SUPPLEMENTARY MATERIAL FOR

Genetic Associations of Psoriasis in a Pakistani Population

P.A. Shaiq[1], P.E. Stuart[2], A. Latif [3], C. Schmotzer[3], A. H. Kazmi[4], M. S. Khan[5], M. Azam[6], T. Tejasvi[2], J.J. Voorhees[2], G.K. Raja[1], J.T. Elder[2,7], R. Qamar[5,6], R.P. Nair[2]

[1]PMAS-Arid Agriculture University Rawalpindi, Rawalpindi, Pakistan
[2]Department of Dermatology, University of Michigan, Ann Arbor, MI, U.S.A.
[3]Rawalpindi Leprosy Hospital, Rawalpindi, Pakistan
[4]Mayo Hospital, Lahore, Pakistan
[5]Shifa College of Medicine, Shifa Tameer-e-Millat University, Islamabad, Pakistan
[6]COMSATS Institute of Information Technology, Islamabad, Pakistan
[7]Ann Arbor Veterans Affairs Hospital, Ann Arbor, MI, U.S.A.

Table S1. Clinical characteristics of the Pakistani psoriasis cases

Variable (unit)	sample size	mean ± standard error
male (%)	351	59.0 ± 2.6
age at exam (years)	351	35.4 ± 0.8
age at onset of psoriasis (years)	349	29.6 ± 0.7
family history (%)	200	28.0 ± 3.2
psoriatic arthritis (%)	200	4.0 ± 1.4

Table S2. Comparison of risk allele frequencies in Pakistan vs. population of disease locus discovery for 30 markers in 24 known psoriasis susceptility loci.

			Frequency of risk allele[3]				
				Discovery Population			
Candidate Gene(s)	Marker[1]	Risk allele[2]	Pakistan	Europe	China	Japan	*P* value[4]
IL28RA	rs4649203	A	0.6865	0.7282	—	—	5.5E-02
IL23R/STAT2	rs2201841	G	0.5083	0.2942	—	—	3.5E-20
IL23R/STAT2	rs11209026	G	0.9789	0.9393	—	—	1.5E-05
LCE3B/LCE3B	LCE3C_LCE3B-del	del	0.6430	0.6486	—	—	7.2E-01
REL	rs702873	G	0.7528	0.8443	—	—	1.7E-06
IFIH1	rs17716942	A	0.9453	0.8443	—	—	1.1E-12
ERAP1	rs27524	A	0.4081	0.3483	—	—	9.7E-03
ERAP1	rs151823	A	0.1498	—	0.4695	—	9.0E-35
IL13/IL4	rs20541	G	0.6934	0.7744	—	—	1.3E-04
TNIP1	rs17728338	A	0.1091	0.0699	—	—	4.3E-03
IL12B	rs2082412	G	0.6865	0.7770	—	—	1.7E-05
IL12B	rs3212227	A	0.6845	0.2203	—	—	6.6E-06
IL12B	rs4379175	C	0.6888	0.6570	—	—	1.6E-01
PTTG1	rs2431697	C	0.4505	0.4195	—	—	2.0E-01
HLA-C	7 SNPs	HLA-Cw6	0.1260	0.0898	—	—	5.2E-04
HLA-C	rs1131151	HLA-Cw1	0.0290	—	—	0.1348	6.1E-08
TRAF3IP2	rs33980500	T	0.0689	0.0897	—	—	1.1E-01
TNFAIP3	rs610604	G	0.3241	0.3259	—	—	9.6E-01
DEFB4/DEFB103	HSPD21	+cn	4.3322	4.5058	—	—	5.5E-02
CSMD1	rs7007032	C	0.3906	—	0.2030	—	6.4E-12
CSMD1	rs10088247	C	0.3230	—	0.2284	—	1.6E-04

IL23A	rs2066807	C	0.9696	0.9288	—	—	7.6E-05
GJB2	rs3751385	T	0.1322	—	0.4365	—	2.0E-33
NFKBIA	rs12586317	T	0.7787	0.7084	—	—	6.9E-04
FBXL19	rs10782001	G	0.6204	0.3549	—	—	2.3E-29
NOS2	rs4795067	G	0.3870	0.3575	—	—	2.0E-01
SERPINB8	rs514315	T	0.6409	—	0.7437	—	1.7E-04
TYK2	rs12720356	A	0.9898	0.8997	—	—	7.5E-20
ZNF816A	rs11084211	G	0.5975	—	0.6523	—	6.0E-02
RNF114	rs495337	C	0.4490	0.5950	—	—	6.9E-10

[1]In addition to SNPs that are denoted by their dbSNP rsid, other markers listed include LCE3C_LCE3B-del, which is a deletion-insertion of 32.2-kb segment encompassing *LCE3C* and *LCE3B* genes; *HLA-Cw6*, which is assayed by seven SNPs in exons 2 and 3 of *HLA-C* (rs28732105, rs1050409, rs1131123, rs1131118, rs1050384, rs17839985, and rs41547419); *HLA-Cw1*, which is uniquely tagged by the A allele of SNP rs1131151 in exon 2 of *HLA-C*; and HSPD21, which is the PRT assay for the beta-defensin CNV described by Aldhous et al. (2010).

[2]Determination of risk allele based on published reports, except for rs4379175, where the positively associated allele in the large Michigan case-control cohort is designated as risk. For HSPD21, an increase in copy number (+cn) is associated with increased risk of psoriasis, and mean copy numbers of the B-defensin CNV are shown instead of allele frequencies (mean computed after fitting of bias-corrected Gaussian mixed model to the distribution of raw copy number estimates).

[3] Risk allele frequencies in Pakistan were estimated from the 545 unaffected Pakistan controls in this study. For the populations where association of the marker with psoriasis was first discovered, estimates of risk allele frequency were estimated primarily from samples in phase 1 (version 3) of the 1000 Genomes project, namely 379 European (GBR, FIN, IBS, TSI), 197 Han Chinese (CHB, CHS), and 89 Japanese (JPT) samples. Risk allele frequencies of the LCE3C_LCE3B-del indel and HLA-Cw6, as well as copy number for the HSPD21 marker, were estimated from the 2,505 unaffected Michigan controls used in this study, which are all of European ancestry.

[4]For all markers except the HSPD21 CNV, the nominal p-value is shown from a Fisher's exact test of the difference in risk allele frequency between Pakistanis and the discovery population. For HSPD21, the nominal p-value for a randomization version of a two sample t-test with pooled variance for the difference in mean copy number is shown. P-values are color coded: black font indicates a corresponding false discovery rate (FDR) > 0.05, cyan font indicates a corresponding FDR ≤ 0.05 and an absolute difference in allele frequency < 0.10, green font indicates a corresponding FDR ≤ 0.05 and an absolute difference in allele frequency of 0.10–0.20, and red font indicates an FDR ≤ 0.05 and an absolute difference in allele frequency > 0.20.