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Dear Doctor,

Greetings from Micro Labs. We are happy to bring you "COSMODERMA TIMES" which contains latest and interesting news in the field of Dermatology.

This issue contains:

Should you require any article or, medical information, please feel free to contact us medicalservices@microlabs.in

Looking forward to your valuable feedback.

Best Regards,

Medical Team, Micro Labs Limited.

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Interplay between AD and hand eczema in the general population

Introduction:

Atopic dermatitis (AD) is a chronic inflammatory skin disease that typically begins in early childhood and may precede other atopic disorders such as asthma, allergic rhinitis, and food allergies. AD commonly manifests between 3 and 6 months of age, with 60% of cases emerging within the first year. The prevalence of AD varies globally, affecting 0.2% to 36% of the pediatric population, with different age groups showing varied anatomical distributions of lesions.[1] In adults, AD can cause significant disease burden and psychiatric comorbidities like depression and anxiety. AD is also linked to an increased risk of developing hand eczema, a condition that includes several subtypes, such as irritant and allergic contact dermatitis, and is often associated with impaired quality of life. Studies suggest a high co-occurrence of AD and hand eczema, with individuals having a history of AD showing a significantly higher likelihood of developing hand eczema.[2] So, this study explored the relationship between AD and hand eczema, focusing on prevalence, disease severity, comorbidities, and contact sensitization, to identify patient subgroups that may benefit from targeted medical attention.

Methods:

This cross-sectional study analyzed 100,000 randomly selected adults (18–75 years) via secure digital mailboxes between May and June 2021 to assess the lifetime prevalence and severity of atopic dermatitis (AD), defined by self-reported physician diagnosis. A modified version of Silverberg et al.'s validated questionnaire was used to identify AD cases, and participants with current or past AD were asked about their disease severity using the Patient-Oriented Scoring for AD (PO-SCORAD). Additional questions addressed hand eczema severity, comorbidities, lifestyle factors, and demographic data. Statistical analyses were performed using IBM SPSS Statistics, including the Mann–Whitney U test, student's t-test, Chi-square test, and logistic regression to assess associations between variables.

Results:

With a 42.7% response rate on the questionnaire, this study found the lifetime prevalence of physician-diagnosed AD to be 9.0%, with a 1-year prevalence of 3.6% and point prevalence of 2.0%. AD was more common in younger individuals and females. Severity was moderate to severe in 31.6% of AD cases. Patch testing was more frequent in AD individuals (39.5% vs. 16.7%), with higher rates of positive reactions to allergens like nickel and chrome. AD was linked to higher asthma and allergic rhinitis prevalence, but lower cardiovascular comorbidities, except for diabetes. Psychiatric conditions, including depression, anxiety, and stress, were more common in AD individuals. Hand eczema had a lifetime prevalence of 22.9%, higher in those with AD (53.3% vs. 19.8%). Lower education levels were associated with a higher prevalence of hand eczema. Individuals with both AD and hand eczema

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reported greater disease severity and more widespread eczema. Self-reported depression, anxiety, and stress were significantly higher in those with both conditions compared to those with AD only. When self-reported disease severity of AD was examined, persons with both AD and hand eczema reported a higher proportion of moderate to severe AD (34.3%) than individuals with only AD (26.9%, p = 0.004, Figure 1).

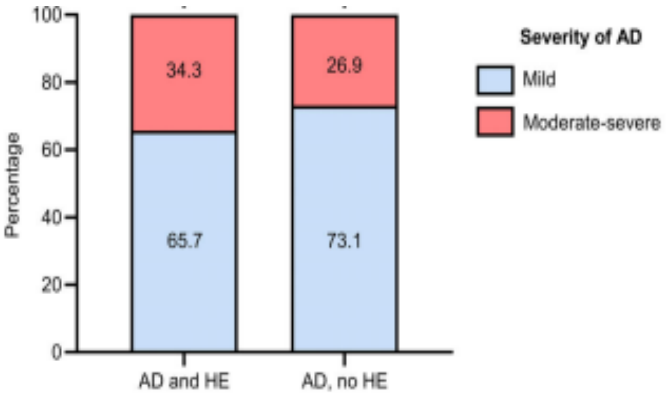

Figure 1: PO-SCORAD severity of current AD in individuals with or without lifetime hand eczema. Mild (≤27) vs. moderate to severe (>27).

Discussion:

This nationwide study reports a lifetime prevalence of 9.0% for atopic dermatitis (AD), with 31.6% of cases classified as moderate to severe. AD was strongly associated with increased hand eczema prevalence, and individuals with both conditions exhibited worse disease severity and higher rates of psychiatric comorbidities, particularly depression and anxiety. These findings align with previous studies, including those from a Dutch cohort and European populations, but also highlighted the challenges in AD prevalence estimation due to differences in study methodologies.[3,4] This study also confirms a higher rate of contact sensitization in individuals with AD compared to those without, although results varied when compared to selected patient populations. Additionally, individuals with both AD and hand eczema reported worse overall health and more widespread eczema compared to those with only one condition.[2]

Conclusion:

This study found a lifetime prevalence of 9.0% of adults reported lifetime atopic dermatitis (AD), with one-third experiencing moderate to severe disease. AD was linked to a higher prevalence of hand eczema, and individuals with both conditions had worse severity and more psychiatric comorbidities. These findings emphasize the need to focus on this vulnerable subgroup.

Individuals with AD and hand eczema are vulnerable groups that physicians should be informed of.

Reference:

1. Eichenfield LF et al. Recent Developments and Advances in Atopic Dermatitis: A Focus on Epidemiology, Pathophysiology, and Treatment in the Pediatric Setting. Paediatr Drugs. 2022 Jul;24(4):293-305.
2. Vinge As et al. Atopic dermatitis and hand eczema in Danish adults: A nationwide population-based study. Contact Dermatitis. 2025 Jan;92(1):21-30.
3. Barbarot S et al. Epidemiology of atopic dermatitis in adults: Results from an international survey. Allergy. 2018 Jun;73(6):1284-1293.
4. Zhang J et al. Prevalence of adult atopic dermatitis in the general population, with a focus on moderate-to-severe disease: results from the Lifelines Cohort Study. J Eur Acad Dermatol Venereol. 2021 Nov;35(11): e787-e790.

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Common characteristics between vitiligo and metabolic systemic disorders

Introduction:

Vitiligo is a chronic depigmenting disorder characterized by the loss of melanocytes, resulting in skin and mucosal pigment dilution. It affects approximately 0.5–2% of the global population, regardless of race or gender, and has significant psychological and quality-of-life impacts.[1] While the condition was viewed as a cosmetic issue traditionally, growing evidence indicates that vitiligo has systemic implications, including the development of metabolic abnormalities such as glucose intolerance and lipid dysregulation. These metabolic changes are associated with an increased risk of conditions like cardiovascular disease and diabetes mellitus, highlighting the systemic nature of vitiligo. Further, the pathogenesis of vitiligo is multifactorial, involving genetic, immunological, and inflammatory factors. Recent studies have demonstrated that vitiligo shares common molecular pathways with metabolic syndrome (MetS), suggesting an association between melanocyte dysfunction and systemic metabolic disturbances.[2] This study explored the common metabolic markers between vitiligo and MetS, focusing on inflammatory profiles, antioxidant enzyme imbalances, and lipid alterations in vitiligo patients, with the goal of understanding and improving patient care.

Methods:

This cohort study enrolled 50 patients with non-segmental vitiligo (19 men, 31 women, mean age 46.3) from the Photobiology Unit of the San Gallicano Institute between December 2022 and February 2024, diagnosed according to Vitiligo Global Issue Consensus Conferences (VGICC) guidelines. The control group consisted of age- and sex-matched healthy individuals. Blood samples were collected, and serum was analyzed for HDL, LDL, total cholesterol, folate, and vitamin D using Roche/Hitachi cobas c 503. Serum levels of insulin growth factor binding proteins 5 (IGFBP5), interleukin-6 (IL-6), chemokine 10 (CXCL10), IL-17, catalase (Cat), superoxide dismutase (SOD), advanced glycation end-products, and cysteine were measured via Enzyme-Linked Immuno Sorbent Assay (ELISA) and colorimetric assays. Plasma fatty acids were extracted, derivatized into fatty acid methyl esters (FAMEs), and analyzed by gas chromatography-mass spectrometry (GCMS). Statistical analysis involved Student’s t-test for group comparisons ($p < 0.05$), and correlation analysis was performed using Spearman's coefficient, with p-values corrected for multiple comparisons using the Benjamani–Hochberg procedure.

Results:

This study found that vitiligo patients exhibited common metabolic syndrome markers, including low vitamin D and folate levels like previous reports. Elevated homocysteine levels were observed, which can impair melanogenesis and contribute to oxidative damage and autoimmunity. Serum cysteine levels, an oxidative stress marker, were also elevated. Inflammatory markers, including IL-6 and CXCL10, were significantly higher in vitiligo patients, supporting the association between systemic inflammation and metabolic syndrome (Figure 1). However, IL-17 levels were lower in vitiligo patients. Oxidative stress was further evidenced by reduced SOD activity, which was correlated with low vitamin D levels, while Cat activity showed a mild increase in vitiligo patients. Advanced glycation end-products (AGEs), another oxidative marker, were elevated in vitiligo serum. Fatty acid analysis revealed a dysregulation in lipid metabolism, with increased γ-linolenic acid (GLA) and arachidonic acid (AA) in the n6-series, along with altered enzyme activity in the n6 and n3 fatty acid pathways. This imbalance between pro-inflammatory n6-series and anti-inflammatory n3-series fatty acids suggests a persistent inflammatory state in vitiligo, contributing to the pathophysiology of the disease.

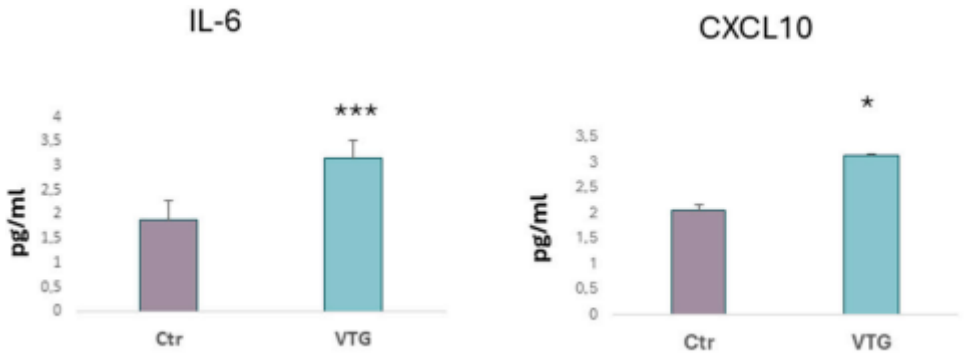

Figure 1. Assessment of Inflammatory State. Protein analysis of pro-inflammatory markers showing elevated levels of IL-6 and CXCL10 in vitiligo patients.

Discussion:

This study reveals that vitiligo is associated with MetS, showing altered metabolic markers such as increased homocysteine, cysteine, inflammatory cytokines (IL-6, CXCL10), and oxidative stress indicators (reduced SOD, elevated AGEs). These findings are consistent with the previous study linking vitiligo to systemic inflammation and metabolic disruptions.[3,4] Additionally, this study observed an imbalance in fatty acid composition, with higher n6-series fatty acids, suggesting a pro-inflammatory state, which aligns with MetS-related lipid metabolism alterations. Overall, this study supports the notion that vitiligo has systemic manifestations beyond skin depigmentation, highlighting the necessity for further research on its metabolic associations.[2]

Conclusion:

This study highlights systemic metabolic abnormalities in vitiligo, reinforcing previous findings of cellular metabolic disruptions. The identified association between vitiligo and metabolic syndrome markers could guide more effective disease management strategies.

Reference:

1. Ezzedine K et al. Vitiligo. Lancet. 2015 Jul 4;386(9988):74-84.
2. Papaccio F et al. Markers of Metabolic Abnormalities in Vitiligo Patients. Int J Mol Sci. 2024 Sep 23;25(18):10201.
3. Abdallah M et al. Egyptian Vitiligo Group. CXCL-10 and Interleukin-6 are reliable serum markers for vitiligo activity: A multicenter cross-sectional study. Pigment Cell Melanoma Res. 2018 Mar;31(2):330-336.
4. Esmaeili Bet al. Expression of IL-17 and COX2 gene in peripheral blood leukocytes of vitiligo patients. Iran J Allergy Asthma Immunol. 2011 Jun;10(2):81-9.

A systemic metabolic alteration in vitiligo patients could be a potential target for establishing a more effective therapy approach.

Association between the skin microbiota and metabolites in Atopic dermatitis patients with scalp involvement

Introduction:

Atopic dermatitis (AD) is a chronic, relapsing inflammatory skin condition affecting 15–30% of children and 2–10% of adults, with onset typically during infancy.[1] While scalp involvement is common in AD, it remains underexplored compared to other affected areas like the flexural regions. Scalp dermatitis often presents as acute eczematous lesions with scaling or dandruff-like appearance. Despite advancements in treatment, challenges specific to scalp dermatitis, such as its visibility and impact on patients' quality of life remain insufficiently addressed. The limited research on scalp dermatitis highlights the need for a deeper understanding of the skin microbiota and metabolites involved.[2] This study investigated the bacterial taxa and metabolites on the scalps of AD patients with scalp involvement and compare them with healthy individuals to identify potential biomarkers for scalp dermatitis and uncover underlying pathophysiological mechanisms.

Methods:

Adult patients with AD and scalp involvement, diagnosed based on Korean AD criteria, were recruited along with healthy controls (HCs) without AD or significant scalp conditions. Exclusion criteria consist of individuals under 18, recent use of antibiotics, antifungal treatments, anti-seborrheic shampoos, and a history of skin cancer. Skin samples were obtained from lesional and non-lesional scalp areas using swabs and D-Squame® tape strips, stored at

−80°C for microbiota and metabolite analysis. Biophysical skin parameters (sebum, pH, erythema) were measured. DNA extraction from swabs was performed using the Mag-Bind® Universal Pathogen Kit, followed by amplification of the V3-V4 regions of the 16S rRNA gene and sequencing on the Illumina MiSeq platform. Data were processed using QIIME2 and DADA2 for quality control and taxonomic classification via Silva138. Alpha diversity (Shannon, Chao1) and beta diversity (Bray-Curti's dissimilarity) were assessed, and statistical analysis was conducted using Kruskal-Wallis and Wilcoxon tests.

Results:

This study included 20 AD patients with scalp involvement and 16 HCs, with 56 skin samples analyzed through bacterial 16S rDNA V3-V4 sequencing. The average read count was 127,378. Alpha diversity indices (Chao1, Shannon) showed no significant differences between lesional

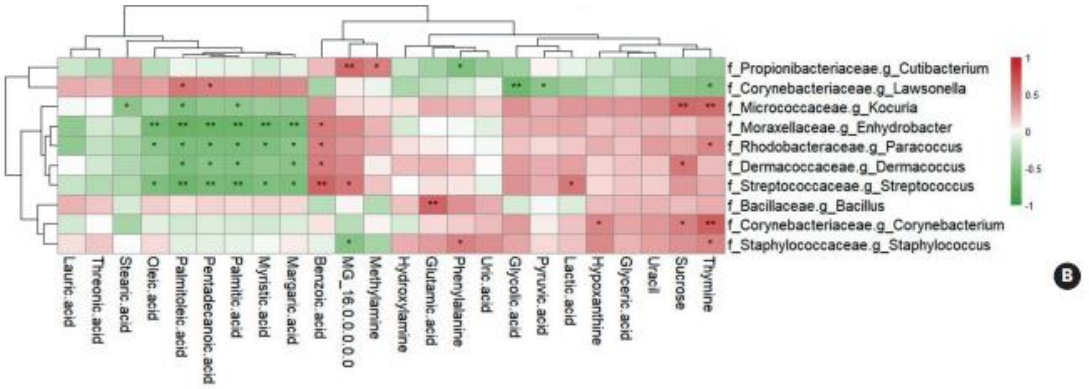

Figure 1. Heatmap of Spearman correlation between skin metabolites and microbiota, with red indicating positive correlations and green representing negative correlations.

(LS), non-lesional (NL) AD skin, and HC groups. However, beta diversity, assessed by Bray-Curti's dissimilarity, revealed significant differences between the groups (P = 0.001, R2 = 0.19297). The scalp microbiota was dominated by Actinobacteria, Firmicutes, and Proteobacteria, with Staphylococcus and Cutibacterium significantly more abundant in LS compared to HC and NL. Skin microbiota correlated with clinical AD severity, with specific genera like Lawsonella and Cutibacterium negatively associated with disease severity. Metabolomic analysis using PCA, PLS-DA, and OPLS-DA showed clear separation between AD and HC groups, with 36 metabolites decreased and 19 increased in LS compared to HC. Comparisons between LS and NL revealed 8 decreased and 7 increased metabolites in LS. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis identified key metabolic pathways, such as phenylalanine, tyrosine, and tryptophan biosynthesis, and alanine, aspartate, and glutamate metabolism, showing significant differences between LS and HC and LS and NL. Correlation analyses revealed associations between metabolites, clinical AD parameters, and microbiota, including positive correlations between glycolic acid, sucrose, thymine, and uracil with AD severity (EASI score). Additionally, certain bacterial genera (Cutibacterium, Lawsonella) correlated with specific metabolites, highlighting complex interactions between the microbiota, metabolites, and AD severity (Figure 1).

Discussion:

This study examined the bacterial microbiota and metabolome of lesional and non-lesional scalp skin in AD patients, compared to HCs. Staphylococcus species were most prevalent in AD lesions, positively correlating with disease severity, consistent with prior research.[3] Metabolically, amino acid biosynthesis pathways (phenylalanine, tyrosine, tryptophan) were downregulated in AD lesions, while glutamine levels were elevated, correlating with disease severity, supporting previous studies on metabolic disruptions in AD.[2]

Conclusion:

This study elucidates the associations between the skin microbiome and metabolome across the LS, NL, and HC groups. Identifying these specific contributions may enhance understanding of the pathogenesis of scalp involvement in AD and offer potential pathways for improving management strategies.

Significant relationships were found between certain bacterial species and particular metabolites.

Reference:

1. Lobefaro F et al. Atopic Dermatitis: Clinical Aspects and Unmet Needs. Biomedicines. 2022 Nov 14;10(11):2927.
2. Kim S et al. Associations Between Skin Microbiome and Metabolome in the Pathogenesis of Atopic Dermatitis Patients with Scalp Involvement. Allergy Asthma Immunol Res. 2024 Nov;16(6):668-681.
3. Woo YR et al. Characterization of Distinct Microbiota Associated with Scalp Dermatitis in Patients with Atopic Dermatitis. J Clin Med. 2022 Mar 21;11(6):1735.

Case Report on Harlequin Ichthyosis in a Preterm Neonate

Introduction:

Harlequin ichthyosis (HI) is a severe subtype of congenital ichthyosis characterized by thick, scaly skin covering the body at birth, leading to flattened ears and a high mortality rate. With an incidence of 1 per 300,000 live births, it is the deadliest form of ichthyosis. HI is an autosomal recessive disorder that results in a thickened stratum corneum, causing impaired skin barrier function, increased transepidermal water loss, and susceptibility to infections.[1] Most neonates with HI die within the first week due to complications such as respiratory failure and sepsis. In resource-limited settings, challenges like inadequate diagnostic facilities and lack of approved treatments hinder effective prenatal diagnosis and management. This case report details the clinical presentation of HI in a newborn in Uganda, focusing on diagnostic approaches and management strategies in a general hospital setting.

Case Presentation:

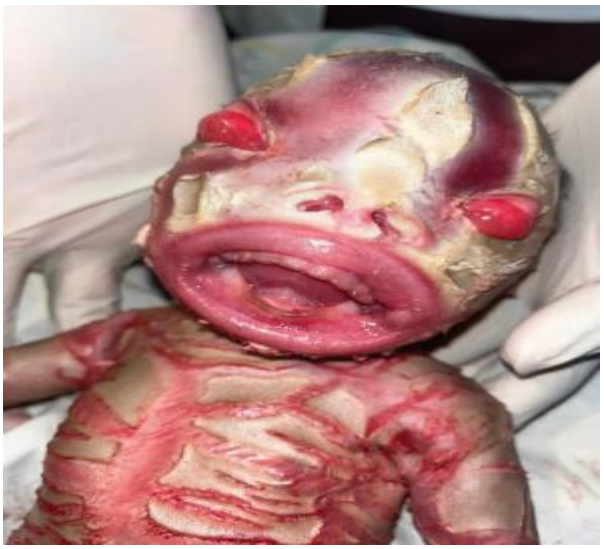

Figure 1: Severe ectropion and eclabium, exposing the conjunctiva, cornea, and oral mucosa

A 5-day-old female neonate, born preterm at 28 weeks of gestation with a birth weight of 1.6 kg, presented with classic signs of Harlequin Ichthyosis (HI). The neonate exhibited thick, yellowish-gray, hyperkeratotic skin scales covering the entire body, with deep erythematous fissures, particularly prominent on the scalp, trunk, and abdomen shown in Figure 1. The facial features included severe bilateral eyelid ectropion, exposing the conjunctivae, and eclabium, which revealed the mucosal lining of the lips. The nose was hypoplastic, with eroded ala, and the ears were small and rudimentary. The neonate had malformed limbs, with constriction bands and hypoplastic digits, particularly in the upper limbs, which were asymmetrical and contracted. Upon examination, the neonate was hypothermic (35.1°C), with respiratory distress, bradycardia, and tachypnea. Given the lack of resources for specialized HI treatments (e.g., retinoids), management focused on supportive care. To enhance fetal lung function and lower the risk of cerebral palsy caused by preterm, the mother received intrapartum dexamethasone and a magnesium sulfate bolus for neuroprotection before cesarean birth. Basic resuscitation, oxygen therapy, intravenous dextrose, and antibiotics were administered postnatally. Supplemental feeding via nasogastric tube and prophylactic treatments for apnea and sepsis were provided. Despite these interventions, the neonate's respiratory condition worsened, leading to death on the fifth day of life due to respiratory complications associated with prematurity. Socioeconomic challenges and social stigma affected the family's acceptance of treatment.

Discussion:

This case of Harlequin Ichthyosis (HI) in an African newborn aligns with typical clinical features, such as thick skin plates, ectropion, and eclabium, similar to the prior report.[3] The neonate's prematurity and subsequent complications, including respiratory distress and infection, contributed to its high mortality rate, which was consistent with previous studies highlighting the poor prognosis of HI in the first week of life.[4]

Conclusion:

Harlequin ichthyosis continues to be linked with a high mortality rate, particularly in resource-limited settings. Key contributing factors include limited access to prenatal diagnostic services, insufficient availability of critical treatments, and inadequate neonatal care infrastructure, all of which significantly worsen outcomes in developing countries.

Harlequin ichthyosis exhibits high mortality in resource-limited settings, emphasizing the need for better diagnostic and care infrastructure.

Reference:

1. Eichenfield LF et al. Recent Developments and Advances in Atopic Dermatitis: A Focus on Epidemiology, Pathophysiology, and Treatment in the Pediatric Setting. Paediatr Drugs. 2022 Jul;24(4):293-305.
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4. Zhang J et al. Prevalence of adult atopic dermatitis in the general population, with a focus on moderate-to-severe disease: results from the Lifelines Cohort Study. J Eur Acad Dermatol Venereol. 2021 Nov;35(11): e787-e790.