NVED abstracs 29-30 January 2026

Posters

P1 – MARIONA OLIVER

MACHINE LEARNING-BASED ANALYSIS OF SMARTPHONE IMAGES FOR REMOTE MONITORING OF PSORIASIS

Mariona Oliver[1,2*], Monika Molnarova[5*], Menthe Bergmans[1], Rahul Ranjan[5], Vasileios Exadaktylos[1], Tessa Niemeyer-van der Kolk[1], Marieke Seyger[6], Deepak M.W. Balak[3], Martijn B.A. van Doorn[1,4], Harald Schnidar[5], Robert Rissmann[1,2,3], Jannik Rousel[1,2], the Next Generation ImmunoDermatology (NGID) consortium

[1]Centre for Human Drug Research, Leiden, The Netherlands; [2]Leiden Academic Centre for Drug Research, Leiden University, Leiden, The Netherlands; [3]Leiden University Medical Centre, Leiden, The Netherlands; [4]Erasmus Medical Center, Rotterdam, The Netherlands; [5]SCARLETRED Holding GmbH, Vienna, Austria; [6]Radboud University Medical Center, Nijmegen, The Netherlands. [*]Authors have contributed equally.

Background Psoriasis requires long-term monitoring to evaluate treatment effectiveness. Traditional tools such as the Psoriasis Area and Severity Index (PASI) are clinic based, time-consuming, and prone to inter-rater variability. Digital health and artificial intelligence (AI) may overcome these limitations by providing remote, objective, and consistent disease evaluation.
Objective This study evaluated the feasibility and accuracy of AI-assisted smartphone imaging for monitoring psoriatic lesions and treatment response.
Methods In a randomized, double-blinded, placebo-controlled trial, 26 patients with mild-to-moderate plaque psoriasis received guselkumab or placebo. Over a 16-week period, patients captured standardized, colour-calibrated images of target lesions at home via smartphone-based medical imaging platform. Physicians also recorded clinical images and evaluated severity with PASI and the Target Lesion Score (TLS). AI-assisted tissue analysis was applied to all images, and a predictive model combining erythema, scaling, and induration was trained on physician-assessed TLS sub-scores to estimate overall TLS.
Results Baseline comparisons showed no significant differences between clinic and home images for erythema and scaling. Guselkumab significantly reduced PASI and TLS compared to placebo, with AI-derived TLS (aiTLS) scores closely aligned with physician-assessed TLS. From week 8 onward, AI analysis detected significant reductions in erythema and scaling in the guselkumab group, consistent across home and clinic images.
Conclusion AI-assisted smartphone imaging offers a reliable, standardized method for remote assessment of psoriasis. By quantifying erythema, scaling, and lesional size, this approach generates comprehensive lesion scores, potentially reducing the frequency of in-clinic assessments and supporting remote monitoring in both research and clinical care.

P2 – JOEY KARREGAT

INCIDENCE OF TATTOO-ASSOCIATED MELANOMA IN THE NETHERLANDS (1991-2023): A NATIONWIDE REGISTRY STUDY

Joey J.J.P. Karregat[1,2], Kim Schipper[1], Albert Wolkerstorfer[1], Elisabeth H. Jaspars[3], Norbertus A. Ipenburg[1], Nicolas Kluger[4,5,6], Yannick S. Elshot[1,7]

[1]Department of Dermatology, Amsterdam University Medical Center, University of Amsterdam, The Netherlands; [2]Department of Molecular Cell Biology and Immunology, Amsterdam University Medical Center, Vrije Universiteit Amsterdam, The Netherlands; [3]Department of Pathology, Amsterdam UMC, University of Amsterdam, Amsterdam, The Netherlands; [4]Department of Dermatology, Helsinki University Hospital, University of Helsinki, Helsinki, Finland; [5]Department of Dermatology, Bichat-Claude Bernard Hospital, Assistance Publique-Hôpitaux de Paris, Paris, France; [6]EADV Task Force on Tattoos and Body Art, Lugano, Switzerland; [7]Department of Dermatology, The Netherlands Cancer Institute - Antoni van Leeuwenhoek, Amsterdam, The Netherlands.

Background Tattooing is an increasingly prevalent practice that is associated with various clinical complications. The carcinogenic potential of tattoo pigments remains unclear. While 45 case reports have described melanomas colocalizing with tattoos thus far, a pathogenetic link between tattoos and melanomas remains unproven. No nationwide epidemiological study has investigated the incidence of tattoo-associated melanoma (TAM).
Objective To determine the incidence of TAM in the Netherlands from 1991 to 2023, analyse TAM characteristics and patient demographics, and compare these findings with melanoma data from the general Dutch population during the same period.
Methods Data were obtained from the nationwide network and registry of histo- and cytopathology in the Netherlands (PALGA). Malignant and benign melanocytic lesions on the tattooed skin were included. Patient demographics and mela-

noma characteristics were extracted and analysed. Data from the Netherlands Cancer Registry were used for comparison.
Results From 1991 to 2023, 94 TAMs and 467 benign melanocytic lesions on tattoos were identified. The annual incidence of TAMs has increased over time. TAMs were diagnosed at an overall median age of 48.0 years, predominantly in males (64.9%). The median Breslow thickness was 0.9 mm, and most TAMs were TNM stage I (76.6%). The number-needed-to-excise was 6.0.
Conclusion This nationwide cohort study found no evidence supporting a causal relationship between tattoos and melanoma.

P3 – ELISE BELJAARDS

OPTICAL COHERENCE TOMOGRAPHY FOR NON-INVASIVE PREDICTION OF RESPONSE TO TOPICAL CHLORMETHINE IN EARLY-STAGE MYCOSIS FUNGOIDES

Elise S.M. Beljaards[1,2], Lisa Bruijnincx[1,3], Selinde S. Wind[1,2], Rianne Rijneveld[1], Tessa Niemeyer-van der Kolk[1], Koen D. Quint[2], Maarten H. Vermeer[2], Robert Rissmann[1,2,3]
[1]Centre for Human Drug Research, Leiden, The Netherlands; [2]Department of Dermatology, Leiden University Medical Center, Leiden, The Netherlands; [3]Leiden Academic Centre for Drug Research, Leiden, The Netherlands.

Background Mycosis fungoides (MF) is the most common cutaneous T-cell lymphoma. Long-term treatment with topical chlormethine is recommended in early-stages, however, some patients fail to respond. Therapeutic response is monitored using invasive biopsies or subjective clinical scores including Composite Assessment of Index Lesion Severity (CAILS).
Objective To evaluate the potential of optical coherence tomography (OCT) as a non-invasive imaging technique to provide an objective, accurate and patient-friendly alternative.
Methods In this open-label interventional study, 21 early-stage MF patients (IA-IIA) and 10 healthy controls were included. Patients applied chlormethine gel for 16 weeks. Clinical scores and OCT imaging of lesional, non-lesional and matched skin sites in controls were performed at weeks -6 and 0 (observational phase) and weeks 4, 8, 12, and 16 (interventional phase). Skin biopsies were obtained at baseline (week 0) and study end (week 16).
Results Lesional skin showed significantly increased epidermal thickness at baseline compared to non-lesional and healthy skin ($p<0.001$), as measured by OCT and histology. Eight patients showed significant reduction in modified CAILS following treatment (Δ-10.5, $p<0.0001$). These responders had significantly thicker epidermis at baseline than non-responders (Δ-83.7 µm, $p<0.05$). OCT measurements correlated significantly with histology (Rrm=0.80, $p<0.001$) and CAILS (Rrm=0.40, $p<0.001$). A subepidermal low echogenic band was observed in seven responders, corresponding to extensive inflammatory infiltrate histologically.
Conclusion OCT reliably measures epidermal thickness and correlates with clinical and histological findings. Our results suggest that epidermal thickness correlates with clinical response to chlormethine, thereby supporting its role as a non-invasive tool for monitoring therapeutic response.

P4 – AGNES GRUTTERS

THE PRICE OF FRAGILE SKIN: A SCOPING REVIEW ON THE ECONOMIC BURDEN OF EPIDERMOLYSIS BULLOSA

L.A. Grutters[1,2], F. Teertstra[2], S. van der Werf[3], A.D.I. van Asselt[4,5], P.C. van den Akker[2], M.C. Bolling[1]
[1]University of Groningen, University Medical Center Groningen, UMCG Centers of Expertise for Blistering Diseases and Genodermatoses, Department of Dermatology, Groningen, The Netherlands; [2]University of Groningen, University Medical Center Groningen, UMCG Centers of Expertise for Blistering Diseases and Genodermatoses, Department of Genetics, Groningen, The Netherlands; [3]University of Groningen, University Medical Center Groningen, Medical Library, Groningen, The Netherlands; [4]University of Groningen, University Medical Center Groningen, Department of Health Sciences Groningen, The Netherlands; [5]University of Groningen, University Medical Center Groningen, Department of Epidemiology, Groningen, The Netherlands.

Background Epidermolysis bullosa (EB) comprises a phenotypically and genetically heterogeneous group of rare skin disorders characterised by mucocutaneous fragility. Currently, EB is incurable, and management focuses on wound care. Emerging genetic therapies offer promising avenues for EB management. However, the high cost of these therapies necessitates robust cost evaluations to support their integration into clinical practice.
Objective This scoping review aimed to provide a comprehensive overview of reported costs, financial magnitude and time investment of EB.
Methods A systematic literature search was performed in the databases MEDLINE, Embase, CINAHL, PsycINFO, Scopus, EBSCO interface and Web of Science Core Collection covering the period until February 2025. English full text published articles from any country or study setting on genetic EB and reporting on cost domains were included.
Results Twenty-two studies from 15 countries, published between 2013 and 2024, were included, encompassing 3128 patients. The majority (77%) employed patient or caregiver-completed questionnaires/interviews for data collection. Direct non-healthcare costs were reported in 73% of studies, direct healthcare costs in 68%, and indirect costs in 27%. Financial magnitude was addressed in 82% of studies, while 45% reported time investment. Annual mean total economic burden per patient ranged from €42,323 to €77,008. Average dressing changes requiring two hours daily.
Conclusion Both financial magnitude and time investment of EB care are substantial. We observed heterogeneity in reported cost domains, which complicated drawing definitive conclusions across EB subtypes. Clarifying the current economic burden of EB care is essential to enable future introduction of high-cost genetic therapies.

P5 – JOSEPHINE AMKREUTZ

THE NORMA 1 STUDY: NO RE-EXCISION IN PT1A MELANOMA

Josephine A.M.P. Amkreutz[1], Elsemieke I. Plasmeijer[1,2], Yvonne M. Schrage[3], Gerrit J. Liefers[4], Remco van Doorn[1,2], Marieke E. Straver[5]

[1]Department of Dermatology, Leiden University Medical Center, Leiden, The Netherlands; [2]Department of Dermatology, Netherlands Cancer Institute - Antoni van Leeuwenhoek (NKI-AvL), Amsterdam, The Netherlands; [3]Department of Surgical Oncology, Netherlands Cancer Institute - Antoni van Leeuwenhoek (NKI-AvL), Amsterdam, The Netherlands; [4]Department of Surgical Oncology, Leiden University Medical Center, The Netherlands; [5]Department of Surgical Oncology, Haaglanden Medical Center, The Hague, The Netherlands.

Background Stage I melanoma accounts for the majority of new melanoma cases and shows the steepest increase in incidence. In the Netherlands, approximately 3,000 patients are diagnosed annually with pT1a melanoma. Standard treatment for pT1a melanoma includes primary excision followed by a re-excision with 1cm margins, aiming to eradicate microsatellites and prevent locoregional recurrence (LR). However, microsatellites are rare and there is insufficient evidence that a re-excision improves survival. The NORMA1-study (NO Re-excision in pT1a MelanomA) will evaluate the omission of re-excision in pT1a melanoma.
Objective To demonstrate that the 5-year LR rate (LRR) remains <5% after omitting re-excision in pT1a melanoma.
Methods The NORMA1-study is a large multicenter, single-arm, prospective interventional study to be conducted in the Netherlands. Adult patients with a completely resected pT1a melanoma choose between omitting or undergoing re-excision. They are monitored annually for 5 years. The experimental arm (no re-excision) requires 650 patients.
Results This abstract describes the study protocol and results are not available yet. The primary endpoint is the 5-year LRR in the experimental arm. Secondary endpoints include survival, quality of life (QoL), cost-effectiveness, as well as complication rates and the 5-year LRR after re-excision.
Conclusion The rationale for re-excision in melanoma treatment is increasingly questioned due to limited supporting evidence alongside its morbidity and healthcare costs. This particularly applies to low-stage melanoma patients with an excellent prognosis. Demonstrating that re-excision can be safely omitted could improve QoL and enhance healthcare efficiency, supporting a paradigm shift in the management of low-risk melanoma worldwide.

P6 – WANDONG WANG

SPATIAL TRANSCRIPTOMIC PROFILING OF THE TUMOUR MICROENVIRONMENT OF ORGAN TRANSPLANT–RELATED VERSUS SPORADIC CUTANEOUS SQUAMOUS CELL CARCINOMA

Wandong Wang[1], Clara Harrs[2], Maria C. Bolling[1], Barbara Horváth[1], Gilles F.H. Diercks[1,2], Emőke Rácz[1]

[1]Department of Dermatology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands; [2]Department of Pathology, Center for Blistering Diseases, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands.

Background Cutaneous squamous cell carcinoma (cSCC) is the second most common skin cancer worldwide. Organ transplant recipients (OTRs) have a 65–200-fold increased risk of developing cSCC compared with the general population. OTRs-cSCC is often more aggressive, with higher recurrence, metastasis, and disease-specific death rates. The mechanisms underlying this aggressiveness remain poorly understood, particularly regarding the tumour microenvironment (TME).
Objective Previous studies have shown that the TME in OTRs differs from sporadic cSCC in exhibiting immune dysfunction characterized by reduced immune cell infiltration, altered T-cell subset composition, and increased immune exhaustion. This study aims to further delineate tumour–stroma–immune interactions and identify spatially defined molecular features contributing to OTRs-cSCC aggressiveness and potential therapeutic targets.
Methods A tissue microarray (TMA) was constructed from formalin-fixed paraffin-embedded (FFPE) tumour samples of metastatic OTRs-cSCC (n=8) and sporadic cSCC (n=8). Tumour sites were matched as closely as possible (OTRs-cSCC: extremities 3/8, head and neck 5/8; sporadic cSCC: extremities 8/8). Sections were analysed using the GeoMx Digital Spatial Profiler, with morphology markers (PanCK, CD45, SYTO13) guiding region-of-interest (ROI) selection in the TME. Spatial transcriptomic profiling was performed using the GeoMx Human Whole Transcriptome Atlas, and sequencing data are currently being processed.
Results Preliminary analyses are expected to reveal differential immune and stromal compositions and distinct gene expression signatures between OTRs-cSCC and sporadic cSCC.
Conclusion We will present our (preliminary) data on the TME of OTRs-cSCC versus sporadic cSCC, and hope hereby to reveal mechanisms of tumour aggressiveness and inform future biomarkers and therapeutic development.

P7 – MARIE-ELINE DEBEUF

BIOLOGICAL CHANGES OF THE SKIN AFTER ABLATIVE LASER THERAPY – A SCOPING REVIEW

Marie-Eline P.H. Debeuf[1,2], Maartje Rauwenhoff[1], Michel van Geel[1,2,3], Peter M. Steijlen[1,2], Valerie L.R.M. Verstraeten[1,2,4]

[1]Department of Dermatology, Centre of Expertise for Genodermatoses, Maastricht University Medical Centre+, Maastricht, The Netherlands; [2]GROW Research Institute for Oncology and Developmental Biology, Maastricht University, Maastricht, The Netherlands; [3]Department of Clinical Genetics, Maastricht University Medical Centre+, Maastricht, the Netherlands; [4]Dermadok Huidkliniek, Antwerp, Belgium.

Background Ablative laser therapy is a widely used interventional tool in dermatology, primarily for skin rejuvenation and scar treatment. The choice between fractional or fully abla-

tive modes is determined by specific indications and patient characteristics. Although research into the clinical effects is growing, the biomolecular mechanisms behind these different laser modes are not fully understood.
Objective To provide a comprehensive overview of the biomolecular changes induced by (fractional) ablative laser therapy on skin.
Methods A literature search was conducted on Pubmed, Embase and Web of Science covering studies from inception until September 2025. Studies focusing on changes in gene and protein expression after ablative laser therapy (10 600 nm CO2 laser, 2940 nm Er:YAG laser, 2790 nm Er:YSGG laser) were included.
Results Twenty studies were included, most focusing on skin rejuvenation. Both fractional and ablative lasers resulted in an inflammatory phase followed by dermal remodelling and neocollagenesis, as characterised by increases in metalloproteinases and collagen. High collagen levels persisted for up to 6 months. Decreases in elastin and increases in tropoelastin indicated a breakdown of old elastic fibres, followed by new elastogenesis, which was more pronounced after full ablation. Superficial Er:YAG micro-ablation, preserving the basal membrane, showed similar biomolecular changes compared to full ablation of the epidermis and superficial dermal layer.
Conclusion Both fractional and ablative laser induced dermal remodelling and neocollagenesis, while elastogenesis was more evident after full ablation. Microablation provided similar results compared to full ablation, highlighting the need for further research in this area.

P8 – KENESHKA ATASH

LEBRIKIZUMAB IN MULTI-THERAPY-REFRACTORY ATOPIC DERMATITIS PATIENTS: A CASE SERIES FROM THE BIODAY REGISTRY

Keneshka Atash[1],, Celeste M. Boesjes[1], Nicolaas P.A. Zuithoff[2], M. de Graaf[1], Marjolein S. de Bruin-Weller[1], Inge M. Haeck[1]
[1]National Expertise Center for Atopic Dermatitis, Department of Dermatology and Allergology, University Medical Center Utrecht, Utrecht, The Netherlands; [2]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht, The Netherlands.

Background Lebrikizumab, a new interleukin-13 inhibitor, has demonstrated efficacy and overall favourable safety in phase-III clinical trials for atopic dermatitis (AD). However, real-world evidence (RWE) regarding lebrikizumab, particularly in multi-therapy-refractory patients is scarce.
Objective To evaluate real-world effectiveness and safety of 28-weeks lebrikizumab in moderate-to-severe AD refractory to multiple conventional/advanced systemic therapies.
Methods Within the BioDay-registry, a prospective case-series analyzed 28-week lebrikizumab outcomes in AD patients from an early access program, who had failed multiple conventional/advanced therapies. Eczema Area and Severity Index (EASI), Numeric Rating Scale (NRS) itch, pain and sleep deprivation, were assessed at baseline, week 4, 16 and 28 using a linear mixed model. Additional clinical outcomes, laboratory parameters, and adverse events (AEs) were analyzed descriptively.
Results Thirteen patients were included. Twelve patients (92.3%) had received prior conventional systemic therapy. All had previously been treated with biologics and/or oral JAK-inhibitors; 8 patients (61.5%) had used ≥ 3 such agents. At week 28, lebrikizumab resulted in a statistically significant mean reduction in EASI from 13.2 (95% CI: 10.3 – 16.2) to 8.4 (95% CI: 5.3 – 11.5); and in NRS itch from 6.7 (95% CI: 5.6 – 7.7) to 5.1 (95% CI: 4.0 – 6.2). In 12 patients (92.3%) 28 AEs occurred, mostly mild and moderate; most commonly ocular surface disease (n=7), myalgia/arthralgia (n=4) and transient eosinophilia (n=4).
Conclusion Lebrikizumab achieved modest yet clinically meaningful improvement in multi-therapy-refractory AD patients with overall tolerable safety. Larger RWE studies are needed to confirm long-term effectiveness and safety of lebrikizumab in broader AD patient populations.

P9 – NIENKE VELDHUIS

DUPILUMAB-ASSOCIATED OCULAR SURFACE DISEASE IN ATOPIC DERMATITIS: RESULTS FROM A LARGE PROSPECTIVE REAL-WORLD COHORT

Nienke Veldhuis[1], Roselie E. Achten[1], Chantal M. van Luijk[2], Coco C. Dekkers1, Nicolaas P. A. Zuithoff[3], Marlot M. van der Wal[4], Femke van Wijk[4], Joke H. de Boer[2], Marlies de Graaf[1], Inge M. Haeck[1], Marjolein S. de Bruin-Weller[1]
[1]Department of Dermatology and Allergology, National Expertise Center for Atopic Dermatitis, University Medical Center Utrecht, Utrecht, The Netherlands; [2]Department of Ophthalmology, University Medical Center Utrecht, Utrecht, The Netherlands; [3]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht, The Netherlands; [4]Center for Translational Immunology, University Medical Center Utrecht, Utrecht University, Utrecht, The Netherlands.

Background Dupilumab-associated ocular surface disease (DAOSD) is a frequently reported side effect in atopic dermatitis (AD) patients treated with dupilumab.
Objective To investigate the frequency and severity of DAOSD, and the effect of dupilumab on conjunctival goblet cells (GCs) in a large prospective real-world cohort.
Methods This prospective study included moderate-to-severe AD patients treated with dupilumab between February 2020 and January 2025 at the UMC Utrecht. Ophthalmological and dermatological examinations were performed at baseline (start of dupilumab), week 4, and week 28. Ocular surface disease (OSD) severity was assessed using the Utrecht Ophthalmic Inflammatory and Allergic disease (UTOPIA) score. DAOSD was defined as a ≥3-point increase from baseline. Conjunctival impression cytology was performed to study the quantity and function of conjunctival GCs.
Results OSD was present in 94.0% (n=141/150) of patients at baseline, while only 60.0% (n=90/150) reported ocular symptoms. During 28 weeks of dupilumab treatment, 30.7% (n=46/150) of patients developed DAOSD. At week 4 and week

28, 56.7% (n=85/150) and 64.7% (n=97/150) of patients regularly used ophthalmic medication, respectively. GC numbers remained stable between baseline and week 28, while Mucin 5AC (MUC5AC) production in Cytokeratin 19-CD45-MUC5AC+ cells significantly decreased.
Conclusion This study highlights the high prevalence of OSD in moderate-to-severe AD patients before dupilumab treatment. DAOSD was observed in 30.7% of patients, despite the potential protective effect of ophthalmic treatment. While conjunctival GC numbers remain stable but low, dupilumab seems to impair GC function.

P10 – KIM DANIËLLE VAN DER GOUW

IMPROVING THE EFFICIENCY OF ANTISENSE OLIGONUCLEOTIDE-MEDIATED EXON SKIPPING OF COL7A1 TO TREAT RECESSIVE DYSTROPHIC EPIDERMOLYSIS BULLOSA

Kim D. van der Gouw[1], Maria C. Bolling[2], Anke H. Maitland-van der Zee[1], Jeroen Bremer[2], Peter C. van den Akker[1]
[1]University of Groningen, University Medical Center Groningen, Department of Genetics, Center of Expertise for Blistering Diseases, Groningen, The Netherlands; [2]University of Groningen, University Medical Center Groningen, Department of Dermatology, Center of Expertise for Blistering Diseases, Groningen, The Netherlands.

Background Recessive dystrophic epidermolysis bullosa (RDEB) is a severe blistering disease caused by mutations in the COL7A1 gene. This gene is mainly expressed by keratinocytes and encodes type VII collagen (C7), a protein that is essential for attaching the epidermis to the dermis. Previously, we demonstrated that antisense oligonucleotides (ASOs) can induce skipping of exon 105 of COL7A1 and restore C7 production in cultured keratinocytes from patients and in patient skin grafts on the backs of mice. However, exon skipping efficiency was only 2.5-5% and this might be too low for clinical benefit.
Objective To increase the efficiency of ASO-mediated exon skipping of COL7A1, by (1) further optimizing the sequence and chemistry of the ASO and (2) improving the delivery of the ASO to keratinocytes.
Methods We will transfect cultured keratinocytes with more than 100 tiled ASOs spanning exon 105 of COL7A1 to assess which ASO induces most exon skipping. We will also compare the efficiency of ASOs with different chemistries. Then, we will use the optimized ASO to explore targeted and non-targeted conjugation approaches. We will evaluate if, and to what extent, these approaches improve ASO delivery to keratinocytes and lead to more efficient exon skipping. Experiments will be performed *in vitro* (in HaCaT cells, primary keratinocytes and 3D human skin equivalents), *ex vivo* (in an intact human skin model) and ultimately *in vivo*.
Conclusion This study will support the development of ASO-mediated exon skipping of COL7A1 as a feasible treatment option for patients with RDEB.

P11 – WOUTER OUWERKERK

BIOMARKER-BASED DIAGNOSIS OF CONTACT DERMATITIS: A STEP TOWARDS MORE ACCURATE AND PATIENT-FRIENDLY TESTING

Sanja Kezic[1], Florentine de Boer[1] , Nariman K.A. Metwally[1,2], Karen Ghauharali-van der Vlugt[3,4,5], Femke S. BeersStet[3,4,5], Wouter Ouwerkerk[6,7], Ivone Jakasa[8], Thomas Rustemeyer[9], Henk F. van der Molen[1]
[1]Public and Occupational Health Department, Amsterdam UMC, University of Amsterdam, Amsterdam Public Health Research, Amsterdam, The Netherlands; [2]Department of Pulmonary Medicine, Amsterdam UMC, University of Amsterdam, Amsterdam, Department of Pediatric Pulmonology and Allergy, Emma Children's Hospital, Amsterdam UMC, Amsterdam, The Netherlands; [3]Amsterdam UMC location University of Amsterdam, Department of Laboratory Medicine and Pediatrics, Laboratory Genetic Metabolic Diseases, Emma Children's Hospital, Amsterdam, The Netherlands; [4]Amsterdam Gastroenterology Endocrinology Metabolism, Inborn errors of metabolism, Amsterdam, The Netherlands; [5]Core Facility Metabolomics, Amsterdam UMC location University of Amsterdam, Amsterdam, The Netherlands; [6]Department of Dermatology, Amsterdam UMC, University of Amsterdam, Amsterdam Infection and Immunity Institute, Amsterdam, The Netherlands; [7]National Heart Centre Singapore, Singapore; [8]Laboratory for Analytical Chemistry, Department of Chemistry and Biochemistry, Faculty of Food Technology and Biotechnology, University of Zagreb, Zagreb, Croatia; [9]Dermato-Allergology and Occupational Dermatology, Amsterdam University Medical Centers, Noord-Holland, The Netherlands.

Background Contact dermatitis (CD) is a highly prevalent inflammatory skin disorder, with two main types; irritant contact dermatitis (ICD) and allergic contact dermatitis (ACD). Overlapping clinical features make subtypes difficult to distinguish. Currently, the gold-standard for distinguishing ICD from ACD is an epicutaneous patch test. Patch tests are a burden on patients, a positive test does not necessarily implicate the allergen and there is a high risk of false-negative results. There is an unmet need for more accurate, objective and patient-friendly diagnostics tools to rapidly distinguish between ICD and ACD.
Objective To develop a prediction tool to discriminate between ACD and ICD in both patch test induced reactions as well as in clinical chronic hand dermatitis.
Methods We collected *stratum corneum* tape strips from a positive patch test reaction to allergens (nickel, chromium, methylisothiazolinone), an irritant lesional skin and a control site of 153 patients. A broad panel of 32, including skin barrier and immunological, biomarkers was measured. We developed multiple classifiers using Bayesian and penalized regression and machine learning methods.
Results We were able to discriminate ACD and ICD in patch test data, with mean AUCs between 0.79 and 0.85. AUC was lower in the classifier validating on lesional data (AUC 0.69-0.72). We could not discriminate between different allergens

in patients with ACD (AUC ~0.5). Most important parameters were Cholesterol (Sulf/Glc), NMF, CEACAM-5, TRAIL, and Amphiregulin.
Conclusion Patch-induced ACD and ICD identified strong discriminators, particularly barrier-related biomarkers. When these patch-derived classifiers were applied to chronic hand-dermatitis, performance decreased.

P12 – LINDA GODDING

EXPERIENCES OF PATIENTS WITH GENERALISED PUSTULAR PSORIASIS: A QUALITATIVE STUDY

L.T.H. Godding[1], L.S. van der Schoot[1], S. van Beugen[2], I. van Ee[3], H.B. Thio[4], E.M.G.J. de Jong[1,5], J.M.P.A. van den Reek[1]
[1]Department of Dermatology, Radboud University Medical Center, Nijmegen, The Netherlands; [2]Health, Medical and Neuropsychology Unit, Institute of Psychology, Leiden University, Leiden, The Netherlands; [3]Psoriasispatiënten Nederland (PN), Nijkerk, The Netherlands; [4]Department of Dermatology, Erasmus Medical Center, Rotterdam, The Netherlands; [5]Radboud University, Nijmegen, The Netherlands.

Background The evolving insights and changing treatment landscape of the severe, chronic inflammatory skin disease generalized pustular psoriasis (GPP) increases the need for a deeper understanding of its disease burden and patients' preferences.
Objective To explore the disease burden and impact of GPP, in both the acute and chronic phase of the disease.
Methods A cross-sectional qualitative study was performed consisting of semi-structured interviews. Patients were recruited through the Dutch Psoriasis Patient Federation and at the outpatient clinic of the Radboud University Medical Centre. Interviews were audio-recorded and transcribed verbatim. Interviews were analysed by inductive thematic analysis using ATLAS.ti software.
Results A total of 10 patients were interviewed. Mean duration of interviews was 51 minutes. Patients had a mean age of 61 years (range 32-75) and a median disease duration of 6 years at the time of interview. Most patients were treated with a combination of topical and systemic treatments (90%), of which 56% with acitretin. Four patients had received spesolimab, a novel interleukin-36 targeting biologic. Based on preliminary results, GPP has a large impact on patients' lives and their social environment. GPP disease flares were reported as extremely distressing events, emphasizing the importance of controlling upcoming flares. The positive experiences of patients who were treated with the newest biologic spesolimab may result in a brighter future perspective for patients with GPP.
Conclusion At the 2026 NVED meeting, final emerging themes resulting from the interviews will be presented.

P13 – BEATRIZ OLIVEIRA FAGUNDES

T CELL EXHAUSTION IN CHRONIC INFLAMMATORY DISEASES – A SCOPING REVIEW

B.O. Fagundes[1,2], L. Loman[1], L.A. Miltner[1], M.L.A. Schuttelaar[1], P. Heeringa[1], Y. Van Sleen[1]
[1]Department of Dermatology, University Medical Center Groningen, Groningen, The Netherlands; [2]Laboratory of Medical Investigation LIM-56, Division of Dermatology, Medical School, University of Sao Paulo (USP), Sao Paulo, Brazil.

Background T cell exhaustion, a dysfunction driven by chronic antigen exposure, is well established in persistent infections and cancer but underexplored in chronic inflammatory diseases. Clarifying how persistent immune activation drives T cell exhaustion may reveal therapeutic strategies. We hypothesize that persistent inflammation promotes exhaustion, contributing to chronic disease sustainment.
Objective To systematically map and summarize the available literature on phenotypic characteristics and functional aspects of exhausted T cells in chronic inflammatory diseases.
Methods A scoping review is being conducted in accordance to JBI methodology and PRISMA-ScR guidelines. PubMed, Embase, Web of Science and Scopus were searched in October 2025 for studies. Title, abstracts, and full texts will be screened independently by two reviewers using JBI SUMARI tool, capturing study characteristics, disease context, biomarkers, mechanisms, and therapeutic interventions. Extracted data will be analyzed descriptively and summarized in tabular and narrative form.
Results Preliminary screening suggests variability in how T cell exhaustion is defined across studies. Common markers include PD-1, TIM-3, CTLA-4, and LAG-3, yet interpretation and defining criteria vary widely. Reports in chronic inflammatory diseases show reduced proliferation and altered cytokine profiles. However, associations with disease severity, prognosis, or treatment response remain inconsistent.
Conclusion This scoping review will provide a comprehensive mapping of T cell exhaustion in autoimmune and chronic inflammatory diseases. By synthesizing evidence on mechanisms, biomarkers, and therapeutic implications, it aims to clarify conceptual boundaries, highlight underexplored conditions, and identify key knowledge gaps. These findings are expected to guide future research and inform the development of targeted immunotherapies.

P14 – FENNA DE BIE

THE EFFECT OF ANTHRACYCLINE TREATMENT ON PRIMARY CUTANEOUS T-CELL LYMPHOMA CELLS

F.J. de Bie[1], M. Dettingmeijer[1], S. de Haan[1], W.H. Zoutman[1], S.Y. van der Zanden[2], C.P. Tensen[1], F.A. Scheeren[1], J. Neefjes[2], M.H. Vermeer[1]
[1]Department of Dermatology, Leiden University Medical Center, Leiden, The Netherlands; [2]Department of Cell and Chemical Biology, ONCODE Institute, Leiden University Medical Center, Leiden, The Netherlands.

Background Cutaneous T-cell Lymphomas (CTCL) are a rare group of extra-nodal mature T-cell-derived lymphomas originating in the skin of which mycosis fungoides (MF) and Sézary syndrome (SS) are the most studied types. Several treatment modalities are available for early stage disease,

however more advanced disease is difficult to treat and requires new therapeutic options. Anthracyclines are widely used in the treatment of various hematologic malignancies and solid tumors. Anthracyclines can cause severe side effects in patients, such as dose-dependent irreversible cardiotoxicity. Aclarubicin (Acla) is an anthracycline that has no cardiotoxic side effects.

Objective Evaluate the cellular toxicity and anti-tumor effects of various anthracyclines on CTCL cell lines and ex vivo CD4+ T-cells derived from CTCL patients.

Methods From 5 CTCL patients of the LUMC Dermatology out-patient clinic peripheral blood was collected, CD4+ T cells were isolated and treated with 4 anthracyclines. Relative cell survival was evaluated by CellTiter-Blue assay and the components of healthy and tumor cells were assessed using spectral flow cytometry.

Results The range IC50 of Acla is 1.0-4.9 µM, of other anthracyclines 3.1-33.6 µM. Flow cytometry analysis revealed that both normal and malignant cells exhibited comparable levels of cell death at equivalent concentrations of anthracycline treatment.

Conclusion Aclarubicin has therapeutic activity against CTCL tumor cells with therapeutic efficacy at lower concentrations than other anthracyclines. These findings suggest that Acla could be an effective treatment in CTCL patients. Given the absence of cardiotoxic side effects of Acla, this treatment warrants further investigation for CTCL patients.

P15 – MYRTHE MOERMANS

UNMET CARE NEEDS AND EXPERIENCES OF PATIENTS WITH BASAL CELL NEVUS SYNDROME AND THEIR PARENTS: A QUALITATIVE INTERVIEW STUDY

Myrthe M.G. Moermans[1,2], Fauve C.A.P. van Veen[1,2], Renée C.P. Schurmans[1], Dorthe O. Klein[3,4], Antoni Gostynski[1,2], Klara Mosterd[1,2]

[1]Department of Dermatology, Maastricht University Medical Centre+, Maastricht, The Netherlands; [2]GROW Research Institute for Oncology and Reproduction, Maastricht University, Maastricht, The Netherlands; [3]Clinical Epidemiology and Medical Technology Assessment, Maastricht University Medical Centre, Maastricht, The Netherlands; [4]CAPHRI Research Institute, Maastricht University, Maastricht, The Netherlands.

Background Basal cell nevus syndrome (BCNS) is a rare genetic disease, with a wide variety of clinical presentations, such as multiple basal cell carcinomas, keratocysts and other extracutaneous manifestations. The nature of the condition requires a rigorous and frequent trajectory of hospital visits and procedures, resulting in a substantial burden on quality of life (QoL).

Objective The objective of this study is to in-depth explore the impact of BCNS on the biological, psychological, and social domains of QoL in patients with BCNS and their parents.

Methods After purposive sampling, semi-structured, individual qualitative interviews were conducted. The interviews were recorded and transcribed verbatim. Interview data were coded and analysed using thematic content analysis in ATLAS.ti version 9.0.

Results Ten patients with BCNS and six parents of children with BCNS were interviewed. Thematic content analysis revealed five major themes related to the impact of BCNS on their QoL. These included: (1) daily impact and physical complaints, (2) experiences with hospital care, (3) being the parent of a child with BCNS, (4) impact on psychological well-being, and (5) impact on social network and relationships.

Conclusion BCNS affects all domains of QoL. However, the degree of impact is highly patient-dependent. Therefore, patient-tailored care should be pursued. Areas for future improvement include creating more disease awareness in the medical and general community, early confirmation of the diagnosis, and attention to psychological and genetic counselling. Patients may benefit from a patient organisation advocating their needs and from a combined patient and physician score to gain more insight into the disease burden.

P16 – JULIA STANKIEWICZ

INVESTIGATING IMMUNOHISTOCHEMICAL MARKERS IN 101 EARLY-STAGE MYCOSIS FUNGOIDES PATIENTS: A RETROSPECTIVE STUDY ON DISEASE PROGRESSION AND PROGNOSTIC FACTORS

J.M. Stankiewicz[1], J.M. Kersten[1], R. Ottevanger[1], P.M. Jansen[2], M.H. Vermeer[1], K.D. Quint[1]

[1]Department of Dermatology, Leiden University Medical Center, Leiden, The Netherlands; [2]Deparment of Pathology, Leiden University Medical Center, Leiden, The Netherlands.

Background Mycosis fungoides (MF) is the most common subtype of cutaneous T-cell lymphomas (CTCLs). Most patients present with patches and plaques (stage Ia/b) and follow an indolent disease course. However, 20-30% of these patients progress to tumor stage (stage IIb) with a 5-year survival rate around 50%. The prognostic value of immunohistochemical markers in early-stage MF remains unclear.

Objective To identify immunohistochemical markers associated with disease progression and poor survival in early-stage MF patients.

Methods Clinical and immunohistochemical data from diagnostic skin biopsies in 101 early-stage MF patients were retrospectively analyzed. Patients were classified as having stable MF (sMF, n=50) or progressive MF (pMF, n=51) based on progression to tumor stage disease during a minimal follow-up of 12 months. Expression of CD4, CD8, CD3, CD5, CD56, TIA-1 and Granzyme B (Gr B) on the tumor cells was retrieved from files in both groups and correlated with disease specific survival (DSS), overall survival and progression free survival (PFS) using univariate and multivariate analysis.

Results Median follow-up time was 121 months. TIA-1 expression was significantly higher in the sMF group and independently associated with improved DSS (HR 0.3, p=.015). Gr B expression correlated with prolonged PFS but did not retain significance in multivariate analysis.

Conclusion Our results suggest that loss of TIA-1 in tumor cells is an independent predictor of worse DSS in early-stage

MF, suggesting its potential as a prognostic marker. Further research is warranted to confirm these findings and to develop a prognostic model integrating immunophenotypic markers and clinical data.

P17 – LINDI KORPELSHOEK

INCIDENCE AND OUTCOME OF OTHER PRIMARY MALIGNANCIES IN 273 PATIENTS WITH PRIMARY CUTANEOUS MARGINAL ZONE LYMPHOMA

Lindi Korpelshoek[1,2], Maarten H. Vermeer[2], Jelle J. Goeman[3], Anne M. R. Schrader[1]

[1]Department of Pathology, Leiden University Medical Center (LUMC), Leiden, The Netherlands; [2]Department of Dermatology, Leiden University Medical Center (LUMC), Leiden, The Netherlands; [3]Department of Medical Statistics, Leiden University Medical Center (LUMC), Leiden, The Netherlands.

Background Primary cutaneous marginal zone lymphoma (PCMZL) is a low-grade B-cell lymphoma with an excellent prognosis. The incidence of other primary malignancies has been investigated in other types of cutaneous lymphoma, but not yet in PCMZL.
Objective This study investigates the incidence of other primary malignancies in PCMZL patients relative to the general population.
Methods We performed a retrospective cohort study including 273 patients diagnosed with PCMZL between 2000 and 2024. Lifetime pathology reports were retrieved from the nationwide Dutch pathology registry and screened for other primary malignancies, either before or after PCMZL diagnosis. Observed rates were compared with population-based expected rates from the Dutch National Cancer Registry. Systemic dissemination or transformation of PCMZL were not classified as OPM.
Results The median observation period was 57.3 years before and 10.3 years after PCMZL diagnosis. Incidence rates were significantly increased for basal cell carcinoma (SIR 1.9, 95%-CI 1.3-2.7) and squamous cell carcinoma (SIR 3.36, 95%-CI 1.4-6.9) before PCMZL diagnosis. After PCMZL diagnosis, significantly increased rates were found for basal cell carcinoma (SIR 3.7, 95%-CI 5.0), squamous cell carcinoma (SIR 3.4, 95%-CI 1.5-6.4), melanoma (SIR 6.1, 95%-CI 2.5-12.6), haematological malignancies (SIR 8.1, 95%-CI 4.9-12.5) and endocrine malignancies (SIR 13.7, 95%-CI 1.7-49.5). Notably, haematological malignancies, both low- and high-grade, predominantly occurred post-diagnosis.
Conclusion This study demonstrates that app. 40% of PCMZL patients is diagnosed with other primary malignancies, with an increased risk of cutaneous, haematological and endocrine malignancies compared with the general Dutch population. Clinicians should be aware of this risk.

P18 – ANNA PATSEA

HEALTH-RELATED QUALITY OF LIFE IN PATIENTS WITH BASAL CELL NEVUS SYNDROME AND HIGH-FREQUENCY BASAL CELL CARCINOMA: A QUESTIONNAIRE STUDY

Anna A.L. Massella Patsea[1], Myrthe M.G. Moermans[1], Babette J.A. Verkouteren[1], Patty J. Nelemans[2], Aimée H.M.M. Arits[3], Marlies Wakkee[4], Emoke Racz[5], Marcel Bekkenk[6], Klara Mosterd[1]

[1]Department of Dermatology, Maastricht University Medical Centre+, Maastricht, The Netherlands; GROW Research Institute for Oncology and Reproduction, Maastricht University Medical Centre+, Maastricht, The Netherlands; [2]Department of Epidemiology, Maastricht University, Maastricht, The Netherlands; [3]Department of Dermatology, Catharina Hospital Eindhoven, Eindhoven, The Netherlands; [4]Department of Dermatology, Erasmus University Medical Center Cancer Institute, Rotterdam, The Netherlands; [5]Department of Dermatology, University Medical Center Groningen, Groningen, The Netherlands; [6]Department of Dermatology, Amsterdam UMC, Amsterdam, The Netherlands.

Background Patients with multiple Basal cell carcinomas (BCCs) require frequent interventions, which impact quality of life (QoL). Multiple BCCs develop from a genetic disease like basal cell nevus syndrome (BCNS) or without known genetic predisposition (high-frequency BCC, HF-BCC). Data on QoL in these patients and the influence of number of BCCs on QoL remain limited.
Objective To evaluate QoL in BCNS and HF-BCC and the impact of BCC burden on QoL.
Methods BCNS patients were recruited through the Maastricht University Medical Centre (MUMC+) and patient/professional associations. HF-BCC patients (≥9 BCCs in 3 years or ≥6 in 10 years) were recruited regionally. QoL was assessed with Skindex-29.
Results 75 BCNS and 59 HF-BCC patients were included. BCNS patients were younger (median 48 vs.74 years), female (61% vs. 34%) and had more BCCs (48% vs. 1% with >100 BCCs), compared to HF-BCC patients. BCNS patients reported more QoL impairment across emotions, functioning and total scores. The mean emotions score (32.2) exceeded the clinically relevant threshold (24). After adjusting for age and sex, the total score remained higher in BCNS, with a between-group difference of 10.0 (95%CI 2.5-17.5). Within BCNS, BCC burden was negatively associated with QoL, a trend absent in HF-BCC.
Conclusions BCNS patients experience greater QoL impairment than other patients with multiple BCCs, particularly in emotional and functional domains. A higher BCC burden further impacts QoL in BCNS, but additional challenges in this group may further impact their psychosocial well-being. These disease-related challenges should be addressed during consultations to improve patient support.

P19 – ANASTASIIA MYRONENKO

TO WHAT EXTENT DOES BEHAVIORAL IMMUNE ACTIVATION INFLUENCE ITCH CONTAGION AND PUBLIC STIGMATIZATION OF PEOPLE WITH PSORIASIS? AN EXPERIMENTAL STUDY

A. Myronenko, S. van Beugen, A.I.M. van Laarhoven
Institute of Psychology, Health, Medical and Neuropsychology Unit, Leiden University, The Netherlands.

Background The behavioral immune system (BIS) plays a key role in detecting and avoiding potential sources of pathogens, often triggering behavioral (e.g., avoidance) and emotional (e.g., disgust) responses to disease-relevant cues, facilitating survival. Previous research suggests involvement of BIS in the perception of contagious itch and stigmatization. However, experimental research on the causal role of BIS activation in contagious itch and stigmatization remains limited.
Objective This study examines whether BIS activation, through visual exposure to pathogen-themed information, increases itch contagion and stigmatizing attitudes toward a person with a chronic skin condition.
Methods In a video vignette experiment (target N = 136), all participants first viewed a person with psoriasis discussing a neutral topic, with lesions concealed. Then, participants were randomly assigned to watch a BIS-activating (pathogen-themed) or neutral control video. After this, participants watched a third video showing the same person from the first video, but now with visible lesions, scratching, and describing intense itch experiences. Outcomes included subjective itch ratings and stigma-related attitudes and behavioral avoidance (social distance).
Results Preliminary results (N = 60) show that participants experienced a significant increase in itch sensations and desire for social distance after viewing the third video when compared to the first video. These effects occurred regardless of prior exposure to the pathogen-themed video, indicating no additive effect of pathogen-themed priming.
Conclusion Preliminary results suggest that the combination of visual skin lesions, scratching, and talking about itch elicits both contagious itch and stigmatizing attitudes, without being amplified by pathogen-related threat cues.

P20 – ZIXIAN LIANG

COMPLEMENT FIXATION TEST IN PEMPHIGOID DISEASES: ASSOCIATION WITH IGG1/IGG4 SUBCLASS PROFILES IN A 1-YEAR PROSPECTIVE STUDY

Z. Liang[1], J. Bremer[1], S.M. van der Molen[1], J. Damman[3], J.M. Meijer[1], G.F.H. Diercks[1,2]
[1]University of Groningen, University Medical Center Groningen, Department of Dermatology, UMCG Center of Expertise for Blistering Diseases, ERN-SKIN, Groningen, The Netherlands; [2]University of Groningen, University Medical Center Groningen, Department of Pathology, UMCG Center of Expertise for Blistering Diseases, ERN-SKIN, Groningen, The Netherlands; [3]Erasmus University Rotterdam, Erasmus Medical Center Rotterdam, Department of Pathology, Rotterdam, The Netherlands.

Background The Complement fixation test (CFT) is an indirect immunofluorescence technique performed on salt-split human skin to detect circulating IgG directed against the basement membrane (BMZ), capable of complement binding. Complement activation contributes to blistering in pemphigoid diseases and depends on IgG subclass, where IgG1 strongly activates complement, whereas IgG4 hardly does.
Objective To assess the association between CFT and IgG subclasses in pemphigoid diseases.
Method In this prospective study, serum samples from suspected pemphigoid patients at UMCG (2023) underwent indirect immunofluorescence on salt-split skin (IIF SSS) for IgG, IgG1, IgG4, and CFT. For CFT, patient serum was incubated on salt-split skin, followed by fresh human serum and fluorescent anti-C3 to detect C3 at the BMZ. Samples that showed IIF SSS-IgG staining intensity of 2+ or 3+ were selected for IgG1 and IgG4 staining.
Results Of 806 tested sera, 113 were strongly positive for IIF SSS-IgG; 61 of these were CFT-positive. In CFT(+) group (n=61), the most common expression pattern was both positive for IgG1 and IgG4 (59.02%, 36/61). However, CFT(-) group (n=52) predominantly showed positivity for only IgG4 (65.38%, 34/52). In CFT(+) group, 57.38% cases exhibited strong IgG1 staining intensity(2+, 3+), while only 1.92% cases (1/52) in the CFT(-) group did($P < 0.0001$). No significant difference in IgG4 staining intensity between the two groups.
Conclusion Complement fixation is strongly associated with IgG1 expression, but not IgG4 subclass. CFT may serve as a functional marker of complement-activating antibody profiles, stratifying patients for complement-targeted therapies, but lacks sensitivity for routine diagnostics.

P21 – OTTE BORGHOUTS

LACK OF CONSENSUS IN REPORTED OUTCOMES FOR EPIDERMAL DIFFERENTIATION DISORDERS: A SCOPING REVIEW

O.J.M. Borghouts[1,2], S.V.J. Rossel[1,2], J. Shourick[3], M.C. Bolling[4], A.M.G. van Pasmooij[4,5], K. Veldman[6], J. J. Kirkham[7], J. Mazereeuw-Hautier[8], A.H. Gostyński[1,2]
[1]Department of Dermatology, Maastricht University Medical Centre+, Maastricht, The Netherlands, Centre of Expertise for Genodermatoses; [2]GROW school for Oncology Reproduction, Maastricht University, Maastricht, The Netherlands; [3]Department of Clinical Epidemiology and Public Health, CHU Toulouse, Toulouse, France; [4]Department of Dermatology, Groningen University Medical Centre, Groningen, The Netherlands, Centre of Expertise for Genodermatoses; [5]Dutch Medicines Evaluation Board, Utrecht, The Netherlands; [6]Vereniging voor Ichthyosis Netwerken, The Netherlands; [7]Centre for Biostatistics, The University of Manchester, Manchester Academic Health Science Centre, Manchester, United Kingdom; [8]Department of Dermatology, CHU de Toulouse, Université Toulouse III, Toulouse, France.

Background Epidermal differentiation disorders (EDDs, formerly known as inherited ichthyosis) comprise a group of rare heterogeneous genodermatoses affecting quality of life.

Although no cure exists, novel treatments are increasingly being investigated. However, heterogeneity in reported outcomes hampers comparison across studies and slows therapeutic progress. Inconsistent or poorly defined outcomes may also contribute to failure to meet trial endpoints. Well-defined outcomes are therefore essential. The Core Outcome Set (COS) for Epidermal Differentiation Disorders aims to establish a minimum list of outcomes and baseline characteristics that should be measured and reported in EDD research.
Objective This scoping review aimed to identify previously reported baseline characteristics and treatment outcomes used in clinical and observational studies on EDDs, serving as a first step in COS development.
Methods The review followed Joanna Briggs Institute (JBI) and PRISMA-ScR guidelines. Medline, EMBASE, CINAHL, Cochrane Library, and Web of Science were searched. Two reviewers independently performed title/abstract and full-text screening, excluding reports on acquired EDDs or studies with fewer than three patients. Data were extracted using a predefined, pilot-tested form.
Results Eighty publications (49 published articles, 31 protocols) were included, reporting 396 baseline characteristics and 259 outcomes, with some degree of overlap. Outcomes were combined and grouped into 10 domains: demographics, anthropometrics, medical history, pregnancy/perinatal, congenital/genetic, skin, extracutaneous manifestations, life impact, resource use, and adverse events.
Conclusion Substantial heterogeneity exists in reported outcomes for EDDs. These findings form the basis for the subsequent e-Delphi and consensus process to define a COS, enabling improved comparability and advancing therapeutic development.

P22 – MARLEEN DE WINTER

VISUALIZING THE EFFECT OF MOGAMULIZUMAB ON T REGULATORY CELLS IN CUTANEOUS T CELL LYMPHOMA USING A MULTIPLEX IMMUNOFLUORESCENCE IMAGING APPROACH

Marleen J. De Winter[1] Veerle A. Merkus[1], Fenna J. de Bie[1], Marieke E. IJsselsteijn[2], Sanne de Haan[1], Ferenc A. Scheeren[1], Noel F.C.C. de Miranda[2], Maarten H. Vermeer[1], Koen D. Quint[1]
[1]Department of Dermatology, LUMC, Leiden, The Netherlands; [2]Department of Pathology, LUMC, Leiden, The Netherlands.

Background Cutaneous T-cell lymphomas (CTCL) are characterized by the proliferation of malignant T cells within the skin. In advanced stages, patients are commonly treated with mogamulizumab, a humanized monoclonal antibody that targets CCR4$^+$ cells. CCR4 is expressed on both malignant T cells and regulatory T cells (Tregs). In peripheral blood, mogamulizumab has been shown to effectively deplete CCR4$^+$ malignant T cells as well as Tregs. However, it remains unclear whether mogamulizumab exerts a similar depleting effect on Tregs within the skin.
Objective This study aims to elucidate the effects of mogamulizumab therapy on Tregs and malignant T cells in the skin of CTCL patients.
Methods A multiplex immunofluorescence antibody panel was used combining T-cell markers (CD3, CD5, CD8) with markers relevant to mogamulizumab's mechanism (FoxP3, identifying Tregs, and CCR4, the therapeutic target). Formalin-fixed paraffin-embedded (FFPE) skin biopsies were collected from CTCL patients before and four months after initiation of mogamulizumab treatment. Image analysis was performed to assess changes in CCR4$^+$ and FoxP3$^+$ cell populations within lesional skin.
Results Preliminary analyses indicate a depletion of CCR4$^+$ cells in the skin following mogamulizumab therapy. Further evaluation of specific cell subsets within the tissue is ongoing.
Conclusion These findings suggest that mogamulizumab effectively depletes CCR4$^+$ cells in the skin, supporting its ability to target CCR4+ cells within the tumor microenvironment.

P23 – JULIETTE FARAI BOLLEMEIJER

CHRONIC PRURITUS IN OLDER ADULTS: PREVALENCE, ASSOCIATIONS, AND PRURITUS-SPECIFIC QUALITY OF LIFE

Juliette F. Bollemeijer[1], Mathijs R. de Veer[1,2], Elke Weisshaar[3], Willem P. Brouwer[4], Lies Lahousse[5,6], David A. Gunn[7], Tamar E.C. Nijsten[1], Luba M. Pardo[1]
[1]Department of Dermatology, Erasmus MC University Medical Center, Rotterdam, The Netherlands; [2]Department of Psychiatry, section Medical Psychology and Psychotherapy, Erasmus MC University Medical Center, Rotterdam, The Netherlands; [3]Division of Occupational Dermatology, Department of Dermatology, University Hospital Heidelberg, Heidelberg, Germany; [4]Department of Gastroenterology and Hepatology, Erasmus MC University Medical Center, Rotterdam, The Netherlands; [5]Department of Epidemiology, Erasmus MC University Medical Center, Rotterdam, The Netherlands; [6]Department of Bioanalysis, Ghent University, Ghent, Belgium; [7]Unilever R&D at King's College London, 28th Floor, Tower Wing, Guy's Hospital, Great Maze Pond, London, UK.

Background Chronic pruritus (itch lasting ≥6 weeks) is a burdensome condition that frequently affects older adults, yet its epidemiology and impact on health-related quality of life (QoL) in the ageing population remain underexplored.
Objective To examine the prevalence of chronic pruritus, its associated factors, and pruritus-specific QoL in the general ageing population.
Methods We included 4,474 participants (median age 72 years; range 48–99; 58.8% female) from the population-based Rotterdam Study. Questionnaires assessed current, 12-month, and lifetime chronic pruritus, along with ItchyQoL scores. Multivariable logistic regression identified factors associated with chronic pruritus, and linear regression assessed factors linked to pruritus-specific QoL. Principal component analysis (PCA) explored the dimensional structure of the ItchyQoL in this older population.
Results Prevalence of chronic pruritus was 8.6% (current), 10.5% (12-month), and 18.6% (lifetime). Female sex, older age, smoking, atopic dermatitis, psoriasis, self-reported dry skin, asthma, steatotic liver disease, polyneuropathy, depressive

symptoms, anxiety, and poor sleep were associated with higher odds of chronic pruritus. Among those with current chronic pruritus, pruritus-specific QoL was moderately impaired, with greater impairment among participants with atopic dermatitis and psychological symptoms. PCA identified four ItchyQoL dimensions, extending beyond the original three domains.
Conclusion Chronic pruritus is a prevalent, multifactorial condition in older adults, with significant psychological impact and implications for multidisciplinary management.

P24 – MARIELLE VAN DER PEET

INVESTIGATING THE RELATIONSHIP BETWEEN GUSELKUMAB TREATMENT AND SIGNALING LIPID LEVELS IN BLISTER AND PLASMA SAMPLES FROM PSORIASIS PATIENTS

M.P. van der Peet[4], J. Rousel[1,4], M.E. Bergmans[1], F. Badmus[5], T. Ederveen[5], T. Niemeyer-van der Kolk[1], P. Maas[4], A. Kindt[4], A.C. Harms[4], M.B.A. van Doorn[1,3], T. Hankemeier[4], R. Rissmann[1,2,4]
[1]Centre for Human Drug Research, Leiden, The Netherlands; [2]Leiden University Medical Centre, Leiden, The Netherlands; [3]Erasmus Medical Centre, Rotterdam, The Netherlands; [4]Leiden Academic Centre for Drug Research, Leiden University, Leiden, The Netherlands; [5]Center for Molecular and Biomolecular Informatics (CMBI), Radboud University Nijmegen, The Netherlands.

Background Psoriasis is a chronic inflammatory skin disease characterized by erythematous, scaly plaques caused by excessive keratinocyte proliferation and immune-mediated inflammation. The IL-23/Th17 axis drives disease pathogenesis through cytokines that promote keratinocyte activation. Guselkumab, a selective IL-23 inhibitor, effectively improves Psoriasis Area and Severity Index scores, but its broader molecular effects remain unclear. Metabolomics can be used to reveal integrated systemic and local disease mechanisms.
Objectives To compare local (suction blister fluid) and systemic (plasma) metabolite profiles to identify treatment-responsive pathways and elucidate psoriasis-related metabolic alterations.
Methods In a randomized, double-blind study, 26 psoriasis patients (20 guselkumab, 6 placebo) and healthy volunteers provided plasma and suction blister samples from non-lesional and peri-lesional skin. Samples were collected at baseline, and after 28 and 112 treatment days. A targeted HPLC-MS approach quantified 250 metabolites, including fatty acids, bile acids, oxylipins, endocannabinoids, and lysophospholipids.
Results We identified 114 metabolites in blister fluid and 127 in plasma. Baseline differences between patients and controls were most pronounced in peri-lesional blisters, emphasizing local metabolic dysregulation. After guselkumab treatment, these differences diminished, particularly in peri-lesional blister fluid, suggesting stronger local than systemic effects. Elevated sphingosine species decreased post-treatment, consistent with reduced keratinocyte activation. Oxylipin profiling indicated predominant lipoxygenase (LOX) over cyclooxygenase (COX) metabolism of arachidonic acid, with LOX activity declining after treatment while COX remained impaired.
Conclusion Guselkumab induces distinct local and systemic metabolic shifts, with pronounced normalization in skin. Paired lipidomic profiling offers mechanistic insight and potential biomarkers for monitoring therapeutic response in psoriasis.

P25 – CHEN LIANG

A SERUM PROTEOMICS-BASED COMPARISON BETWEEN BULLOUS PEMPHIGOID AND NONBULLOUS PEMPHIGOID

Chen Liang[1], Miranda Nijenhuis[1], Jeroen Bremer[1], Peter Heeringa[2], Barbara Horváth[1], Gilles Diercks[1,2], Joost Meijer[1]
[1]University of Groningen, Department of Dermatology, UMCG Center of Expertise for Blistering Diseases, European Reference Network for Rare Skin Diseases (ERN SKIN), University Medical Center Groningen, Groningen, The Netherlands; [2]University of Groningen, Department of Medical Biology and Pathology, University Medical Center Groningen, Groningen, The Netherlands.

Background Bullous pemphigoid (BP) is a common autoimmune subepidermal blistering disease that typically presents with tense bullae and intense pruritus. However, some patients do not develop bullae, a presentation referred to as nonbullous pemphigoid (NBP). The pathogenesis of BP is complex, and it remains unclear why some patients do not develop blisters. It is hypothesized NBP and BP differ in disease mechanism, or reflect a disease phase with differences in intensity of the inflammatory response.
Objective To explore and compare the proteomic profiles in serum of BP and NBP patients with the aim of elucidating their differences and uncovering the mechanisms that drive blister formation.
Methods Serum samples from 27 patients with BP, 29 patients with NBP, and 28 healthy controls (HCs) were analyzed using the multiplex Olink Reveal NGS based proteomics.
Results multiplex proteomics analysis revealed significant differences and trends related to proinflammatory mediators and immune function. In detail analysis will indicate the exact role in disease pathomechanism of BP and NBP.
Conclusion multiplex proteomics may contribute to elucidate potential differences in disease mechanism between the clinical phenotypes of BP and NBP.

P26 – CARIN SMIT

EVALUATING LABORATORY ABNORMALITIES IN ATOPIC DERMATITIS PATIENTS TREATED WITH JAK-INHIBITORS

Carin Smit[1], Nicolaas P.A. Zuithoff[2], Juliette Bras[3], Dirk Jan Hijnen[3,4], Octavian I. Bacoş-Cosma[5], Marie-Louise Schuttelaar[5], Nikita van Dijk[1], Phyllis Spuls[6], Marijke Kamsteeg[4], Simone Stadhouders-Keet[7], Marjolein S. de Bruin-Weller[1], Louise A.A. Gerbens[6#], Marlies de Graaf[1#]
[1]National Expertise Center for Atopic Dermatitis, Department of Dermatology and Allergology, University Medical Center Utrecht, Utrecht, The Netherlands; [2]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht, The Netherlands; [3]Department of Dermatology, Erasmus Medical Center, Rotterdam, The Netherlands;

[4]*Department of Dermatology, Radboud University Medical Center, Nijmegen, The Netherlands;* [5]*Department of Dermatology, University Medical Center Groningen, Groningen, The Netherlands;* [6]*Department of Dermatology, Amsterdam UMC, University of Amsterdam, The Netherlands;* [7]*Department of Dermatology, Reinier de Graaf Hospital, Delft, The Netherlands.* [#]*Authors share joint senior authorship.*

Background Real-world evidence on laboratory abnormalities in patients with atopic dermatitis (AD) treated with Janus kinase inhibitors (JAKi) is scarce.
Objective To evaluate the frequency, severity, and clinical impact of laboratory abnormalities in adults with moderate-to-severe AD treated with JAKis in routine clinical practice, providing insight for optimized patient monitoring.
Methods This multi-center observational study included adults with moderate-to-severe AD treated with a JAKi between January 1, 2021, and August 31, 2024, in five Dutch hospitals participating in the BioDay and TREAT NL registries. Laboratory parameters were assessed at baseline and at weeks 4, 16, 28, 40, and 52. The severity of abnormalities was graded according to the Common Terminology Criteria for Adverse Events (CTCAE).
Results 282 adult patients with a total of 404 treatment episodes were included. The most common CTCAE grade ≥2 abnormalities were elevated CPK (9.0%), increased triglycerides (4.3%), and decreased lymphocytes (2.6%). Severe abnormalities (grade ≥3) were rare, observed in 0.35% of all tests (49/13,927), mainly in patients receiving abrocitinib 200 mg, upadacitinib 15 mg, or baricitinib 4 mg. The most frequent severe findings were elevated CPK, increased triglycerides, and lymphopenia. Treatment discontinuation due to abnormalities occurred in two episodes (0.5%), both with upadacitinib 15 mg.
Conclusion This study showed that severe lab abnormalities are rare in AD patients treated with JAKis in daily practice, aligning with phase III trial data. These findings support reconsidering the need for routine laboratory monitoring of parameters with limited clinical relevance.

P27 – ANGELIKI BIRMPILI

RESTORATION OF MOLECULAR PROFILES IN PSORIATIC SKIN FOLLOWING GUSELKUMAB TREATMENT

Angeliki Birmpili, Ron Heeren, Rob Vreeken, Eva Cuypers
Maastricht Multimodal Molecular Imaging Institute (M4i), University of Maastricht, The Netherlands.

Background Psoriasis is a chronic inflammatory skin disease characterized by keratinocyte hyperproliferation and immune dysregulation. Alterations in skin lipid metabolism play a major role in barrier dysfunction and disease pathogenesis. Although Guselkumab, an anti–IL-23 monoclonal antibody, effectively restores clinical and histological features of psoriatic skin, its impact on the skin lipidome remains poorly understood.
Objective This study aims to investigate the molecular effects of Guselkumab treatment on the spatial distribution and composition of lipids in psoriatic skin using mass spectrometry imaging.
Methods Biopsies from psoriatic lesions were collected at baseline and after 16 weeks of Guselkumab therapy. Matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) MSI was employed to spatially map lipid species across skin layers. Data were analyzed by multivariate statistical analysis to identify treatment-related lipid changes relative to healthy control skin.
Results Guselkumab treatment markedly normalized the lipidome of psoriatic skin, with the vast majority of ceramide species restored toward healthy profiles. Principal component analysis (PCA) revealed a clear shift of post-treatment samples toward the healthy cluster, indicating molecular recovery. Nevertheless, several phospholipid and triglyceride species, particularly within the dermis and hypodermis, remained altered, suggesting incomplete metabolic normalization in deeper skin layers.
Conclusion In conclusion, guselkumab substantially restores psoriatic skin lipid composition, supporting the therapeutic normalization of epidermal lipid metabolism. Persistent lipid alterations in deeper layers may represent biomarkers of residual disease activity or potential targets for adjunctive therapy. MALDI-TOF MSI emerges as a powerful approach for monitoring molecular resolution in psoriasis treatment.

P28 – OLIVIA STEIJLEN

THE DUTCH SQUAMOUS CELL CARCINOMA AND METASTASIS (D-SQUAME) STUDY: TWO NATIONWIDE COHORTS WITH A NESTED CASE-CONTROL DESIGN FOR PROGNOSTIC MODEL DEVELOPMENT AND VALIDATION

O.F.M. Steijlen[1], B. Rentroia-Pacheco[1], A.L. Mooyaart[2], M. Wakkee[1], L.M. Hollestein[1,3]
[1]Department of Dermatology, Erasmus MC Cancer Institute, University Medical Center Rotterdam, Rotterdam, The Netherlands; [2]Department of Pathology, Erasmus University Medical Center, Rotterdam, The Netherlands; [3]Department of Research & Development, Netherlands Comprehensive Cancer Organization (IKNL), Utrecht, The Netherlands.

Background Current clinical risk stratification systems are limited in their predictive value for metastasis in cutaneous squamous cell carcinoma. Progress requires large representative datasets integrating clinical, pathological, and molecular data.
Objective To describe a nationwide study design that enables collection of two large and well-defined sets of CSCC samples with long follow-up and sufficient metastatic events to support prognostic research.
Methods Linked data of the Netherlands Cancer Registry and the Dutch Nationwide Pathology Databank were used to collect two nationwide CSCC cohorts and perform nested case–control studies. In the discovery cohort (first CSCC diagnosis 2007-2009), each metastatic case was matched to a non-metastatic control with similar metastatic risk. In the validation cohort (first CSCC diagnosis 2017-2018), each case was matched to both a random and a risk-matched control. Tissue sections were performed for Haematoxylin & Eosin staining, RNA/DNA sequencing, and spatial proteomics.
Results The discovery cohort included 19,120 CSCC patients with ten years of follow-up and 472 samples (236 case-control sets) with a median time to metastasis of 1.1 (IQR 0.5-2.1) years. The validation cohort included 25,921 CSCC patients with at least five years of follow-up and 349 samples (~175 sets with 2 types of controls). These datasets provide the basis for the development of absolute risk prognostic models that combine clinical, pathological, and molecular data, paving the way towards more personalised treatment approaches for CSCC patients.
Conclusion This design enabled large-scale CSCC sample collection with a sufficient number of events, supporting robust prognostic research.

P29 – ELISE LEEMAN

EVALUATION OF DUPILUMAB IN PEMPHIGOID GESTATIONIS WITH PLACENTAL PATHOLOGY AND LITERATURE REVIEW

Elise J. Leeman[1], Joost M. Meijer[1], Lisette M. Prens[1], Dominika Grabik[1], Silke Bouwman[1], Jelmer R. Prins[2], Sanne J. Gordijn[2], Mirthe H. Schoots[3], Maria C. Bolling[1], Gilles F.H. Diercks[1,3], Jeroen Bremer[1], Barbara Horváth[1]
[1]Department of Dermatology, University Medical Center Groningen, UMCG Center of Expertise for Blistering Diseases, European Reference Network for Rare Skin Diseases (ERN SKIN), Groningen, The Netherlands; [2]Department of Obstetrics and Gynaecology, University Medical Center Groningen, Groningen, The Netherlands; [3]Department of Pathology, University Medical Center Groningen, Groningen, The Netherlands.

Background Pemphigoid gestationis (PG) is a rare autoimmune subepidermal blistering disease of pregnancy. PG likely results from loss of maternal immune tolerance, with antibodies to placental BP180 cross-reacting with maternal cutaneous BP180, driving eosinophil-mediated inflammation and blister formation. Given its Th2-skewed pathogenesis, dupilumab has emerged as a potential therapy.
Objective To report four cases of PG refractory to corticosteroids treated with dupilumab, including placental pathology, and a literature review.

Methods Prospective case series of pregnant women with PG by IgG and/or C3 deposits along the basement membrane zone by direct immunofluorescence and identification of circulating autoantibodies on salt-split skin and by ELISA against NC16A. Dupilumab was administered as a 600 mg loading dose followed by 300 mg biweekly (one patient weekly). Outcomes included clinical response, BP180 titers, placental pathology, and a review of reported PG cases treated with dupilumab.
Results Four women with severe PG were included. Dupilumab led to rapid improvement of itch, cessation of blistering, and corticosteroid tapering (prednisolone discontinued in three; one reduced topical use). Two women delivered healthy infants; two pregnancies are ongoing. BP180 titers increased in three of four patients during treatment and declined after delivery in one of two patients. Placental pathology in one case showed chronic villitis, multifocal histiocytic intervillositis, low-grade fetal vascular malperfusion, and chorangiosis. In total, eleven PG cases treated with dupilumab during pregnancy have been reported to date.
Conclusion Dupilumab appears to be an effective corticosteroid-sparing therapy for refractory PG. Placental abnormalities, possibly reflecting maternal immune activation, warrant further study.

P30 – CLARA HARRS

SPATIALLY RESOLVED WHOLE-TRANSCRIPTOMIC PROFILING OF AGGRESSIVE CUTANEOUS SQUAMOUS CELL CARCINOMA IN EPIDERMOLYSIS BULLOSA

C. Harrs[1], B. Horváth[2], L.C.L.T. van Kempen[1,3], M.C. Bolling[2], W. Wang[2], Emőke Rácz[2#], G.F.H. Diercks[1,2#]
[1]Department of Pathology and Medical Biology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands; [2]Department of Dermatology, Center for Blistering Diseases, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands; [3]University of Maastricht, Maastricht University Medical Center+, Department of Pathology, Maastricht, The Netherlands. #Authors share joint senior authorship.

Background A serious complication in epidermolysis bullosa (EB) is the development of aggressive cutaneous squamous cell carcinoma (EB-cSCC), characterized by a high metastatic risk and poor survival. The biological behaviour of these tumours is more aggressive than conventional UV-induced cSCCs, but the underlying pathogenesis remains unclear. A permissive tumour microenvironment (TME) may play a critical role in driving the development of aggressive EB-cSCCs. Spatial transcriptomics is a novel technique enabling gene expression profiling of specific TME compartments, including immune or stromal cells. This approach may shed light on intrinsic and extrinsic TME processes contributing to EB-cSCC aggressiveness and can lead to the optimization of therapeutic interventions.
Objective Analysing spatial features of the TME in EB-cSCC to unravel the underlying pathogenesis and to identify novel biomarkers and anticancer targets.
Methods Spatial transcriptomics is being performed using the NanoString GeoMx Digital Spatial Profiler on formalin-fixed paraffin-embedded tissues of EB-cSCC (n=8) and UV-induced cSCC (n=8). The TME was segmented into tumour, immune, and stromal compartments based on staining with fluorescently labelled antibodies. These selected regions of interest were UV-illuminated to release oligonucleotide tags from RNA probes hybridized to target transcripts. These tags were collected and next-generation sequencing is currently conducted. Thereafter, data analysis will be performed, enabling spatial gene expression profiling within the defined regions to characterize and compare the TME between EB-cSCC and UV-induced cSCC.
Results/conclusions After finishing data analysis, it is estimated that preliminary results and conclusions of the spatial gene expression profiling can be presented at the NVED meeting.