



Symposium

Genetic polymorphisms and their association with atopic dermatitis in skin of color – A comprehensive review

Sahana P. Raju¹

¹Department of Dermatology, Bangalore Medical College and Research Institute, Bengaluru, Karnataka, India.

ABSTRACT

Atopic dermatitis (AD) is a chronic inflammatory skin disease with a multifactorial etiology, including genetic, environmental, and immunological components. The disease disproportionately affects children and contributes significantly to the global disease burden, especially in high-income countries. While several genetic factors have been established in European populations, limited research exists on the genetic landscape of AD in individuals with skin of color (SOC), which includes Asian, African, Latin, Pacific Islander, and Indigenous populations. SOC is under-represented in dermatologic research, contributing to diagnostic, therapeutic, and epidemiologic gaps. Genetic heterogeneity and pigment-related diagnostic challenges complicate the clinical management of AD in these groups. This review aims to summarize current knowledge on genetic polymorphisms associated with AD; highlight differences in genetic susceptibility and mutation profiles in SOC populations, particularly in Indian patients; discuss clinical implications of identified polymorphisms for disease onset, severity, and treatment response; identify limitations in existing research; and propose future directions for inclusive genetic studies. Filaggrin (FLG) mutations, particularly loss-of-function variants, play a crucial role in AD susceptibility. Indian studies reveal novel FLG mutations not previously identified in other populations, with significant association with early disease onset and high Immunoglobulin E (IgE) levels. Other single-nucleotide polymorphisms in immune and barrier genes (e.g., Interleukin-4 [IL-4], IL-13, serine protease inhibitor Kazal type 5, toll-like receptor 2) further contribute to ethnic-specific risk profiles. SOC populations show lower prevalence of common European FLG mutations but unique mutations with distinct clinical outcomes. Understanding the genetic architecture of AD in SOC is critical for early diagnosis, risk stratification, and personalized therapy. Future directions include inclusive multi-omics research, creation of biobanks, and better ethnic representation in genomic databases.

Keywords: Atopic dermatitis, Genetic polymorphisms, Skin of color

INTRODUCTION

Atopic dermatitis (AD) is a chronic inflammatory skin condition with a multi-factorial etiology. It has significant global health implications, especially in children. Skin of color (SOC) refers to Asian, including Indian skin, African, Latin, Hawaiian, Pacific Islanders, Native Americans, Chinese, Japanese, Hispanics, and other people of Indigenous descent.^[1] SOC is generally under-represented across all dermatological conditions, especially in AD. There are variations in the genetic make-up, pathogenesis, epidemiology, clinical features, complications, and management of AD in SOC, compared to Caucasian skin.^[2] A combination of genetic predisposition and environmental triggers contributes to the onset and progression of AD within an individual. This intricate interplay accounts for the wide variation seen in the disease's presentation, severity, and progression. Factors such as ethnicity, geographic location,

climate, pollution levels, and occupational exposures play key roles in shaping these differences.^[3] Genetic factors play a pivotal role in the pathogenesis of AD, accounting for almost 82% of the risk.^[4] Children with a strong family history of atopy in both parents are at a 5 times higher risk of developing early-onset AD.^[5] Genetic risk factors vary across ethnic groups, indicating the need for population-specific studies. Recognizing the distinct clinical manifestations of AD across various ethnic groups, along with the genetic polymorphisms that affect disease susceptibility and treatment response, is essential for effectively managing a growingly diverse patient population. Studying AD in SOC populations presents unique challenges due to underrepresentation in clinical and genetic research. Variations in pigmentation can mask classic signs like erythema, leading to delayed or missed diagnoses.^[6] Differences in healthcare access and cultural perceptions of skin disease further contribute to disparities. In addition, most genomic studies have focused on European

*Corresponding author: Sahana P. Raju, Department of Dermatology, Bangalore Medical College and Research Institute, Bengaluru, Karnataka, India. sahanapraju@gmail.com

Received: 05 June 2025 Accepted: 08 July 2025 Epub Ahead of Print: 30 August 2025 Published: 26 September 2025 DOI: 10.25259/IJSA_39_2025

This is an open-access article distributed under the terms of the Creative Commons Attribution-Non Commercial-Share Alike 4.0 License, which allows others to remix, transform, and build upon the work non-commercially, as long as the author is credited and the new creations are licensed under the identical terms. ©2025 Published by Scientific Scholar on behalf of Indian Journal of Skin Allergy

populations, limiting the applicability of findings to diverse ethnic groups.^[7] This review aims to cover the genetic basis and specific genetic polymorphisms of AD in the under-represented SOC, with more focus on genetic variability in Indian skin.

GENETIC BASIS OF AD

Heritability estimates from family and twin studies suggest that genetic factors contribute significantly (70–80%) to the risk of developing AD, underscoring its polygenic and multifactorial nature rather than a simple familial inheritance. Monozygotic twins exhibit concordance rates as high as 86%, compared to 21–23% in dizygotic twins. A landmark discovery in the genetics of AD is the identification of loss-of-function mutations in the *Filaggrin* (*FLG*) gene, which compromise skin barrier function. These mutations are common in Northern Europeans but occur at much lower frequencies in populations of African ancestry. Beyond *FLG*, several other genetic variants have been linked to AD, particularly those involved in the Th2 immune pathway, including interleukin-4 (*IL-4*), *IL-13*, and *IL4R*, as well as serine protease inhibitor Kazal type 5 (*SPINK5*), which is implicated in Netherton syndrome. Genome-wide association studies (GWAS) have further expanded the genetic landscape of AD, identifying over 30 risk loci, many associated with epidermal barrier integrity and immune regulation. Some loci are located in non-coding regions, indicating the need for functional follow-up studies. Phenome-wide association studies have demonstrated that *FLG* mutations are also associated with other atopic conditions such as asthma and allergic rhinitis. Whole-exome and genome sequencing efforts have revealed rare variants in genes such as *general transcription factor IIIH subunit 5* (*GTF2H5*), *A disintegrin and metalloproteinase domain containing protein 33* (*ADAM33*), *envoplakin* (*EVPL*), *NLR family pyrin domain containing 1* (*NLRP1*), underscoring the genetic heterogeneity of AD and the need for ancestry-specific research.^[8]

The epidermal differentiation complex (EDC), located on chromosome 1q21, is a key genomic region involved in maintaining skin barrier structure and function. This region spans about 1.9 megabases and includes nearly 45 genes, which are mainly categorized into three groups: Cornified envelope precursor proteins such as loricrin, involucrin, and late-stage small proline-rich proteins; the S100 calcium-binding protein family; and the S100 fused-type proteins (SFTPs), which include *FLG*, *FLG-2*, trichohyalin, trichohyalin-like protein 1, hornerin, repetin, and cornulin. Among these, the SFTP family is particularly significant in the context of AD, due to its central role in skin differentiation and immune barrier function. Beyond the genes located within the EDC, whole genome sequencing has highlighted *SID1* transmembrane family member 2 (*SIDT2*) (on chromosome 11q23.3) and *RBBP8NL* (on 20q13.33) as

important modulators of keratinocyte-mediated antiviral defense, particularly in response to herpes simplex virus type 1.^[9]

Other single-nucleotide polymorphisms (SNPs) in AD

SNPs are considered significant genetic contributors in allergic diseases and can influence an individual's susceptibility to AD. Research on SNPs has identified several genetic loci associated with AD risk, including *FLG*, *IL-4*, *IL-4* receptor alpha (*IL-4R α*), and *SPINK5*. However, most of these studies have concentrated on isolated polymorphisms and have often yielded inconsistent or conflicting results. Nine SNPs have shown a positive correlation with AD susceptibility (*FLG* R501X, deletion at *FLG* 2282, chromosome 11q13.5 rs7927894, *IL-17A* rs2275913, *IL-18-137* G/C, toll-like receptor 2 [*TLR2*] rs5743708, *TLR2* A-16934 T, *SPINK5* Asn368Ser, interferon- γ T874A) and one was negatively associated with AD susceptibility (*IL-4-1098* T/G).^[10]

The genes involved in AD can be broadly categorized into those involved in immune regulation and epithelial barrier function.

Immune-related genes

Genetic variations in components of both innate and adaptive immunity – especially those involved in Th2 signaling – play a crucial role in the development of AD and exhibit notable differences across ethnicities. Variants in Th2-associated genes such as *IL-4*, *IL-13*, *IL-31*, and their receptors (*IL-4R α* , *IL13R α 1*) are linked to a heightened risk of AD due to disruptions in signaling cascades. Elevated expression of *IL-4* and *IL-13* can also suppress *FLG* expression, compromising the skin barrier even in the absence of *FLG* mutations. In Egyptian individuals, specific polymorphisms in *IL-4* and *IL-4R α* are associated with AD susceptibility. Similar associations involving *IL-4*, *IL-13*, and *IL13R α 1* have been documented in Japanese, Chinese, and Korean populations. The other immune-related genes are enumerated in Table 1.^[11-14]

Genes involved in epithelial barrier function

FLG loss-of-function mutations are among the most thoroughly investigated genetic factors associated with AD across different populations. The other genes involved in epithelial barrier function are enumerated in Table 2.^[15-22]

ROLE OF FLG IN AD

The *FLG* gene, situated on chromosome 1q21 within the EDC, encodes *FLG*, a critical protein in the stratum corneum (SC). Research from European and Asian populations has consistently shown that *FLG* loss-of-function mutations are a major risk factor for AD, identified in nearly 50% of European and about 27% of Asian patients with the condition.^[23] Individuals carrying these mutations often

Table 1: Genes involved in immune regulation of atopic dermatitis.

Gene	Locus	Population and key findings
<i>DEFB1</i> (<i>Defensin beta 1</i>)	8p23	Single-nucleotide polymorphisms of <i>DEFB1</i> at 668 C and 1836 A alleles correspond to an earlier age of onset and increased severity in the Mexican population. ^[11]
<i>FCERIA</i> (Fc fragment of IgE receptor Ia)	1q23	Japanese patients of atopic dermatitis with the 315CT/TT genotype tend to have higher total serum IgE levels. ^[12]
<i>TSLP</i> (Thymic Stromal Lymphopoietin)	5q22	<i>TSLP</i> and its receptors - <i>IL7R</i> and <i>TSLPR</i> increase the risk of AD and Eczema herpeticum in African-American patients ^[13]
<i>STAT6</i> (Signal Transducer and Activator of Transcription 6)	12q13	<i>IL-4</i> , <i>IL-4Rα</i> , and <i>STAT6</i> gene polymorphisms showed increased risk of AD in Saudi-Arabians. ^[14]

AD: Atopic dermatitis, IgE: Immunoglobulin E, *DEFB1*: Human beta-defensin 1, *STAT6*: Signal transducer and activator of transcription 6, *TSLP*: Thymic stromal lymphopoietin receptor, *IL*: Interleukin-4

Table 2: Genes involved in epithelial barrier function in atopic dermatitis.

Gene	Locus	Population and key findings
<i>FLG</i>	1q21	Multiple studies show a strong association between <i>FLG</i> mutation and increased AD risk in African-American, Chinese, Japanese, and Korean populations ^[15-18]
<i>FLG-2</i>	1q21	Showed an increased risk of AD mainly in Ethiopian patients. ^[19]
<i>SPINK5</i>	5q31	Mutations in <i>SPINK5</i> exons 13, 14, and 26 show increased risk of developing AD, other atopic conditions, asthma, and hand eczema, along with <i>IL-31</i> polymorphisms in Taiwanese, Japanese, and Chinese patients. ^[20-22]
<i>TCHH</i> , <i>CRNN</i> , <i>HRNR</i>	1q21.3	Shows a weak association with AD in the Ethiopian population ^[19]

AD: Atopic dermatitis, *IL*: Interleukin, *FLG*: Filaggrin, *SPINK5*: Serine protease inhibitor, kazal-type 5, *TCHH*: Trichohyalin, *CRNN*: Cornulin, *HRNR*: Hornerin

present with an earlier onset of AD, more severe symptoms, increased susceptibility to eczema herpeticum, and a higher likelihood of other atopic conditions compared to those without the mutations.^[24]

FLG-2, a member of the S-100 protein family and part of the polyfilament group, is derived from profilaggrin through processes involving dephosphorylation and proteolytic cleavage. A deficiency of *FLG-2* has been associated with

abnormalities in the structural organization and maturation of the lipid bilayers, a reduction in the cohesion of corneocytes, and increased permeability of the SC.^[25] *In vitro* experiments using reconstructed human epidermal models demonstrated that silencing *FLG2* expression through short hairpin RNA (shRNA) resulted in a significant reduction of natural moisturizing factor (NMF) components such as urocanic acid and pyrrolidone carboxylic acid, which are essential for absorbing ultraviolet (UV) radiation and contribute to protection against UVB-induced damage. Furthermore, reduced *FLG2* expression led to structural changes in the epidermis, including a denser SC with parakeratosis, the presence of abnormal intracellular vesicles, and an increase in surface pH, which are features consistent with a weakened skin barrier and could predispose to conditions like AD.^[26] However, there are no studies currently that directly link standalone mutations in *FLG2* and the development of AD.

The most prevalent *FLG* mutations (R501X, 2282del4, S3247X, and R2447X) are found in 7–10% of White Europeans, whereas Asian populations tend to have distinct *FLG* null mutations specific to their ethnic backgrounds. In populations of African descent, the link between *FLG* mutations and AD remains less definitive. *FLG* mutations appear to be approximately 6 times less frequent in African Americans than in European Americans. The four most common *FLG* null mutations are found in fewer than 5.8% of African-Americans, compared to 27.5% in European Americans. Interestingly, the mutation frequency is higher among African-Americans diagnosed with both AD and ichthyosis vulgaris, with one study reporting a 22.2% mutation rate in this subgroup. Similar to European populations, lower intragenic copy number in *FLG* is associated with more severe disease in African-Americans, with each additional *FLG* monomer reducing the risk of AD by 12%.

Genetic basis of AD in the Indian population

A landmark Indian study studying the *FLG* gene polymorphisms in children detected loss-of-function mutations in *FLG* in 26 out of 75 children, indicating a prevalence of 34.7%. Among the *FLG* null variants detected, 16 (80%) were novel and had not been previously reported in Asian or European populations. These novel mutations included nonsense mutations such as p.Gln447Ter, p.Arg572Ter, p.Gln2314Ter, p.Tyr3105Ter, p.Gly427Ter, p.Gly2593Ter, p.Tyr2478Ter, p.Ser3640Ter, p.Trp1064Ter, and p.Ser2344Ter; frameshift deletions such as p.Gln1672ArgfsTer34, p.Gly2023HisfsTer67, p.Arg992SerfsTer31, and p.His2864CysfsTer5; a frameshift insertion p.Glu1605ThrfsTer103; and a splice-site variant c.139-1G>A. A statistically significant association was found between *FLG* variants and an early age of onset of

AD and elevated serum IgE levels, whereas no significant correlation was observed between the number of FLG null variants and the severity of AD, as measured by the SCORing in atopic dermatitis (SCORAD) index.^[27] Another Indian study specifically identified FLG exon 3 variants in 63% of participants, out of which 23% had pathogenic or likely pathogenic mutations, and 45% had novel mutations. This study did not detect common FLG mutations prevalent in Western populations, such as R501X and 2282del4, highlighting ethnic differences in FLG mutation profiles and emphasizing the necessity for population-specific genetic research to inform targeted diagnostic and therapeutic strategies.^[28] The other Indian studies on genetic mutations in AD are summarized in Table 3.^[29-33]

CLINICAL IMPLICATIONS OF GENETIC POLYMORPHISMS

Effect of FLG deficiency on the epidermis: Loss-of-function mutations in the *FLG* gene result in truncated profilaggrin that cannot be processed into functional FLG monomers. This deficiency disrupts the skin barrier by affecting keratin filament organization, lamellar body secretion, and lipid layering in the SC. It also impairs tight junction formation by reducing the expression of key proteins such as (Zonula Occludens 1) ZO-1 and occludin, weakening the skin's structural integrity. FLG breakdown products contribute to NMFs, and their absence increases transepidermal water loss, raises skin pH, and reduces hydration. Elevated pH

Table 3: Summary of key findings in Indian studies on genetic mutations in atopic dermatitis.

Study	Population	Filaggrin mutations studied	Key findings	Regional insights
Rajeshwari <i>et al.</i> , 2023 ^[29]	30 children with AD, 15 healthy controls	Full <i>FLG</i> gene sequencing	Identified 22 amino acid changes; 17 novel mutations (e.g., P2238N, R2239W, V2243L in 70%; S2231E in 67%) - Common mutations R501X and 2282del4 absent - Stop codon mutation (S2366STOP) in one patient - No mutations in controls	Highlights a unique FLG mutation profile in South Indian children, distinct from other ethnic groups
Chawla <i>et al.</i> , 2023 ^[30]	180 participants (60 AD, 60 Ichthyosis vulgaris, 60 controls) aged 3 months–60 years	R501X and 2282del4	R501X in 31.6% (AD) and 23.3% (IV) - 2282del4 in 18.3% (AD) and 13.3% (IV) - Combined genotype in 10% (AD) and 5% (IV) - No mutations in controls - R501X is linked with higher SCORAD severity	Indicates the presence of European-reported mutations in Central Indian populations, supporting the association between FLG mutations and disease severity
Handa <i>et al.</i> , 2019 ^[31]	Patients with hand eczema	Common FLG variants (e.g., R501X, 2282del4)	Reported a prevalence of 33.7% for FLG variants (S2889X, 2282del4, R501X, Q2417X) associated with hand eczema	Suggests a significant role of FLG mutations in hand eczema among the Indian population
Chauhan <i>et al.</i> , 2020 ^[32]	90 children with allergic diseases (asthma, eczema), 81 healthy controls	R501X	5.5% (5/90) of allergic children were homozygous mutant (AA) for R501X - 43.3% had heterozygous or homozygous mutant genotype - No homozygous mutants in controls - 3.3% of children with asthma and 2.2% with asthma and eczema had the mutant R501X genotype	Indicates a modest prevalence of R501X mutation among North Indian children with allergic diseases, emphasizing the need for broader genetic screening.
Nath <i>et al.</i> , 2020 ^[33]	Indian AD patients	FLG missense variants and skin microbiome analysis	Identified “potentially damaging” FLG alleles-Damaging allele dosage positively correlated with Proteobacteria abundance and negatively with Firmicutes (including <i>Staphylococcus aureus</i>) -Enriched microbial pathways associated with skin barrier permeability and inflammation	Indicates a link between FLG genotypes and skin microbiome dysbiosis in Indian AD patients, suggesting potential for personalized treatment strategies

AD: Atopic dermatitis, FLG: Filaggrin, SCORAD: SCORing in Atopic Dermatitis

Table 4: Risk of atopic dermatitis in various single-nucleotide polymorphisms (SNP).

SNP	Gene	Association type
rs17454584	<i>IL2</i> (Interleukin 2)	Increased risk
rs17389644	<i>IL21</i> (Interleukin 21)	Increased risk
rs11741861	<i>IRGM</i> (Immunity-related GTPase M)	Increased risk
rs6682925	<i>IL23R</i> (Interleukin 23 receptor)	Increased risk
rs7622183	<i>IL5RA</i> (Interleukin 5 receptor α)	Protective
rs6473227	<i>ZBTB10</i> (Zinc finger BTB domain 10)	Protective
rs221243	<i>EMSY</i> (BRCA2 interacting repressor)	Protective

BRCA: Breast cancer gene

further impairs lipid-processing enzymes, worsening the barrier defect. Moreover, a weakened barrier allows allergens to penetrate more easily, triggering local inflammation and systemic sensitization. Studies in FLG-deficient mice have demonstrated enhanced allergen absorption and elevated antigen-specific IgE levels. This supports the idea that FLG mutations can accelerate progression along the atopic march by facilitating allergic sensitization through the skin.^[34] Understanding the clinical implications of genetic polymorphisms in AD is crucial for moving toward a personalized approach to diagnosis, prognosis, and therapy. Specific gene variants can influence not only susceptibility to AD but also its severity, chronicity, and response to treatment. Identifying such polymorphisms, particularly in populations with SOC, allows for better risk stratification and may guide tailored interventions in the future. Table 4 summarizes key single-nucleotide polymorphisms (SNPs) found to be associated with either increased risk or protective effects.^[35]

Limitations in current research

Aberrant epigenetic regulation has been linked to differences in gene expression between lesional and non-lesional AD skin, particularly in genes related to barrier integrity and innate immunity. In addition, non-coding RNAs such as microRNAs add another layer of post-transcriptional regulation, with several miRNAs found to be differentially expressed in AD. Despite these insights, a significant limitation in the current research is the paucity of large-scale, longitudinal epigenetic studies in diverse populations, particularly in SOC, which hampers our ability to fully understand and translate epigenetic findings into targeted therapies. Most GWAS and candidate gene studies are conducted in populations of European descent, in which subgroup analysis by ethnicity is often lacking. In addition, in SOC

populations, environmental exposure, nutritional status, and access to healthcare are not adequately controlled in studies, which vary widely and may influence gene/environment interactions. Countries with high SOC populations often lack access to advanced genomic infrastructure and technology, limiting large-scale sequencing efforts. These limitations underscore the need for more exclusive research that considers the genetic, environmental, and socio-economic contexts of SOC populations pertaining to AD.

Future perspectives

Future research on AD in SOC must prioritize the development of ethnically inclusive research consortia to address the current gaps in genetic data across diverse populations. A comprehensive understanding of the complex gene-environment interactions underlying AD can be achieved by integrating multi-omics approaches, including genomics, epigenomics, and transcriptomics. Special attention should be given to the role of epigenetic regulation and microbiome-gene interactions, particularly in the context of early-life exposures that may influence disease onset and progression in SOC populations. In addition, the establishment of regional biobanks and genetic registries in areas with significant SOC representation is crucial to enable large-scale, population-specific studies that can inform tailored therapeutic strategies and equitable healthcare outcomes.

CONCLUSION

The study of gene mutations in atopic dermatitis affecting skin of color is still an under-represented area of research. This review throws light on certain genetic mutations specific to Indian and other ethnic skin populations, compared to the western cohort. Clinically recognizing these genetic differences may pave the way for risk prediction, and improved patient outcomes. Further research on region specific bio-banks and inclusive genomic studies in Indian skin are essential to bridge the knowledge gap.

Ethical approval: Institutional Review Board approval is not required.

Declaration of patient consent: Patient's consent is not required as there are no patients in this study.

Financial support and sponsorship: Nil.

Conflicts of interest: There are no conflicts of interest.

Use of artificial intelligence (AI)-assisted technology for manuscript preparation: The author confirms that there was no use of artificial intelligence (AI)-assisted technology for assisting in the writing or editing of the manuscript and no images were manipulated using AI.

REFERENCES

1. Iwuala C, Taylor SC. Structural and functional differences in skin of colour. *Clin Exp Dermatol* 2022;47:247-50.
2. Wilson BN, Sun M, Shah R, Murrell DF, Murase JE. Purposeful inclusion of

- skin of colour in published literature for improved dermatology education: A call to action. *Clin Exp Dermatol* 2022;47:409-10.
3. Criado PR, Miot HA, Bueno-Filho R, Ianhez M, Criado RF, De Castro CC. Update on the pathogenesis of atopic dermatitis. *An Bras Dermatol* 2024;99:895-915.
 4. Thomsen SF, Ulrik CS, Kyvik KO, Hjelmborg JV, Skadhauge LR, Steffensen I, *et al.* Importance of genetic factors in the etiology of atopic dermatitis: A twin study. *Allergy Asthma Proc* 2007;28:535-9.
 5. Roduit C, Frei R, Depner M, Karvonen AM, Renz H, Braun-Fahrlander C, *et al.* Phenotypes of atopic dermatitis depending on the timing of onset and progression in childhood. *JAMA Pediatr* 2017;171:655-62.
 6. Kolb L, Ferrer-Bruker SJ. *Atopic dermatitis*. Treasure Island, FL: StatPearls Publishing; 2025.
 7. Peterson RE, Kuchenbaecker K, Walters RK, Chen CY, Popejoy AB, Periyasamy S, *et al.* Genome-wide association studies in ancestrally diverse populations: Opportunities, methods, pitfalls, and recommendations. *Cell* 2019;179:589-603.
 8. Brown SJ, Elias MS, Bradley M. Genetics in atopic dermatitis: Historical perspective and future prospects. *Acta Derm Venereol* 2020;100:adv00163.
 9. Stefanovic N, Irvine AD. Filaggrin and beyond: New insights into the skin barrier in atopic dermatitis and allergic diseases, from genetics to therapeutic perspectives. *Ann Allergy Asthma Immunol* 2024;132:187-95.
 10. Huang Y, Zhou W, Liu S, Zeng D, Zhou W. Association between polymorphisms and atopic dermatitis susceptibility: A systematic review and meta-analysis. *Gene* 2024;913:148397.
 11. Prado-Montes De Oca E, García-Vargas A, Lozano-Inocencio R, Gallegos-Arreola MP, Sandoval-Ramírez L, Dávalos-Rodríguez NO, *et al.* Association of beta-defensin 1 single nucleotide polymorphisms with atopic dermatitis. *Int Arch Allergy Immunol* 2007;142:211-8.
 12. Niwa Y, Potaczek DP, Kanada S, Takagi A, Shimokawa N, Ito T, *et al.* FcεpsilonR1alpha gene (FCER1A) promoter polymorphisms and total serum IgE levels in Japanese atopic dermatitis patients. *Int J Immunogenet* 2010;37:139-41.
 13. Gao PS, Rafaels NM, Mu D, Hand T, Murray T, Boguniewicz M, *et al.* Genetic variants in thymic stromal lymphopoietin are associated with atopic dermatitis and eczema herpeticum. *J Allergy Clin Immunol* 2010;125:1403-7.
 14. Tsunemi Y, Saeki H, Nakamura K, Sekiya T, Hirai K, Kakinuma T, *et al.* Interleukin-13 gene polymorphism G4257A is associated with atopic dermatitis in Japanese patients. *J Dermatol Sci* 2002;30:100-7.
 15. Margolis DJ, Apter AJ, Gupta J, Hoffstad O, Papadopoulos M, Campbell LE, *et al.* The persistence of atopic dermatitis and filaggrin (FLG) mutations in a US longitudinal cohort. *J Allergy Clin Immunol* 2012;130:912-7.
 16. Wang JJ, Lin TJ, Kuo CF, Lin SL, Lee YL, Chen PC. Filaggrin polymorphism P478S, IgE level, and atopic phenotypes. *Br J Dermatol* 2011;164:791-6.
 17. Nemoto-Hasebe I, Akiyama M, Nomura T, Sandilands A, McLean WH, Shimizu H. FLG mutation p.Lys4021X in the C-terminal imperfect filaggrin repeat in Japanese patients with atopic eczema. *Br J Dermatol* 2009;161:1387-90.
 18. Park J, Jekarl DW, Kim Y, Kim J, Kim M, Park YM. Novel FLG null mutations in Korean patients with atopic dermatitis and comparison of the mutational spectra in Asian populations. *J Dermatol* 2015;42:867-73.
 19. Taylan F, Nilsson D, Asad S, Liedner A, Wahlgren CF, Winge MC, *et al.* Whole-exome sequencing of Ethiopian patients with ichthyosis vulgaris and atopic dermatitis. *J Allergy Clin Immunol* 2015;136:507-9.e19.
 20. Lan CC, Tu HP, Wu CS, Ko YC, Yu HS, Lu YW, *et al.* Distinct SPINK5 and IL-31 polymorphisms are associated with atopic eczema and non-atopic hand dermatitis in Taiwanese nursing population. *Exp Dermatol* 2011;20:975-9.
 21. Kato A, Fukai K, Oiso N, Hosomi N, Murakami T, Ishii M. Association of SPINK5 gene polymorphisms with atopic dermatitis in the Japanese population. *Br J Dermatol* 2003;148:665-9.
 22. Zhao LP, Di Z, Zhang L, Wang L, Ma L, Lv Y, *et al.* Association of SPINK5 gene polymorphisms with atopic dermatitis in Northeast China. *J Eur Acad Dermatol Venereol* 2012;26:572-7.
 23. Kaufman BP, Guttman-Yassky E, Alexis AF. Atopic dermatitis in diverse racial and ethnic groups-variations in epidemiology, genetics, clinical presentation and treatment. *Exp Dermatol* 2018;27:340-57.
 24. Drislane C, Irvine AD. The role of filaggrin in atopic dermatitis and allergic disease. *Ann Allergy Asthma Immunol* 2020;124:36-43.
 25. Wang Z, Chen H, Wang Y, Wu C, Ye T, Xia H, *et al.* Recombinant filaggrin-2 improves skin barrier function and attenuates ultraviolet B (UVB) irradiation-induced epidermal barrier disruption. *Int J Biol Macromol* 2024;281:136064.
 26. Li L, Liu Y, Chang R, Ye T, Li Z, Huang R, *et al.* Dermal Injection of recombinant filaggrin-2 ameliorates UVB-induced epidermal barrier dysfunction and photoaging. *Antioxidants (Basel)* 2024;13:1002.
 27. Srinivas SM, Dhar S, Gowdra A, Saha A, Sundararajan L, Geetha TS, *et al.* Filaggrin gene polymorphisms in Indian children with atopic dermatitis: A cross-sectional multicentre study. *Indian J Dermatol Venereol Leprol* 2023;89:819-27.
 28. Somasundaram A, Chiramel MJ, Chapla A, Sathishkumar D, Athiyarath R, Mathew L, *et al.* Targeted filaggrin gene (FLG) sequencing: A pilot study among Indian children with atopic dermatitis. *Indian Dermatol Online J* 2025;16:263-9.
 29. Rajeshwari KA, Thomas MM, Nagaraj G. Filaggrin gene mutation in pediatric patients with atopic dermatitis: A look into Indian gene pool, a pilot study. *Indian J Dermatol* 2023;68:135-40.
 30. Chawla HS, Kosta S, Namdeo C, Kataria R, Bhatia K, Sahu R, *et al.* Genotype study of filaggrin gene loss-of-function mutations in central India population with atopic dermatitis and Ichthyosis vulgaris. *Indian Dermatol Online J* 2023;14:611-5.
 31. Handa S, Khullar G, Pal A, Kamboj P, De D. Filaggrin gene mutations in hand eczema patients in the Indian subcontinent: A prospective case-control study. *Contact Dermatitis* 2019;80:359-64.
 32. Chauhan A, Panigrahi I, Singh M, Attri SV, Agarwal A, Singh M. Prevalence of filaggrin gene R501X mutation in Indian children with allergic diseases. *Indian J Pediatr* 2020;87:587-90.
 33. Nath S, Kumari N, Bandyopadhyay D, Sinha N, Majumder PP, Mitra R, *et al.* Dysbiotic lesional microbiome with filaggrin missense variants associate with atopic dermatitis in India. *Front Cell Infect Microbiol* 2020;10:570423.
 34. Tenn MW, Ellis AK. The clinical relevance of filaggrin mutations: Effect on allergic disease. *Ann Allergy Asthma Immunol* 2016;117:483-9.
 35. Kim JH, Lee SY, Kang MJ, Yoon J, Jung S, Cho HJ, *et al.* Association of genetic polymorphisms with atopic dermatitis, clinical severity and total IgE: A replication and extended study. *Allergy Asthma Immunol Res* 2018;10:397-405.

How to cite this article: Raju SP. Genetic polymorphisms and their association with atopic dermatitis in skin of color – A comprehensive review. *Indian J Skin Allergy*. 2025;4:117-22. doi: 10.25259/IJSA_39_2025