chronic itch is a common symptom of a number of conditions, it remains challenging to assess and treat because of its complexity.[2] Calls to action by consensus groups have resulted in the successful development and validation of four Patient-Reported Outcomes Measurement Information System® item banks for adults,[3] but what about itch in children and young people? Little is currently known about what concepts are most important to them, how their experiences differ from those of adults, and what aspects of itch and its impact should be measured.

In this issue of the *BJD*, Fang *et al.* used an in-depth approach to understand the lived experiences of young people aged 6–17 years.[4] Using semistructured interviews with children and parents, authors found that quality, intensity, duration and triggers are key aspects of itch. Participants also reported that impact on daily life was profound, and affected clothing choices, relationships with peers and family, and sleep. This foundational understanding provides both important insight for clinicians treating children who experience itch and supports the need for measures that fully capture paediatric itch and its impacts. The authors express a commitment to developing *de novo* paediatric measures for this purpose.

By incorporating qualitative feedback from patients and their caregivers, the authors utilize a patient-centred approach to measure development, which is essential to ensure that any future survey reflects the voices and experiences of children and young people.[5] In that same vein, it is important for the authors to continue to carefully consider the demographics of their sample. As the authors point out, the current cohort in Fang *et al.* is primarily male and white. This lack of diversity may influence the ultimate content validity of any resulting measure by not fully reflecting the voices of certain groups (for example gender differences in self-reported health-related quality of life seen in adolescence).[6] Additionally, socioeconomic status was not captured, but could influence priority areas identified by children and their families (e.g. cost of trying multiple treatments).

Ultimately, the study performed by Fang *et al.* provides the initial foundation for the development of a rigorous, patient-centred outcome measure for children experiencing itch. This goal is extremely important to both clinical care and future clinical trials for these populations, as itch can be a high-priority outcome. For example, patients with eczema receiving dupilumab who developed negative side-effects, such as paradoxical head and neck erythema, were still satisfied with their treatment because of reductions in itch.[7] As work on this outcome measure develops, it will be important to continue to centre the patient's voice and pay particular attention to the generalizability of item banks across demographic groups, age cohorts and self vs. proxy measures. Furthermore, we agree with the authors that whatever is developed must integrate the work by Harmonising Outcome Measures for Eczema (http://www.homeforeczema.org) and other core outcome sets, and ultimately take into account patient burden and interpretation of scores.

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A growing family of outcome measurement proposals for hidradenitis suppurativa

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Hidradenitis suppurativa (HS) seems to originate within the hair follicle infundibulum. Occlusion is followed by

inflammation and development of the disease. For treatment, surgery is the gold standard,[1] but it is not always practical, and in randomized controlled trials (RCTs), an anti-tumour necrosis factor-α agent was promising for HS.[2] Genetics and other factors, such as smoking, microbes and adiposity, contribute to the disease phenotype, which includes boils, noduli, scars, secreting or nonsecreting fistulae ('tunnels'), and inflammation mainly of inverse areas.[3]

It is of outmost importance to monitor disease activity over time, for both the clinician and the researcher. Carefully designed outcome measurement instruments and staging systems provide functioning benchmark tools for assessment of primary and secondary outcomes of interventional trials and to guide treatment selection properly. A motley clinical picture of HS has complicated the search for uniform outcome variables, and work has been ongoing for at least two decades. The classic Hurley clinical grading system[4] has three stages: one or more abscesses with no sinus tract or cicatrization (stage I), one or more widely separated recurrent abscesses, with a tract and scarring (stage II), and the most severe cases, with multiple interconnected tracts and abscesses throughout an entire affected area (stage III). The Hurley grading system is useful for overall classification of cases and may form the basis for selection of appropriate treatment in selected anatomical regions, but it is not sufficiently dynamic in RCTs to compare treatment effects. A plethora of scores have been devised but not fully validated, and a few will be discussed here.

In this issue of the *BJD*, Goldfarb *et al.*[5] describe the Hidradenitis Area and Severity Index Revised (HASI-R), a new method inspired by the old Psoriasis Area and Severity Index. Their aim is to minimize time-consuming lesion counts, to estimate the body surface area of involved skin at predetermined anatomical regions, and to incorporate the signs of HS inflammation (erythema, thickness, drainage and tenderness). The original HASI and Severity and Area Score for Hidradenitis (SASH) instruments were merged into HASI-R with the addition of tunnel counting. SASH included inflammatory colour change, induration and the amount of open skin surface with an estimate of involved body surface area. During the rating session the outcome measurement systems mentioned in this commentary were included for comparison. According to Goldfarb *et al.* HASI-R had better interrater reliability than the other HS physical sign outcome measures. Furthermore, HASI-R had the highest intrarater reliability and good construct validity, and showed known-groups validity. The HASI-R was also the most preferred tool by the raters during the session. We all look forward to clever studies like the one from Goldfarb *et al.*, and prospective clinical trials using HASI-R in order to find its place in the growing family of outcome measurements proposed for HS.

In collaboration with Professor Gregor Jemec, all three authors of this commentary proposed a system for severity scoring, in which involved anatomical preselected regions are counted, and both inflammatory and noninflammatory lesions are classified and weighted according to type. Extra points are given for the longest distance between two lesions within each anatomical region and for regions containing Hurley stage III. The points are added to give an overall severity score.[6] Later this system was modified.[7]

The HS-Physician Global Assessment (HS-PGA) is a simple objective total count, an anchored six-point PGA based on lesion counts in predilection areas.[8] Hidradenitis Suppurativa Severity Score System (HS4) and International HS4 are two versions of a proposal for scoring developed through ambitious Delphi voting procedures involving more than 40 participants with special interest and expertise in HS, from all over the world.[9] Nodules, abscesses and draining fistulas ('tunnels') are counted and weighted according to type. Hidradenitis Suppurativa Clinical Response (HiSCR), meant for RCTs, but not allowing direct comparisons between different centres, is another approach.[2] HiSCR is a lesion count, designed retrospectively on the basis of results from a phase II clinical trial with adalimumab.

In a recent publication, nine common outcome measurement instruments showed very wide intervals for agreement even among experienced raters.[10] Much work is needed to reach consensus on how to measure the physical signs of HS. At the moment we would like to recommend the clinician to use the PGA, perhaps in combination with a visual analogue scale of the most troublesome region and the Dermatology Life Quality Index. Finally, ask the patient about the number of boils (or exacerbations) during the latest month.

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Identification of keratinocyte subpopulations in transcriptome to evaluate drug effects in atopic dermatitis

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Publicly available transcriptome data have been widely used to achieve a systems-level understanding of the complex pathogenesis of atopic dermatitis (AD).[1] The transcriptome data are interpreted not only by individual gene-level analysis to identify differentially expressed genes between two sample sets (e.g. before and after drug administration), but also by gene-set analysis (GSA)[2] to extract information on biological functions. GSA evaluates associations between the expression profiles and predefined gene sets with known biological functions using different statistical methods (e.g. gene-set enrichment analysis[3] and gene-set variation analysis[4]).

A new computational approach, Cell-type Identification By Estimating Relative Subsets Of RNA Transcripts (CIBERSORT), was developed in 2015 by Newman *et al.* to estimate the relative fractions of prechosen cell types in tissue samples using their transcriptome data.[5] CIBERSORT applies linear support vector regression to deconvolute the transcriptome data into fractions of the cell types according to a predefined matrix of gene signatures for the cell types. CIBERSORT has already been applied to understand the pathogenesis of various diseases,[6,7] including AD.[8] Those studies used the established gene signatures validated by comparison between the estimated fractions of the cell types and the fractions that were experimentally measured, for example, by flow cytometry.[5,8]

In this issue of the *BJD*, Clayton *et al.* applied CIBERSORT to evaluate the effects of dupilumab and ciclosporin on the inflammatory profiles of keratinocytes in patients with AD, using publicly available transcriptome datasets in the Gene Expression Omnibus (GEO).[9] They chose putative keratinocyte subpopulations according to their expression profiles in response to cytokine stimulation (e.g. a keratinocyte subpopulation stimulated by interleukin-22), and then defined their own gene signatures that corresponded to cutaneous cell types including the keratinocyte subpopulations. The estimated results by CIBERSORT suggested treatment-dependent modification of keratinocyte subpopulations and generated new testable hypotheses.

Clayton *et al.* demonstrate a new method to evaluate drug effects on the keratinocyte subpopulations using multiple public GEO datasets. As Newman *et al.* pointed out in their original CIBERSORT paper, the accuracy of the estimation by CIBERSORT largely depends on the quality of the predefined gene signatures.[5] The study by Clayton *et al.* may inspire the development of a novel method to measure the fraction of putative keratinocyte subpopulations to validate the proposed gene signatures. Open source, open data and open science will drive innovation by leveraging multidisciplinary approaches that can effectively improve our understanding of AD pathogenesis and drug effects.[10]

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