioners, in the same period, which suggests that traditional eye medicine was not a direct cause of pterygium^[106]. Individuals who use African traditional medication are likely to follow certain traditions^[109] such as first degree cousin marriage^[102]. Reproduction between cousins increases the risk of occurrence of hereditary conditions present in an extended family^[103]. The following of the tradition of first degree cousin marriage^[102] is the reason for the association of traditional eye treatment with pterygium and so, the use of traditional medication may implicate heredity in pterygium occurrence^[106].

The ratio between the unaffected and pterygium-affected individuals in the combined family of pterygium probands was 9:7^[106], which suggests digenic inheritance (the simplest form of multifactorial inheritance^[97]). Table 1 shows the depicted genotypes of affected and unaffected offspring. A and B indicate active alleles whereas a and b indicate inactive alleles. Bold font indicates predicted genotypes of a pterygium patient. The appearance of only two letters represents predicted alleles in the gametes of the parents. The genotypes of the two parents are AaBb and AaBb. Each letter

Table 1 Depicted genotypes of affected and unaffected offspring

Genotypes	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
Ab	AAbB	AAbb	AabB	Aabb
aB	aABB	aABb	aaBB	aaBb
ab	aAbB	aAbb	aabB	aabb

whether capital or small represents one type of gene. This table suggests that pterygium cases have at least one type of gene having both alleles inactive (determinant gene). The signals for fibroblast mitosis, generated by fibrogenic growth factors are regulated by inhibitory smad proteins [72,73] and smurf proteins [74,75]. These proteins are genetically determined [76,77] and so it is possible that pterygium fibroblasts undergo vibrant mitosis [62] because of genetic lack of inhibitory smads or smurf proteins.

Figure 1 depicts a pedigree of a pterygium proband. Oval empty drawings illustrate unaffected females and the shaded oval drawings illustrate affected females. Rectangular empty drawings illustrate unaffected males and the shaded rectangular drawing indicates an affected male. The arrow points at the proband. As 2 generations were affected autosomal dominant with incomplete penetrance in the first generation is likely [87]. As only the second and third generations had pterygium patients it is possible that this was due to autosomal recessive mode of inheritance whereby the first generation and the spouse of the proband were carriers [40]. It is also possible that sex linked inheritance was the mode of inheritance since the proband, a male, might have inherited a recessive gene from his carrier mother and he transmitted this gene to his daughter whose mother was a carrier [95]. Because this pedigree does not show a consistent Mendelian pattern Mendelian inheritance is unlikely in pterygium occurrence. Rather, the most likely mode of inheritance is multifactorial because it was determined from a large sample [90,110]. The proband had a short recurrence time (Less than 3mo after surgery [108]) and his daughter was 16 years old. These observations indicate that multifactorial mode of inheritance follows the polygenic model [92]. A short recurrence time and an early onset are signs of severe pterygium [8]. The skipping of the first generation and only one individual in the third generation being affected might suggest the presence of few genes [92]. However, the small size of a pedigree [90] most likely caused it to appear that all siblings in the second generation and only one in the third generation were pterygium patients because alleles may or may not be transmitted. All pterygium patients are predisposed and they may have unaffected relatives [106]. The proportion of the pterygium-affected relatives seems to depend on the proportion of determinant genes (polygenic model [100]). These findings suggest that predisposition to pterygium is unlikely to be the deficiency of Dlg-5 [82] because more than one gene seems to be involved in

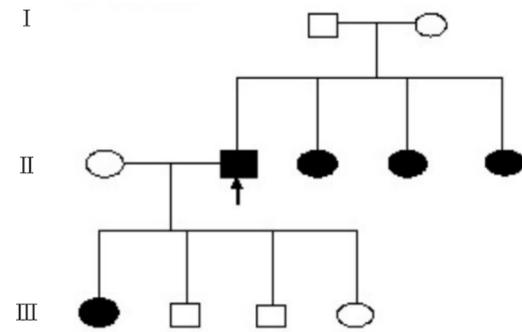


Figure 1 Pterygium pedigree.

pterygium development whereas Dlg-5 deficiency involves only one gene.

Age and small pterygium extent seem to be associated with pterygium recurrence after surgery perhaps due to the patients' selection criteria [108]. Also, large pterygium extent seems to be associated with recurrence perhaps due to inadequate treatment [111]. It is possible that pterygium size has no relationship with post-surgical recurrence. Pterygium fleshiness appears to be associated with pterygium recurrence after excision probably because excision was not followed by adjunctive treatment [112] otherwise, fleshiness has no relationship with post-surgical recurrence [108]. Since it is likely that pterygium occurrence is due to dormant genes post-surgical recurrence (pterygium progression [108]) can be explained by continued genetic inactivity [113]. The patient's age, pterygium size, and its fleshiness most likely depend on pterygium progression to be associated with post-surgical recurrence. However, genes controlling pterygium occurrence have yet to be established.

Sunlight exposure is only a trigger for pterygium to occur All the participants had been exposed to sunlight and excessive exposure had no relationship with pterygium occurrence [106], which is similar to recent reports [32,34]. Since sunlight damage may induce chronic inflammatory cell infiltration in the conjunctival stroma [26] the presence of chronic inflammatory cells in all pterygium samples, and the inhibition of MMPs in all pterygia and controls [107] support the finding that all pterygium patients as well as controls had been exposed to sunlight [106]. As the inflammatory cell infiltrate varied in pterygia that had collagen degeneration (sign of prolonged UV radiation [54]) this shows that the degree of infiltration was not related to the level of exposure to the sun. Sunlight irrespective of its degree of exposure may be only a trigger for pterygium occurrence in those predisposed to pterygium formation [106]. This may occur by inducing oxidative stress at the ocular surface [28]. Also, sunlight may be only a trigger for pterygium recurrence after excision [108].

Chronic inflammation is only a promoter of pterygium enlargement Inflammatory cell infiltration in pterygium samples is a sign of inflammation [46]. Although the inflammatory cell count was correlated with pterygium size,

which suggests that inflammation may contribute to pterygium enlargement inflammation is unlikely to be a determinant of enlargement because pterygia irrespective of their size tended to have a low count ^[107]. The degree of the inflammatory cell infiltration may indicate the severity of inflammation rather than pterygium size ^[107]. Inflammation irrespective of its severity may be just a promoter of pterygium enlargement. Because pterygia tended to be mildly inflamed this suggests that epithelial mesenchymal transition is unlikely to be the mechanism for pterygium to occur as epithelial mesenchymal transition requires that inflammation be severe for it to occur^[81].

Inhibition of MMPs in the fibroblasts and stroma of all pterygium samples and controls is most likely to be due to inflammation ^[107]. Inflammation activates TGFβ ^[47,48], which stimulates the fibroblasts to synthesize collagen ^[49,50]. In addition, TGFβ inhibits MMPs ^[51,52]. The synthesized collagen is deposited randomly, which causes previously transparent tissues to become opaque ^[53]. Collagen is the reason that pterygia are fleshy and it is the reason for the cap. Inhibition of MMPs minimizes collagenolysis ^[12] and it suggests that the collagen degeneration which was present in most of the pterygia and controls was not due to MMPs. This contradicts previous studies ^[20,56] perhaps because the participants in the present study had not used spectacles^[107]. Transforming growth factor-beta up-regulates VEGF ^[59], which stimulates neovascularisation^[60] hence, inflammation in addition promotes pterygium neovascularisation.

Limbal stem cell damage was not associated with pterygium^[107]. This suggests that DNA damage^[19,29] is unlikely to be a factor in pterygium development. The predisposition to DNA damage ^[23,24] is unlikely to be the predisposition to pterygium occurrence.

Proposed Model of Pterygium Development Figure 2 shows the proposed model of pterygium development, which is a flow chart showing that pterygium development is influenced by heredity in conjunction with sunlight exposure. Sunlight exposure, *via* oxidative stress induces growth factor production, angiogenesis, chronic inflammation, and collagenolysis. Bold black font indicates determinant factors, bold black font in italics indicates promoting factors, and bold black arrows show the determinant pathway. Normal black font in italics indicates a trigger and bold yellow arrows show the triggering pathway. Heredity^[105,106] influences growth factors to cause vibrant fibroblast mitosis^[63]. Sunlight induced oxidative stress triggers growth factors ^[28,61] and it triggers angiogenesis by directly stimulating capillaries to grow^[65]. Oxidative stress triggers inflammation^[18,41] in sunlight exposed conjunctivas ^[106], and it causes collagenolysis also ^[41,107]. Vibrant mitosis produces many fibroblasts ^[62], which are stimulated by inflammation ^[47] to collectively synthesize collagen ^[49] exuberantly. Excessive collagen is deposited in

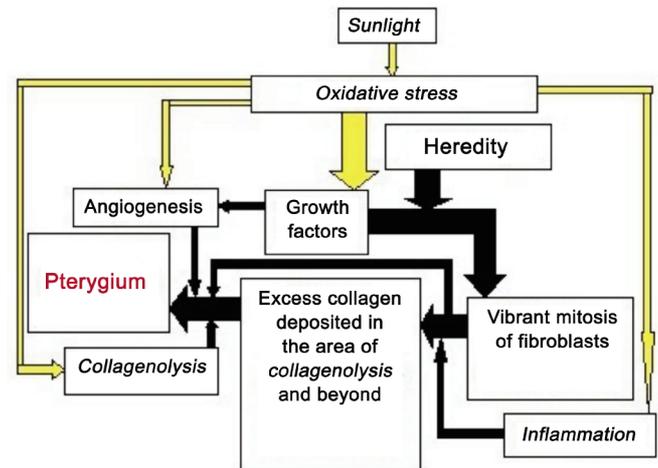


Figure 2 Proposed model of pterygium development.

the damaged area and beyond the margins of the damaged matrix to develop the pterygium cap. The excessive collagen is invaded by fibroblasts, and new blood vessels stimulated by growth factors and ROS to develop pterygium. Cap collagenolysis^[41] facilitates the fibroblasts and new blood vessels to invade the stroma. Bowman's membrane probably gets fragmented due to the location of the cap in it^[4,6]. Pterygium onset is at the surgical limbus probably because of the numerous endothelial cells ^[10], which generate abundant ROS after sunlight exposure^[28].

Figure 3 depicts sub-model 1, which is a flow chart showing that heredity sustains pterygium development *via* oxidative stress generated by proliferating fibroblasts and endothelial cells. Bold font indicates determinant factors, bold font in italics shows promoting factors, and orange arrows indicate pathways involving ROS, and a plain arrow indicates a subsidiary pathway for growth factor production. After sunlight has triggered pterygium onset the proliferating fibroblasts generate ROS, through which production of fibrogenic and angiogenic growth factors is sustained ^[61]. Through ROS the proliferating fibroblasts sustain inflammation ^[18,39,41,42]. Matrix damage ^[41,107] and angiogenesis (by directly stimulating capillary growth ^[65]) are also sustained. The replicating endothelial cells generate oxidative stress thereby stimulating endothelial cells and fibroblasts to produce fibrogenic and angiogenic growth factors ^[61]. Also, capillary growth is directly stimulated ^[65]. Angiogenic growth factors are also induced by inflammation ^[57,58]. It seems that sustenance of pterygium development can be terminated if hereditary predisposition is halted, perhaps by activation of previously dormant genes^[99,108].

Because the conjunctiva and Tenon's fascia are loosely attached before the surgical limbus, thereafter the two, fused, are firmly attached to the episclera ^[9], and the limbus and cornea are compact^[11], it is most likely that there is increasing centripetal resistance to the expanding fibrovascular mass, which causes it to be shaped like a wing. The role of

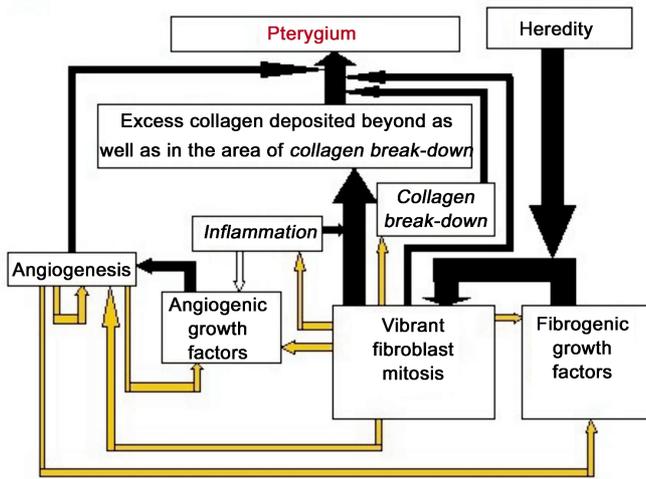


Figure 3 Sub-model 1.

pterygium inflammation is to promote pterygium enlargement [107] and fleshiness by stimulating collagen synthesis^[49,50] and its conservation^[107].

Figure 4 depicts sub-model 2, which is a flow chart showing that heredity determines pterygium severity. Bold font indicates determinant factors. Double arrows indicate interaction. Normal arrows show normal outcome and bold single arrows show an abnormal outcome. The genes involved in pterygium occurrence may be those for inhibitory smad proteins [76] or for smurf proteins [77]. Because the inhibition of signals for mitosis, generated by growth factors is independent of receptor inhibition [72] it may be that interaction between inactive genes for inhibitory smads and inactive genes for smurfs or, between inactive genes for inhibitory smads and active genes for smurf proteins causes severe pterygium to occur. Because degradation of growth factor type 1 receptors depends on smad 7 [74] it may be that a mild pterygium occurs if active genes for smad 7 proteins interact with inactive genes for smurf proteins.

Since numerous fibrogenic growth factors are present in pterygium^[15-17] it is possible that pterygium size is determined by the proportion of growth factors lacking inhibitory smads or smurf proteins (polygenic model^[100]). Severity in large pterygia may be determined by the proportion of growth factors lacking inhibitory smad proteins (polygenic model^[92]).

CONCLUSION

Hereditary predisposition is fundamental for the onset and sustenance of pterygium. Pterygium size and severity are most likely to be determined by hereditary factors. Predisposition to pterygium occurrence most likely follows multifactorial mode of inheritance, which is of the polygenic model. It is possible that two types of genes, one for inhibitory smad proteins and the second for smurf proteins are inactive thereby predisposing to pterygium occurrence. It seems that fibrogenic growth factors are crucial for pterygium to develop, and it seems that pterygium

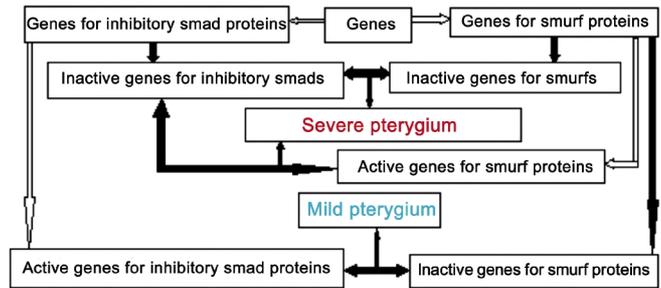


Figure 4 sub-model 2.

angiogenesis follows fibroblast proliferation, collagen synthesis, and collagenolysis.

Sunlight is only a trigger for pterygium to occur, perhaps *via* reactive oxygen species. It appears that inflammation and collagen damage, which are most likely to be due to oxidative stress only promote pterygium enlargement.

Recommendations Genetic counselling to advise family members regarding risks for pterygium development seems far off at present although it might play a role with further investigation in high risk communities. Studies to determine the molecular nature of predisposition are recommended.

Control of sunlight exposure by use of spectacles/sunglasses in predisposed individuals is encouraged. Control of collagen synthesis seems to be an attractive option to minimize enlargement of the fibrovascular mass in those predisposed.

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