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Atopic dermatitis (AD) is caused by a complex interplay between immune and barrier abnormalities. Murine models of AD are essential for preclinical assessments of new treatments. While many models have been used to simulate AD, their transcriptomic profiles are not fully understood, and a comparison of these models with the human AD transcriptomic fingerprint is lacking. We sought to evaluate the transcriptomic profiles of six common murine models and determine how they relate to human AD skin. Transcriptomic profiling was performed using microarrays and qRT-PCR on biopsies from NC/Nga, flaky-tail, Flg-mutated, ovalbumin-challenged, oxazolone-challenged, and IL-23-injected mice. Gene expression data of AD, psoriasis, and contact dermatitis were obtained from previous patient cohorts. Criteria of fold-change/FCH≥2 and false discovery rate/FDR≤0.05 were used for gene arrays. IL-23-injected, NC/Nga, and oxazolone-challenged mice show the largest homology with our human meta-analysis derived AD (MADAD) transcriptome (37%, 18%, 17%, respectively). Similar to human AD, robust Th1, Th2, and also Th17 activation are seen in IL-23-injected and NC/Nga mice, with similar, but weaker, inflammation in ovalbumin-challenged mice. Oxazolone-challenged mice show a Th1-centered reaction and flaky-tail mice demonstrate a strong Th17 polarization. Flg-mutated mice display FLG down-regulation without significant inflammation. No single murine model fully captures all aspects of the AD profile; instead, each model reflects different immune or barrier disease aspects. Overall, among the six murine models, IL-23-injected mice best simulate human AD; still, the translational focus of the investigation should determine which model is most applicable. When testing new drugs for atopic dermatitis, murine models might be used to study barrier or immune features, but human trials are needed to determine effects on actual disease profile.

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