**Research Directions in Genetic Predispositions to Stevens-Johnson Syndrome/**

**Toxic Epidermal Necrolysis**

Running title: Research Directions in SJS/TEN

Teri A. Manolio, M.D., Ph.D.1, Carolyn M. Hutter, Ph.D.1, Mark Avigan M.D., C.M.2, Ricardo Cibotti Ph.D.3, Robert L. Davis, M.D., M.P.H.4, Joshua C. Denny, M.D., M.S.5, Lois La Grenade , M.D., M.P.H.2, Lisa M. Wheatley, M.D., M.P.H.6, Mary N. Carrington, Ph.D.7, Wasun Chantratita, Ph.D.8, Wen-Hung Chung, M.D., Ph.D.9, Andrea D. Dalton, J.D.10, Shuen-Iu Hung, Ph.D.11, Ming Ta Michael Lee, Ph.D.12, J. Steven Leeder, Pharm.D., Ph.D.13, Juan J. L. Lertora, M.D., Ph.D.14, Surakameth Mahasirimongkol, M.D., Ph.D.15, Howard L. McLeod, Pharm.D.16, Maja Mockenhaupt, M.D., Ph.D.17, Michael Pacanowski, Pharm.D., M.P.H.2, Elizabeth J. Phillips, M.D.18,19, Simone Pinheiro, Sc.D., M.Sc.2, Munir Pirmohamed M.B. Ch.B., Ph.D.20, Cynthia Sung, Ph.D.21, Wimon Suwankesawong, B.Sc., M.A.22, Lauren Trepanier , D.V.M., Ph.D.23, Santa J. Tumminia, Ph.D.24, David Veenstra, Pharm.D., Ph.D.25, Rika Yuliwulandari, M.D., Ph.D.26, Neil H. Shear, M.D.27

1 Division of Genomic Medicine, National Human Genome Research Institute, Bethesda MD

2 Center for Drug Evaluation and Research, U.S. Food and Drug Administration, Silver Spring MD

3 Division of Skin and Rheumatic Diseases, National Institute of Arthritis and Musculoskeletal and Skin Diseases, Bethesda MD

4 Center for Biomedical Informatics, University of Tennessee Health Science Center, Memphis TN

5 Departments of Biomedical Informatics and Medicine, Vanderbilt University, Nashville TN

6 Division of Allergy, Immunology, and Transplantation, National Institute of Allergy and Infectious Diseases, Bethesda MD

7 Cancer and Inflammation Program, Laboratory of Experimental Immunology, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research, Frederick, MD and Ragon Institute of MGH, MIT and Harvard, Cambridge, MA

8 Medical Genomic Center, Ramathibodi Hospital, Mahidol University, Bangkok, Thailand

9 Department of Dermatology, Drug Hypersensitivity Clinical and Research Center, Chang Gung Memorial Hospitals, Taipei, Linkou, and Keelung, and College of Medicine, Chang Gung University, Taoyuan, Taiwan

10 Stevens-Johnson Syndrome Foundation, Westminster CO

11 Institute and Department of Pharmacology, National Yang-Ming University, Taipei, Taiwan

12 Genomic Medicine Institute, Geisinger Health System, Danville PA

13 Division of Clinical Pharmacology, Toxicology and Therapeutic Innovation, Children’s Mercy Hospital, Kansas City MO

14 Clinical Pharmacology Program, National Institutes of Health Clinical Center, Bethesda MD

15 Medical Genetics Center, Medical Life Sciences Institute, Department of Medical Sciences, Ministry of Public Health, Nonthaburi, Thailand

16 DeBartolo Family Personalized Medicine Institute, Moffitt Cancer Center, Tampa FL

17 Dokumentationszentrum schwerer Hautreaktionen (dZh), Department of Dermatology, Medical Center and Medical Faculty - University of Freiburg, Freiburg, Germany

18 Department of Medicine, Pharmacology, Oates Institute for Experimental Therapeutics, Department of Pathology, Microbiology and Immunology, Vanderbilt University, Nashville TN

19 Institute for Immunology and Infectious Diseases, Murdoch University, Murdoch, Australia

20 Institute of Translational Medicine, University of Liverpool, Liverpool UK

21 Duke-National University of Singapore Medical School, Singapore

22 Health Product Vigilance Center, Thai Food and Drug Administration, Nonthaburi, Thailand

23 School of Veterinary Medicine, University of Wisconsin Madison, Madison WI

24 Office of the Director, National Eye Institute, Bethesda MD

25 Department of Pharmacy, University of Washington, Seattle WA

26 YARSI Research Institute, YARSI University, Jakarta, Indonesia

27 Department of Medicine (Dermatology and Clinical Pharmacology and Toxicology), University of Toronto, Toronto Canada

This paper summarizes the deliberations of a symposium convened by the National Human Genome Research Institute (NHGRI) on March 3-4, 2015 to examine gaps and priorities for future research to eliminate genetically mediated SJS/TEN globally.

Correspondence:

Teri Manolio, M.D., Ph.D.

Director, Division of Genomic Medicine

National Human Genome Research Institute

5635 Fishers Lane, Room 4113, MSC 9305

Bethesda, MD 20892-9305

Phone: 301-402-2915

E-mail: manolio@nih.gov

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**Introduction**

 Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) is one of the most devastating of adverse drug reactions (ADRs) and was, until recently, essentially unpredictable. With the discovery of several risk alleles for drug-induced SJS/TEN and the demonstration of effectiveness of screening in reducing incidence, the stage is set for implementation of preventive strategies in populations at risk. Yet much remains to be learned about this potentially fatal complication of commonly used drugs.

**Key words: Stevens-Johnson syndrome, toxic epidermal necrolysis, severe cutaneous adverse reactions, medical genomics, implementation, prevention, pharmacogenomics, precision medicine, HLA, MHC, T-cell receptor, peptide, idiosyncratic drug toxicity**

**Background**

Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) is a rare but devastating skin reaction to a number of commonly used drugs. Occurring in roughly one per million of the general population in Europe and the U.S., and 2-4 times that in Asia [1], risk is up to 1,000 times greater in patients with AIDS [2]. The great majority (>80%) of cases is believed to be genetically mediated in response to specific drugs. In 2004, Chung and colleagues identified *HLA-B\*15:02* as a potent risk factor, associated with greater than 100-fold increased risk among users of carbamazepine [3]. This variant has a high frequency in Han Chinese and other Southeast Asian ancestry groups but is uncommon outside that region [Figure]. Following the initial discovery of the *HLA-B\*15:02* association, several other risk variants have been identified in relation to carbamazepine and other drugs [Supplementary Table 1], and efforts to screen and prevent the condition have been shown to be effective in regions with high disease incidence, high negative predictive value (approaching 100%), and high risk allele frequencies [1].

The epidemiology and clinical features of SJS/TEN have been described extensively and the reader is referred to recent excellent reviews [2,4]. Much less is understood, however, about the pathogenesis, variability, modulating factors, or penetrance of risk alleles for SJS/TEN. Research efforts are limited and isolated, particularly in the U.S. where the condition is perceived to be extremely rare, though some recent estimates are 1-2 orders of magnitude higher than the one per million quoted above [5].

To explore needs for further research into the epidemiology, pathogenesis, treatment, and prevention of SJS/TEN, the National Human Genome Research Institute (NHGRI) and several other Institutes and Centers of the National Institutes of Health (see Acknowledgments) in collaboration with the U.S. Food and Drug Administration (FDA) convened 30 international experts to examine the role of genomics in the etiology, treatment, and eradication of preventable cases and to identify gaps, unmet needs, and priorities for future research with the ultimate aim of eliminating genetically mediated drug-induced SJS/TEN globally.

**Role of Genomics in Etiology and Prevention**

 Considerable progress has been made in the 13 years since the first causative allele for SJS/TEN was identified [3], including recognition of additional drug-specific risk alleles [1], improved diagnostic criteria [4], and implementation of effective screening programs in high-risk populations [1]. Understanding of the immunopathogenesis is continuing to evolve and has recently been reviewed [1,2,6]. In addition, continued advances in next-generation sequencing and related technologies have greatly expanded the precision and speed with which genetic variants associated with drug response can now be identified [7].

 One of the most promising recent advances in the genomics of SJS/TEN, a condition that was previously believed to be entirely idiosyncratic and unpredictable [1,6], has been the translation of genetic associations into effective screening and prevention strategies. Groups in several countries including Singapore, Taiwan, and Thailand have demonstrated the effectiveness of genetic screening for *HLA-B* risk alleles in reducing the incidence of SJS/TEN [1,6], similar to the effective use of *HLA-B\*57:01* screening to prevent abacavir hypersensitivity.

**Research Gaps and Needs**

 Advances in understanding of basic pathogenesis, risk variant identification, clinical implementation, and pharmacosurveillance have brought risk prediction and prevention of SJS/TEN into the realm of possibility, at least for some causative drugs, but many barriers remain. Chief among these are the rarity of the condition, the suddenness of onset, and the rapidity of progression. While several national and international consortia have been established [8-9], none is sufficiently large or ancestrally diverse to permit identification of risk alleles of modest effect or minor allele frequencies much below 5%.

 High priority research needed to address these challenges can be grouped into overarching and facilitative research as well as basic, clinical, and pharmacovigilance/epidemiologic research (Table 1). Many of the research priorities listed there (in rough priority order) could be facilitated through an expanded international collaboration or global registry of ancestrally diverse and well-phenotyped patients using standardized protocols. Biospecimen collection should include appropriately processed and cryopreserved peripheral blood mononuclear cells (PBMCs) and blister fluid collected early in the course, before massive de-epithelialization has occurred, for analysis of drug-specific CD8+ T cell responses. While blister fluid collection is challenging given that SJS/TEN develops suddenly and its differential diagnosis is difficult in early stages, heightened awareness and increased diagnostic suspicion could enable aspiration of intact bullae to help in characterizing the immunopathogenic cascade [2]. Needed infrastructure would include specialized centers to receive, process, and characterize samples and standard consent forms to facilitate sharing of data and samples across national borders. Public-private funding models sharing responsibility with the pharmaceutical industry, similar to those developed in Japan and Taiwan, are the most sustainable. They are also firmly in industry’s interests as SJS/TEN leads not only to disability and death of patients but the “death” or withdrawal of promising new therapeutic agents [6].

Key gaps in basic knowledge that can be translated to early diagnostic and prognostic markers and effective therapeutics include the cellular processes leading to the development of drug neoantigens, the co-factors that drive immunogenicity, and the lack of reliable and effective *in vitro* drug challenge tests. SJS/TEN patients, particularly those being treated for infections such as HIV/AIDS or tuberculosis, are often started on multiple drugs at once making determination of the causative agent much more difficult. At present identification of the culprit drug in such cases is often a hit-or-miss affair, requiring cessation of all drugs and gingerly adding them back in hopes the causative agent will declare itself before too much additional damage is done. An *in vitro/ex vivo* test with high specificity and sensitivity that could quickly determine the specific causative drug would be an enormous advance.

The international network described above could address a variety of needs in clinical research and care, including development of an affordable pharmacogenomic assay, piloting pre-emptive testing to assess impact, and incorporating genotypic information and decision support directly into the medical record and medication prescribing and dispensing systems. The network could also facilitate genome-wide association studies of other implicated drugs, such as oxicam-type non-steroidal anti-inflammatory agents, sulfonamide antimicrobials, and lamotrigine, for which robust genomic risk factors have yet to be characterized.

 The epidemiology and burden of SJS/TEN is unknown in many populations, particularly ethnic subgroups in the U.S. and African ancestry and non-European indigenous populations worldwide. Studies in Asian-Americans and Asians immigrating to other environments in other parts of the world would seem particularly important. Studies in implementation and cost-effectiveness should expand beyond one-gene-one-drug risk assessments as the cost of genome-wide assessment declines, in the expectation that multi-gene tests or genome sequencing will soon be more favorable economically.

 Despite the development of new pharmacovigilance methods such as NEISS-CADES [https://www.healthypeople.gov/2020/data-source/national-electronic-injury-surveillance-system-cooperative-adverse-drug-event] and Sentinel [https://www.fda.gov/safety/fdassentinelinitiative/ucm2007250.htm], extraordinary gaps remain in basic epidemiologic data on SJS/TEN in the U.S. Addressing these gaps will require adopting uniform methods for effective identification and assessment of potential cases, particularly through electronic medical records. Existing large databases and integrated medical systems should be queried using standardized data collection processes for reliable case identification and validation. Similar efforts should also be undertaken using databases in other countries. Immediate needs include improved collection of race/ethnic data in databases (including key nation- or region-specific subgroups); adoption of standardized case definitions and e-algorithms; and a minimum set of clinical, diagnostic, and drug exposure criteria for use in retrospective studies. Methods to identify potential retrospective cases against gold standard case definitions should be developed, recognizing the potential for inaccurate classification when clinical data may be incomplete.

 Follow-up of SJS/TEN survivors would enable study of outcomes and their predictors. Improved clinician education and awareness of SJS/TEN and engaging patients and their families in specialized research early in their course will help promote early detection, appropriate treatment, and further knowledge and evidence generation.

 Whether a common research approach will be generalizable across all implicated drugs is currently unknown, but course and outcome in clinically recognized SJS/TEN are so similar that at present a common framework seems to be the most reasonable. Highest priority drugs for risk identification and prevention would be those in widest use, such as allopurinol, co-trimoxazole, and non-steroidal anti-inflammatory agents, or drugs with risk alleles of known high population frequency.

**CONCLUSION**

 The identification of major risk alleles for SJS/TEN and the implementation of effective screening and prevention strategies, particularly in Southeast Asia, have provided a compelling example of the power of personalized medical care to improve drug safety. The relatively localized nature of these successes to date, however, impels us to find and apply effective approaches in other population groups, for which we must identify additional risk predictors and develop needed infrastructure for implementation. Extension of such approaches to other genetically mediated severe adverse reactions such as drug-induced liver and kidney injury should be explored.

Such efforts are within our grasp, particularly as genomic technology and medical informatics improve in economy and efficiency, making feasible widespread screening and effective interdiction of culprit drugs in susceptible individuals, even prior to drug approval and release. As these are in essence iatrogenic events, however unintentional, we as physicians and health care providers must take responsibility for them. It is our obligation, and now our great good fortune, to seize the opportunities for clinical translation and prevention presented by the new discoveries and future prospects described briefly here. Such efforts could serve as a paradigm for broader ADR prevention strategies. By expanding these investigations to other population groups and causative drugs, and extending our knowledge of pathogenic mechanisms and population trends, we should aim for a real reduction in the incidence of genetically-mediated drug-induced SJS/TEN, and indeed, someday, for its global eradication.

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**Figure Legend**: Global frequency of drug-specific HLA alleles. Allele frequencies in percents are shown in red for *HLA-B\*57:01*, in blue for *HLA-B\*58:01*, and in black for *HLA-B\*15:02*.

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