Allergic rhinitis is the most common clinical presentation of allergy, affecting 400 million people worldwide, with increasing incidence in westernized countries. To elucidate the genetic architecture and understand the underlying disease mechanisms, we carried out a meta-analysis of allergic rhinitis in 59,762 cases and 152,358 controls of European ancestry and identified a total of 41 risk loci for allergic rhinitis, including 20 loci not previously associated with allergic rhinitis, which were confirmed in a replication phase of 60,720 cases and 618,527 controls. Functional annotation implicated genes involved in various immune pathways, and fine mapping of the HLA region suggested amino acid variants important for antigen binding. We further performed genome-wide association study (GWAS) analyses of allergic sensitization against inhalant allergens and nonallergic rhinitis, which suggested shared genetic mechanisms across rhinitis-related traits.

Future studies of the identified loci and genes might identify novel targets for treatment and prevention of allergic rhinitis.

General information
State: Published
Organisations: Department of Biotechnology and Biomedicine, Disease Systems Immunology, Department of Bio and Health Informatics, Immunoinformatics and Machine Learning, Imperial College London, University of Greifswald, Icahn School of Medicine at Mount Sinai (ISMMS), University of California at San Francisco, University of Southern California, Erasmus University Rotterdam, University of Melbourne, University of Liege, Telethon Kids Institute, University of Oulu, University Children’s Hospital Regensburg (KUNO), National Institute for Health and Welfare, Ludwig Maximilian University of Munich, University of Copenhagen, Helmholtz Zentrum Muenchen German Research Center for Environmental Health, University of Manchester, 23andMe Inc., University of Chicago, Hospital Universitario Nuestra Senora de Candelaria, Vrije Universiteit Amsterdam, Barcelona Institute for Global Health Foundation (ISGlobal), Kiel University, University of Arizona, Polytechnic University of Catalunya, University of Basel, University of Bristol, Henry Ford Health System, deCODE Genetics, University of Helsinki
Number of pages: 9
Pages: 1072-1080
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Nature Genetics
Volume: 50
Issue number: 8
ISSN (Print): 1061-4036
Ratings:
BFI (2019): BFI-level 3
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Impact factor 27.125
BFI (2016): BFI-level 2
Web of Science (2016): Impact factor 27.959
Scopus rating (2017): CiteScore 21.12 SJR 22.243 SNIP 5.867
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 20.83 SJR 21.979 SNIP 6.709
Web of Science (2016): Indexed yes
Web of Science (2015): Impact factor 31.616
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 22.76 SJR 23.98 SNIP 6.332