**A Genome-Wide Association Study implicates *NR2F2* in Lymphangioleiomyomatosis Pathogenesis**

Wonji Kim1\*, Krinio Giannikou2\*, Sungho Won1,3,4\*, John R. Dreier2, Sanghun Lee5, Magdalena E. Tyburczy2, Edwin K. Silverman2,6, Elżbieta Radzikowska7, Shulin Wu8, Chin-Lee Wu8 , Elizabeth P. Henske2, Gary Hunninghake2, Havi Carel9, Antonio Roman10, Miquel Angel Pujana11, Joel Moss12, David J. Kwiatkowski2

1Interdisciplinary Program of Bioinformatics, Seoul National University, Seoul, Korea

2Division of Pulmonary and Critical Care Medicine and of Genetics, Brigham and Women’s Hospital and Harvard Medical School, Boston, 02115, Massachusetts, United States of America

3Department of Public Health Sciences, Seoul National University, Seoul, Korea

4Institute of Health and Environment, Seoul National University, Seoul, Korea

5Department of Medical Consilience, Graduate School, Dankook University, Seoul, Korea

6Channing Division of Network Medicine, Department of Medicine, Brigham and Women’s Hospital and Harvard Medical School, Boston, MA, 02115, USA

7National Tuberculosis and Lung Diseases Research Institute, Warsaw, Poland

8Urology Research Laboratory, Massachusetts General Hospital, Boston, MA, 02114, USA

9Department of Philosophy, University of Bristol, UK

10Vall d'Hebron University Hospital, CIBERES, Barcelona, Spain

11 ProCURE, Catalan Institute of Oncology, Oncobell, Bellvitge Institute of Biomedical Research (IDIBELL), Barcelona, Spain

12 Cardiovascular and Pulmonary Branch, National Heart Lung and Blood Institute, National Institutes of Health, Bethesda, MD

Corresponding author:

David J. Kwiatkowski

20 Shattuck Street, Division of Pulmonary Medicine, Brigham and Women’s Hospital, Boston, MA 02115

[dk@rics.bwh.harvard.edu](mailto:dk@rics.bwh.harvard.edu)

phone: 8573070781 fax: 6173942769

\*equal contribution

Author contributions:

Contributions to the conception and design of the work: SW, EKS, GH, DJK

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Short running head: LAM GWAS implicates *NR2F2*

**ABSTRACT**

**Rationale:** Lymphangioleiomyomatosis is a rare aggressive low-grade neoplasm which affects almost exclusively women and causes cystic lung destruction. Lymphangioleiomyomatosis can either be associated with Tuberous Sclerosis Complex or be sporadic. Risk factors for development of sporadic Lymphangioleiomyomatosis (S-Lymphangioleiomyomatosis) are unknown.

**Objectives:** We hypothesized that DNA sequence variants outside of *TSC2*/*TSC1* might be associated with susceptibility/risk for Lymphangioleiomyomatosis, and performed an S-Lymphangioleiomyomatosis Genome Wide Association Study.

**Methods:** Saliva DNA samples from 479 S-Lymphangioleiomyomatosis subjects were genotyped on the Infinium OmniExpress-24 v1.2 BeadChip, and compared with genotype data for 1,261 COPDGene controls. Standard quality controls were employed, and both standard and conditional logistic regression for matched cases and controls was done. A replication study was performed. RNA-seq and immunohistochemistry analyses were also performed.

**Measurements and Main Results:** Two non-coding SNPs met genome-wide significance; rs4544201 (minor allele frequency (MAF) 0.166 in cases vs. 0.275 in controls, P-value=8.51×10 -10) and rs2006950 (MAF 0.142 in cases vs. 0.253 in controls, P-value=3.92×10 -10), which are in the same 35kb linkage disequilibrium block. This association was replicated in an independent cohort. *NR2F2,* a nuclear receptor and transcription factor, was the only nearby protein-coding gene. *NR2F2* expression was higher by RNA-seq analysis in kidney angiomyolipoma, a Lymphangioleiomyomatosis-related tumor, than any cancer type available, and immunohistochemistry showed strong nuclear expression in both Lymphangioleiomyomatosis and angiomyolipoma.

**Conclusions:** SNPs on chr15q26.2 are associated with S-Lymphangioleiomyomatosis, and chromatin and expression data suggest that this association may occur through effects on *NR2F2* expression, which potentially plays an important role in S-Lymphangioleiomyomatosis development.

Abstract word count is 249.

**KEYWORDS**

TSC2*,* GWAS, S-LAM, LAM, NR2F2

**INTRODUCTION**

Lymphangioleiomyomatosis (LAM) is a rare aggressive low-grade neoplasm which affects almost exclusively women at reproductive age or older and causes progressive cystic lung destruction leading to fatal respiratory failure in subjects with severe disease [1-6]. LAM is characterized by an abnormal proliferation of smooth muscle-like and epithelioid cells in innumerable tiny clusters in the lungs, in association with thin-walled cysts and lung parenchymal destruction [7, 8]. Progressive cyst enlargement and inflammation contribute to decline in lung function measured as both decreased FEV1 and DLCO. The diagnosis of LAM is based on clinical features, chest computed tomography findings of thin-walled cysts, and either pathology seen on lung biopsy or elevated serum vascular endothelial growth factor D (VEGF-D) levels.

LAM occurs at high frequency (> 40%) in women with Tuberous Sclerosis Complex (TSC); and at much lower frequency in women (about 1 in 100,000) without that disorder, in which it is called sporadic (S-LAM). TSC is due to germline or mosaic mutations in either *TSC1* (25%) or *TSC2* (75%) [9]. Tumor development in TSC follows the classic Knudson model of a germline mutation complemented by a somatic second hit mutation in the other corresponding allele in tumors [9, 10]. Limited data are available for S-LAM, but it appears that *TSC2* mutations are seen in the vast majority of S-LAM lesions. About 50% S-LAM subjects have kidney angiomyolipoma, a tumor which is very common in TSC. Angiomyolipoma share histologic, expression, and genetic features with LAM, though are not identical pathologic lesions.

Treatment options for women with LAM include rapamycin and related drugs (rapalogs), which have been shown to provide significant benefit in stabilizing lung function. Lung transplant is also an option for patients with severe and progressive disease [11-13]. Although rapalog therapy is beneficial, prolonged treatment is necessary, since cessation of therapy leads to recurrence of progressive respiratory functional decline [11-14].

Genome-wide association studies (GWAS) are utilized to identify genetic variants and susceptibility loci associated with human complex traits and common disease. Although there is no precedent for genetic influence on the development of S-LAM, we hypothesized that DNA sequence variants outside of *TSC2*/*TSC1* might be associated with disease risk, and go unrecognized due to the low frequency of this disorder.

**METHODS**

**Discovery cohort**

Over 600 female S-LAM patients were identified and collected through international solicitation. S-LAM was diagnosed using standard diagnostic criteria [1-3, 7-8] by their treating physicians. Subjects were recruited from 2010 to 2014 from 14 countries: Australia, Canada, Colombia, France, Germany, Israel, Italy, Panama, Poland, Puerto Rico, Scotland, Spain, United Kingdom, and the USA (Supplemental Table 1). Genomic DNA was extracted from saliva using the QIAamp DNA mini kit (Qiagen), and 479 S-LAM DNA samples were genotyped with the Infinium OmniExpress-24 v1.2 BeadChip, which assesses 716,503 SNPs across the entire genome at the Harvard Cancer Center Highthroughput Genotyping Core, Harvard T.H Chan School of Public Health. The S-LAM patient cohort consisted of 445 females of European ancenstry and 34 non-white females, and non-white females were excluded from our analyses.

Genotype data from the same genotyping chip were available for 1261 healthy female volunteers from the COPDGene Consortium, and were obtained from dbGaP (phs000951.v2.p2.c1). These COPDGene participants had smoked at least 10 pack years and were 45 to 80 years old, and were without known COPD [13, 15].

**Quality control analyses of SNP genotype data**

We evaluated the quality of SNPs and subjects in the discovery data set using standard methods, the PLINK [16] and ONETOOL [17] which are the analysis toolsets for genetic data. We excluded all SNPs for which: the Hardy-Weinberg equilibrium test [18] gave P < 1×10-5; minor allele frequency (MAF) was < 0.05; or genotype call rates were less than 95%. We also discarded any subjects whose missing genotype rates were > 5%, or showed identity-by-state > 80% with any other subject. These filtering procedures were first applied separately to cases and controls, and then cases and controls were pooled/merged, and this procedure was repeated on the pooled dataset. In addition, any SNP showing a difference in missing data rate between cases and controls by Fisher’s exact test [19], with P < 1×10-5 was removed. Last, EIGENSTRAT [20] was applied to the pooled data and principal component (PC) scores were calculated. PC scores were used to detect subjects with an outlying genetic background, and outliers were then removed. These filters led to retention of 426 S-LAM cases and 852 female controls for analysis in the discovery phase with 549,599 SNP genotypes (Figure 1).

**Replication data**

Replication analysis was done on an additional independent set of 196 non-Hispanic white (NHW) female S-LAM subjects, for the two SNPs identified in the discovery study. All S-LAM subjects for replication data were NHWs from USA (supplementary Table 1). Genotyping was performed by TaqMan SNP genotyping assays C\_832391\_10 and C\_27296040\_10 for SNPs rs2006950 and rs4544201, respectively (ThermoFisher Scientific). Nine randomly selected S-LAM subjects from the discovery study were also genotyped by this method to confirm the accuracy of genotyping in the replication analysis. Their discovery study genotypes matched the TaqMan analysis genotypes perfectly. Those 9 subjects were not included in the replication analyses. 409 NHW healty females in COPDGene Consortium who were not used for discovery analyses were used as controls for the replication study.

**Statistical analyses with genetic data**

GWAS analyses with discovery data were conducted using conditional logistic regression (CLR).

PC scores were estimated with EIGENSTRAT [20], and used to adjust population substructure. CLR requires matching of cases and controls, and matching quality is affected by the number of PC scores matching. Each case was matched with two controls, and matching was conducted with *Matching* R package [21]. Supplementary Figure 1 shows that matching with age and two PC scores corresponding to the 2 greatest eigenvalues provide the variance inflation factor closest to 1. Thus CLR was conducted with cases and controls matched with age and 2 PC scores.

CLR analyses were performed using conditional logistic regression in the R package *survival* [22]{Team, 2016 #31;Therneau, 2017 #94}, respectively. Genome-wide significance was assessed by P-value < 5×10-8 between cases and controls.

We also conducted gene-based analyses to identify genes with significant association with S-LAM using the optimal sequence kernel association test (SKAT-O) [23]. SNPs within each gene were used to provide a SNP set file, and age, squared age and 10 PC scores were included as covariates.

**Genotype imputation and statistical analyses with imputed genotypes**

We imputed untyped SNPs located within 1 mega-base of the two genome-wide significant SNPs on chromosome 15 to do fine-mapping. Imputation was conducted using the Sanger Imputation Service (<https://imputation.sanger.ac.uk>). We used Haplotype Reference Consortium release v1.1 and considered predominantly European ancestry [24] which consists of 64,940 haplotypes as reference panel. Pre-phasing and imputation was conducted with SHAPEIT [25] and the PBWT package [26], respectively, and imputation accuracy was evaluated with the INFO metric [27]. Imputed SNPs were filtered out if INFOs, MAFs or P-values for the Hardy-Weinberg equilibrium test were < 0.3, 0.05, or 1×10-5, respectively. Linkage disequilibrium (LD) blocks were chosen by using Haploview with default options [28] and we applied CLR to all SNPs in the LD block with the genome-wide significant SNPs from the initial genotyping. Furthermore, we applied Probabilistic Identification of Causal SNPs (PICS) software to imputed and genotyped SNPs within the 34kb LD block containing the genome-wide significant SNPs and calculated PICS probability for each SNP. PICS assumes that there is a single causal SNP, and calculates the probability of each individual SNP being the causal SNP [29].

**Topologically associated domains (TADs) and chromatin interactions**

To identify chromatin interactions in the region of interest on chromosome 15q26.2, we used a publicly available web-based query tool, 3D genome browser ([www.3dgenome.org](http://www.3dgenome.org)). 3D genome browser predicts TADs using 86 published high-throughput chromosome conformation capture data sets with a pipeline provided by Dixon *et al* [30]. We checked for TADs around the genome-wide significant SNPs and protein coding genes belonging to each TAD were investigated. We analyzed TADs from four cell lines/tissues judged closest to LAM: (i) human fetal lung fibroblast (IMR90), (ii) lung-related tissues (LUNG), (iii) H1 derived mesenchymal stem cells (H1-MSC), and (iv) Human Umbilical Vein Endothelial Cells (HUVEC).

**Statistical analyses with RNA sequencing data**

Whole transcriptome RNA-Seq analysis was performed on one abdominal LAM tumor and four kidney angiomyoliopomas at the Broad Institute of Harvard and MIT. Briefly, mRNA-Seq was performed using polyA cDNA capture followed by cDNA library synthesis (Illumina Truseq RNA Library Prep Kit), and sequencing on Illumina machines, following the same methods and in the same facility in which the GTEx RNA-seq project occurred [31]. Read data was processed into FASTQ files with standard QC methods, and aligned to the genome (hg19, NCBI37) using Tophat v2.0.10 [31]. R package *DESeq2* [32] yielded RPKM. Fastq files were also converted into RSEM format by David Marron and Joel Parker (UNC) [33]. RSEM values were compared to RNA-seq data from 2463 tumors of 27 different histologic types from the TCGA [34]. RPKM values for *NR2F2* were compared to the GTEx data set of normal human tissues (~7,000 samples from 53 normal tissue types, v6p release) [35].

**Immunohistochemistry analyses**

Immunochistochemistry was performed as described elsewhere [36] using a primary mouse monoclonal antibody against *NR2F2* [Abcam Cat.Num # ab41859 Concentration 1:100 (10ug/ml) ]. Briefly, 5 µm sections of formalin-fixed, paraffin-embedded tumor specimens were deparaffinized in xylene, rehydrated with graded concentrations of alcohol to distilled water, washed with Tris-buffered saline with 0.1% Tween 20 (TBST), and antigen retrieval was performed in EDTA (pH 8.0, Diagnostic BioSystems) using a pressure cooker. Endogenous peroxidase activity was blocked with 3% H2O2, blocking was done with 5% goat serum for 30 minutes, followed by incubation overnight with antibody at 4°C, washing three times in TBST, incubation with anti-goat secondary antibody (Vector Labs, Burlingame, CA) at a dilution of 1:300. The peroxidase reaction was developed using DakoCytomation Liquid DAB plus Substrate Chromogen System (DakoCytomation). Both LAM lung samples and kidney angiomyolipomas were stained by similar methods.

**RESULTS**

**GWAS analysis of S-LAM identifies two intergenic SNPs on chromosome 15**

After multiple filtration steps and elimination of SNPs and samples as described in the methods, GWAS was performed on 426 S-LAM subjects and 852 control subjects for 549,599 SNPs using CLR. Two non-coding SNPs rs4544201 and rs2006950 on chromosome 15 met genome-wide significance (rs4544201: P-value=8.5110-10; rs2006950: P-value=3.9210-10).

Quantile-quantile plots for CLRs demonstrated that the distribution of observed P-values met the expected distribution (Figure 2a), with the exception of the two SNPs (Figure 2b), indicating that the analyses were free of systematic P-value inflation and likely robust. Multi-dimensional scaling plots indicates genetic similarity between cases and controls in the discovery analyses(Supplementary Figure 2). All controls in the discovery analyses are smokers, and the genome-wide association analyses can be confounded with nicotine addiction. We identified SNPs associated with nicotine addiction from GWAS catalog [37], and p-values for SNPs in our discovery analyses of which correlations are larger than 0.8 were provided in supplementary Table 3. None of them were significant at the 0.05 significance level, which indicates that our analyses are not confounded with smoking status. Manhattan plots of the genome demonstrated that only the two SNPs met genome-wide significance. Table 1 provides summaries for the two genome-wide significant SNPs.

SNPs rs4544201 and rs2006950 are located on 15q26.2, 11,563 nt apart, in an intergenic gene desert between *MCTP2* (1.1Mb away) and *NR2F2* (700kb away), that contains many lncRNAs (Figure 3b). Both SNPs have minor and major alleles of A and G, and showed lower MAFs in S-LAM cohort than the control population. The odds ratios (ORs) of a single minor allele in the S-LAM cohort were 0.49 and 0.47 respectively, in comparison to the control population (Table 1). ORs for genome-wide significant SNPs tend to be inflated by the Winner’s curse. To adjust for this potential effect, bias-adjusted ORs for rs4544201 and rs2006950 were calculated using br2 [38] and were still highly significant at 0.57 and 0.53, respectively.

Replication was performed for the 2 SNPs with association with LAM using 196 additional S-LAM patients and 409 NHW healthy females from COPDGene participants who were not used for discovery analyses. A similar OR for association of the minor allele of these SNPs with S-LAM was seen in the replication data (Table 1, ORrs4544201=0.33, ORrs2006950 = 0.28), confirming the results from the initial GWAS. Furthermore we compared the MAFs of the 2 SNPs in LAM patients with those in other cohort data. Supplementary Table 4 shows that MAFs of the 2 SNPs in LAM patients are significantly smaller than those in other cohort participants.

rs4544201 and rs2006950 belong to the same LD block on 15q26.2 [28], and are strongly correlated (*D*’=0.977, *r*2=0.854; Supplementary Figure 3). To examine the potential association of other SNPs in this region with S-LAM, we used the genotyped SNP data to impute genotype data for all SNPs within 1 megabase of these two SNPs. Eighteen imputed SNPs in the 34kb LD block had P-values for association with LAM similar to the two genotyped SNPs (Table 2).

To attempt to identify the causal SNP among these SNPs with low P-values, we performed PICS analysis for all SNPs in Table 2, and the original two SNPs showing association. rs41374846 had both significant association with LAM, and the largest PICS probability (PPICS=0.65, Supplementary Table 2), suggesting that it is the candidate causal SNP in this association [29].

**Association of GWAS-significant SNPs with *NR2F2***

To assess potential mechanisms by which these SNP alleles are associated with LAM development, several analyses were performed.

First, we considered the chromatin TAD which contained these SNPs. TADs are defined using high-throughput chromosome conformation capture data to identify in a global manner regions of chromatin that have physical interaction through looping. It is postulated that the majority of SNPs associated with human disease or other phenotypes cause the association through interaction with regulatory elements of a coding gene within the TAD containing the SNP [39]. To identify the TAD containing these SNPs, we used TAD information available for four tissues: IMR90 cells, a fetal lung myofibroblast cell line; lung tissue; H1-MSC, a mesenchymal stem cell line; and HUVEC, human umbilical vein endothelial cells (Supplementary Figures 4-7). In all four of these cells/tissues, *NR2F2* was the only protein-coding gene within or near the boundary of the TAD containing the GWAS SNPs. This suggests that this SNP region may influence expression of *NR2F2* as its mechanism of association with S-LAM.

To examine this possibility in further detail, we conducted gene-based analyses of association of SNPs within all three protein-coding genes in the 2 MB region of chromosome 15 surrounding the GWAS-SNPs using SKAT-O. *NR2F2* was the only one of the three genes located in this chromosomal region that showed a significant association (P-value=0.03, Table 3).

*NR2F2*, also known as COUP-transcription factor II, encodes a member of the steroid/thyroid hormone superfamily of nuclear receptors [40], and plays important roles in many developmental processes, including the human neural crest [41], which is considered a potential candidate cell of origin of LAM [42], as well as in lymphangiogenesis and in angiogenesis [43]. Hence, we considered it a potential target of regulation by one of the SNPs showing a strong association with LAM (Table 2), and performed further studies.

**Analysis of *NR2F2* in angiomyolipoma and LAM**

Using RNA-seq data, we compared the gene expression of 4 kidney angiomyolipoma and 1 abdominal LAM tumor with an extensive set of human cancers (from TCGA [34]), and normal tissues (from GTEX [35]) (Figure 4). *NR2F2* was more highly expressed in the LAM-related tumors than in any TCGA cancer (Figure 4a), and was also relatively highly expressed in LAM-related tumors in comparison to normal tissues (Figure 4b, P-value=6.38×10-6). In contrast, two other genes, *SPATA8* and *MCTP2*, that were next closest to the SNP region showing association with LAM (1.1 and 1.2Mb distant, Figure 3b) had no expression in the LAM-related tumors (data not shown).

Immunohistochemistry (IHC) analysis also demonstrated strong nuclear expression of *NR2F2* in both LAM lung and kidney angiomyolipoma sections (Figure 5).

**DISCUSSION**

LAM occurs almost exclusively in women of childbearing age. Most LAM patients presenting with symptoms are sporadic cases without TSC, and the origins of LAM in S-LAM patients are completely unknown. In the present study, we conducted a GWAS in a large cohort of LAM subjects. Two intergenic SNPs, rs4544201 and rs2006950, were identified in a 34kb LD block on chromosome 15, that met genome-wide significance for association with LAM (Table 1). Eighteen other SNPs in this 34kb region were also strongly associated with LAM as assessed by genotype imputation analysis (Table 2). The association was replicated in a validation population. Despite these findings, there were limitations to our study. Although our cohort of samples was large for a rare disease such as LAM, it was of only moderate size for GWAS. Second, to collect sufficient LAM subjects, we employed a successful worldwide recruitment strategy. However, our controls were all from the USA. Hence, we employed EIGENSTRAT to identify genetic outliers, and make our control and LAM subject sets more uniform from a genetic background perspective.

The SNPs with association to S-LAM lie in a gene desert on distal chromosome 15. The nearest protein-coding gene is *NR2F2*, 700kb away, and other nearby protein-coding genes are *MCTP2*, 1.2Mb away, and *SPATA8,* 1.1Mb away. Consideration of chromatin TADs in this region indicates that only *NR2F2* is in/on the border of the TAD region containing the SNPs showing association with S-LAM in four relevant cells/tissues, suggesting that these SNP alleles may influence *NR2F2* expression as the potential mechanism of their association with S-LAM development. Furthermore *NR2F2* is highly expressed in LAM and angiomyolipoma by RNA-Seq analysis in comparison to large cancer and normal tissue data sets, and *NR2F2* shows high expression with nuclear localization in both LAM and angiomyolipoma by IHC. Although we did not identify an eQTL relationship for any of the 20 SNPs associated with S-LAM for any gene in any normal tissue or cancer type [35], it is possible that such an eQTL relationship exists for LAM cells. We also note that the region of these SNPs also contains several non-coding long RNAs, some antisense transcripts, and microRNA miR1469 (Figure 4a). It is possible that expression of one or more of these noncoding genes are affected by these SNP alleles, and have a role in LAM development.

*NR2F2* is an orphan nuclear receptor known to play important roles in both normal tissue development and in tumorigenesis [44], making it a promising candidate driver gene in LAM pathogenesis. LAM occurs nearly exclusively in women, and estrogen levels influence LAM development and progression [45, 46]. siRNA knockdown of ERα (Estrogen Receptor) in MCF-7 breast cancer cells decreased *NR2F2* expression, while treatment with estradiol increased its expression [47]. This interaction between ERα and *NR2F2* may also play a role in LAM development.

Lymphatic involvement in LAM is a hallmark pathologic feature with LAM cell clusters in the lung showing marked enrichment for lymphatic vessels [48, 49]. VEGF-D is a probable driver of lymphatic vessel growth in LAM, as serum VEGF-D levels are increased in the majority of LAM patients, and serves as a diagnostic biomarker of LAM [50]. In mice, *NR2F2* has been shown to be required, with *SOX18*, for the polarized expression of *PROX1* in a subset of endothelial cells (ECs) within the cardinal vein at embryonic day 9.5, an event that leads to development of the lymphatic endothelium [51]. Hence there is also a potential connection between *NR2F2*, VEGF-D, lymphatic development, and LAM pathogenesis.

In conclusion, our GWAS has identified non-coding SNPs on chr15q26.2 whose alleles are associated with S-LAM, that are located in a TAD containing the orphan nuclear receptor *NR2F2*, suggesting a model in which these SNP alleles may influence *NR2F2* expression and thereby LAM pathogenesis. *NR2F2* is relatively highly expressed in LAM and LAM-related tumors. *NR2F2* has not previously been associated with LAM pathogenesis, and these findings will hopefully lead to further analysis of its role in LAM, leading to better insight into this often progressive and lethal lung disorder.

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**Data and Code Availability**

The primary GWAS and replication data will be made available on publication of this work through dbGaP.

**REFERENCES**

1. Kitaichi M, Nishimura K, Itoh H, Izumi T. Pulmonary lymphangioleiomyomatosis: a report of 46 patients including a clinicopathologic study of prognostic factors. *American journal of respiratory and critical care medicine* 1995: 151(2): 527-533.

2. Chu SC, Horiba K, Usuki J, Avila NA, Chen CC, Travis WD, Ferrans VJ, Moss J. Comprehensive evaluation of 35 patients with lymphangioleiomyomatosis. *CHEST Journal* 1999: 115(4): 1041-1052.

3. Urban T, Lazor R, Lacronique J, Murris M, Labrune S, Valeyre D, Cordier J-F. Pulmonary lymphangioleiomyomatosis: a study of 69 patients. *MEDICINE-BALTIMORE-* 1999: 78: 321-337.

4. Cunha B, Conceição DM, Cabo C, Jesus N, Santos L, de Carvalho A. Pulmonary Lymphangioleiomyomatosis on a Post-Menopausal Woman with Chronic Lymphocytic Leukaemia. *Case Reports in Clinical Medicine* 2016: 5(03): 101.

5. Youssef AL, Alami B, Sahnoun F, Boubbou M, Kamaoui I, Maâroufi M, Houssaini NS, Amara B, Tizniti S. Lymphangioleiomyomatosis: An unusual age of diagnosis with literature review. *International Journal of Diagnostic Imaging* 2014: 1(1): 17.

6. Soler-Ferrer C, Gómez-Lozano A, Clemente-Andrés C, De Cendra-Morera E, Custal-Teixidor M, Colomer-Pairés J. Lymphangioleiomyomatosis in a post-menopausal women. *Archivos de Bronconeumología ((English Edition))* 2010: 46(3): 148-150.

7. Taylor JR, Ryu J, Colby TV, Raffin TA. Lymphangioleiomyomatosis. *New England Journal of Medicine* 1990: 323(18): 1254-1260.

8. Kalassian KG, Doyle R, Kao P, Ruoss S, Raffin TA. Lymphangioleiomyomatosis: new insights. *American journal of respiratory and critical care medicine* 1997: 155(4): 1183-1186.

9. Giannikou K, Malinowska IA, Pugh TJ, Yan R, Tseng Y-Y, Oh C, Kim J, Tyburczy ME, Chekaluk Y, Liu Y. Whole exome sequencing identifies TSC1/TSC2 biallelic loss as the primary and sufficient driver event for renal angiomyolipoma development. *PLoS genetics* 2016: 12(8): e1006242.

10. Carsillo T, Astrinidis A, Henske EP. Mutations in the tuberous sclerosis complex gene TSC2 are a cause of sporadic pulmonary lymphangioleiomyomatosis. *Proceedings of the National Academy of Sciences* 2000: 97(11): 6085-6090.

11. Harari S, Elia D, Torre O, Bulgheroni E, Provasi E, Moss J. Sirolimus therapy for patients with lymphangioleiomyomatosis leads to loss of chylous ascites and circulating LAM cells. *Chest* 2016: 150(2): e29-e32.

12. Cai X, Pacheco-Rodriguez G, Haughey M, Samsel L, Xu S, Wu H-P, McCoy JP, Stylianou M, Darling TN, Moss J. Sirolimus decreases circulating lymphangioleiomyomatosis cells in patients with lymphangioleiomyomatosis. *Chest* 2014: 145(1): 108-112.

13. Moss J, Avila NA, Barnes PM, Litzenberger RA, Bechtle J, Brooks PG, Hedin CJ, Hunsberger S, Kristof AS. Prevalence and clinical characteristics of lymphangioleiomyomatosis (LAM) in patients with tuberous sclerosis complex. *American journal of respiratory and critical care medicine* 2001: 164(4): 669-671.

14. Black J, Ge Q, Boustany S, Johnson P, Poniris M, Glanville A, Oliver B, Moir L, Burgess J. In vitro studies of lymphangioleiomyomatosis. *European Respiratory Journal* 2005: 26(4): 569-576.

15. Regan EA, Hokanson JE, Murphy JR, Make B, Lynch DA, Beaty TH, Curran-Everett D, Silverman EK, Crapo JD. Genetic epidemiology of COPD (COPDGene) study design. *COPD: Journal of Chronic Obstructive Pulmonary Disease* 2011: 7(1): 32-43.

16. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, De Bakker PI, Daly MJ. PLINK: a tool set for whole-genome association and population-based linkage analyses. *The American Journal of Human Genetics* 2007: 81(3): 559-575.

17. Song YE, Lee S, Park K, Elston RC, Yang H-J, Won S. ONETOOL for the analysis of family-based big data. *Bioinformatics* 2018: 1: 3.

18. Wigginton JE, Cutler DJ, Abecasis GR. A note on exact tests of Hardy-Weinberg equilibrium. *The American Journal of Human Genetics* 2005: 76(5): 887-893.

19. Raymond M, Rousset F. An exact test for population differentiation. *Evolution* 1995: 49(6): 1280-1283.

20. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. *Nature genetics* 2006: 38(8): 904.

21. Sekhon JS. Multivariate and propensity score matching software with automated balance optimization: the matching package for R. 2011.

22. Therneau TM, Lumley T. Package ‘survival’. *R package version* 2017: 2.41-43.

23. Lee S, Emond MJ, Bamshad MJ, Barnes KC, Rieder MJ, Nickerson DA, Team ELP, Christiani DC, Wurfel MM, Lin X. Optimal unified approach for rare-variant association testing with application to small-sample case-control whole-exome sequencing studies. *The American Journal of Human Genetics* 2012: 91(2): 224-237.

24. Consortium HR. A reference panel of 64,976 haplotypes for genotype imputation. *Nature genetics* 2016: 48(10): 1279-1283.

25. Delaneau O, Marchini J, Consortium GP. Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature communications* 2014: 5: 3934.

26. Durbin R. Efficient haplotype matching and storage using the positional Burrows–Wheeler transform (PBWT). *Bioinformatics* 2014: 30(9): 1266-1272.

27. Marchini J, Howie B. Genotype imputation for genome-wide association studies. *Nature reviews Genetics* 2010: 11(7): 499.

28. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* 2004: 21(2): 263-265.

29. Farh KK-H, Marson A, Zhu J, Kleinewietfeld M, Housley WJ, Beik S, Shoresh N, Whitton H, Ryan RJ, Shishkin AA. Genetic and epigenetic fine mapping of causal autoimmune disease variants. *Nature* 2015: 518(7539): 337-343.

30. Dixon JR, Selvaraj S, Yue F, Kim A, Li Y, Shen Y, Hu M, Liu JS, Ren B. Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* 2012: 485(7398): 376-380.

31. Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome biology* 2013: 14(4): R36.

32. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology* 2014: 15(12): 550.

33. Li B, Dewey CN. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC bioinformatics* 2011: 12(1): 323.

34. Network CGAR. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature* 2008: 455(7216): 1061.

35. Lonsdale J, Thomas J, Salvatore M, Phillips R, Lo E, Shad S, Hasz R, Walters G, Garcia F, Young N. The genotype-tissue expression (GTEx) project. *Nature genetics* 2013: 45(6): 580-585.

36. Bongaarts A, Giannikou K, Reinten RJ, Anink JJ, Mills JD, Jansen FE, Spliet GW, den Dunnen WF, Coras R, Blümcke I. Subependymal giant cell astrocytomas in Tuberous Sclerosis Complex have consistent TSC1/TSC2 biallelic inactivation, and no BRAF mutations. *Oncotarget* 2017: 8(56): 95516.

37. MacArthur J, Bowler E, Cerezo M, Gil L, Hall P, Hastings E, Junkins H, McMahon A, Milano A, Morales J. The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). *Nucleic acids research* 2016: 45(D1): D896-D901.

38. Poirier JG, Faye LL, Dimitromanolakis A, Paterson AD, Sun L, Bull SB. Resampling to Address the Winner's Curse in Genetic Association Analysis of Time to Event. *Genetic epidemiology* 2015: 39(7): 518-528.

39. Grubert F, Zaugg JB, Kasowski M, Ursu O, Spacek DV, Martin AR, Greenside P, Srivas R, Phanstiel DH, Pekowska A. Genetic control of chromatin states in humans involves local and distal chromosomal interactions. *Cell* 2015: 162(5): 1051-1065.

40. Qiu Y, Krishnan V, Zeng Z, Gilbert DJ, Copeland NG, Gibson L, Yang-Feng T, Jenkins NA, Tsai MJ, Tsai SY. Isolation, characterization, and chromosomal localization of mouse and human COUP-TF I and II genes. *Genomics* 1995: 29(1): 240-246.

41. Rada-Iglesias A, Bajpai R, Prescott S, Brugmann SA, Swigut T, Wysocka J. Epigenomic annotation of enhancers predicts transcriptional regulators of human neural crest. *Cell stem cell* 2012: 11(5): 633-648.

42. Julian LM, Delaney SP, Wang Y, Goldberg AA, Doré C, Yockell-Lelièvre J, Tam RY, Giannikou K, McMurray F, Shoichet MS. Human Pluripotent Stem Cell–Derived TSC2-Haploinsufficient Smooth Muscle Cells Recapitulate Features of Lymphangioleiomyomatosis. *Cancer research* 2017: 77(20): 5491-5502.

43. Qin J, Chen XP, Xie X, Tsai MJ, Tsai SY. COUP-TFII regulates tumor growth and metastasis by modulating tumor angiogenesis. *P Natl Acad Sci USA* 2010: 107(8): 3687-3692.

44. Xu MF, Qin J, Tsai SY, Tsai MJ. The role of the orphan nuclear receptor COUP-TFII in tumorigenesis. *Acta Pharmacol Sin* 2015: 36(1): 32-36.

45. Juvet SC, Hwang D, Downey GP. Rare lung diseases I--Lymphangioleiomyomatosis. *Canadian respiratory journal* 2006: 13(7): 375-380.

46. McCormack FX, Gupta N, Finlay GR, Young LR, Taveira-DaSilva AM, Glasgow CG, Steagall WK, Johnson SR, Sahn SA, Ryu JH, Strange C, Seyama K, Sullivan EJ, Kotloff RM, Downey GP, Chapman JT, Han MK, D'Armiento JM, Inoue Y, Henske EP, Bissler JJ, Colby TV, Kinder BW, Wikenheiser-Brokamp KA, Brown KK, Cordier JF, Meyer C, Cottin V, Brozek JL, Smith K, Wilson KC, Moss J, Lymphangioleiomyomato AJC. Official American Thoracic Society/Japanese Respiratory Society Clinical Practice Guidelines: Lymphangioleiomyomatosis Diagnosis and Management. *American Journal of Respiratory and Critical Care Medicine* 2016: 194(6): 748-761.

47. Riggs KA, Wickramasinghe NS, Cochrum RK, Watts MB, Klinge CM. Decreased chicken ovalbumin upstream promoter transcription factor II expression in tamoxifen-resistant breast cancer cells. *Cancer Res* 2006: 66(20): 10188-10198.

48. Glasgow CG, Taveira-DaSilva AM, Darling TN, Moss J. Lymphatic involvement in lymphangioleiomyomatosis. *Ann Ny Acad Sci* 2008: 1131: 206-214.

49. Seyama K, Mitani K, Kumasaka T. Lymphangioleiomyoma Cells and Lymphatic Endothelial Cells Expression of VEGFR-3 in Lymphangioleiomyoma Cell Clusters. *Am J Pathol* 2010: 176(4): 2051-2052.

50. Young LR, Lee HS, Inoue Y, Moss J, Singer LG, Strange C, Nakata K, Barker AF, Chapman JT, Brantly ML, Stocks JM, Brown KK, Lynch JP, Goldberg HJ, Downey GP, Swigris JJ, Taveira-DaSilva AM, Krischer JP, Trapnell BC, McCormack FX, Grp MT. Serum VEGF-D concentration as a biomarker of lymphangioleiomyomatosis severity and treatment response: a prospective analysis of the Multicenter International Lymphangioleiomyomatosis Efficacy of Sirolimus (MILES) trial. *Lancet Resp Med* 2013: 1(6): 445-452.

51. Srinivasan RS, Geng X, Yang Y, Wang Y, Mukatira S, Studer M, Porto MP, Lagutin O, Oliver G. The nuclear hormone receptor Coup-TFII is required for the initiation and early maintenance of Prox1 expression in lymphatic endothelial cells. *Genes & development* 2010: 24(7): 696-707.

**Table 1. Genome-wide significant SNPs.**

|  |  |  |
| --- | --- | --- |
|  | **rs4544201** | **rs2006950** |
| ***Chromosome*** | 15q26.2 | 15q26.2 |
| ***SNP position (hg19)*** | 96167827 | 96179390 |
| ***Minor / Major alleles*** | A / G | A / G |
| ***Minor allele frequency*** | | |
| S-LAM | 0.1655 | 0.1420 |
| Control | 0.2750 | 0.2529 |
| ***Genotype counts  (AA / AG / GG / Missing)*** | | |
| S-LAM | 16 / 108 / 299 / 3 | 11 / 99 / 316 / 0 |
| Control | 62 / 343 / 444 / 3 | 58 / 315 / 479 / 0 |
| ***Discovery data*** |  |  |
| Odds ratio |  |  |
| Original | 0.4916 | 0.4732 |
| Bias adjusted | 0.5677 | 0.5315 |
| P-value | 8.5110-10 | 3.9210-10 |
| ***Replication data*** | | |
| Odds ratio | 0.3288 | 0.2731 |
| P-value | 4.32×10-5 | 1.5610-5 |

Definition of abbreviations: SNP = Single-Nucleotide Polymorphism; S-LAM = Sporadic Lymphangioleiomyomatosis;CLR = Conditional Logistic Regression.

**Table 2. Statistical analyses of imputed SNPs with CLR.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| CHR | SNP | POS | Alleles\* | MAF | INFO† | P-value for CLR‡ |
| 15 | rs41374846 | 96143559 | A/G | 0.2605 | 0.9097 | 3.43210-9 |
| 15 | rs59125351 | 96144157 | G/T | 0.2510 | 0.9771 | 3.22910-10 |
| 15 | rs17581137 | 96146414 | C/A | 0.2336 | 0.9893 | 1.38410-10 |
| 15 | rs6496126 | 96148439 | C/G | 0.2330 | 0.9890 | 1.81410-10 |
| 15 | rs2397810 | 96148765 | C/T | 0.2330 | 0.9890 | 1.81410-10 |
| 15 | rs10520790 | 96151040 | T/G | 0.2478 | 0.9958 | 3.57110-10 |
| 15 | rs55804812 | 96151256 | A/T | 0.2475 | 0.9952 | 4.17810-10 |
| 15 | rs16975389 | 96153782 | C/T | 0.2463 | 0.9967 | 5.80110-10 |
| 15 | rs16975396 | 96158705 | G/T | 0.2466 | 0.9983 | 9.59210-10 |
| 15 | rs4628911 | 96167905 | T/C | 0.2472 | 1.0000 | 5.14710-10 |
| 15 | rs6496128 | 96168303 | G/A | 0.2472 | 1.0000 | 5.14710-10 |
| 15 | rs8029996 | 96168770 | A/G | 0.2472 | 0.9998 | 5.14710-10 |
| 15 | rs4551988 | 96169589 | C/G | 0.2472 | 0.9998 | 5.14710-10 |
| 15 | rs58878263 | 96171069 | A/C | 0.2493 | 0.9979 | 6.36110-10 |
| 15 | rs8040665 | 96175692 | G/T | 0.2487 | 0.9976 | 7.35610-10 |
| 15 | 15:96175733 | 96175733 | A/G | 0.2466 | 0.9975 | 5.22410-10 |
| 15 | rs8040168 | 96176096 | G/C | 0.2466 | 0.9981 | 5.22410-10 |
| 15 | rs17504029 | 96177670 | T/A | 0.2478 | 0.9876 | 1.90010-10 |

Definition of abbreviations: CHR = Chromosome; POS = SNP Position according to NCBI genome build 37 (hg19); MAF = Minor allele frequency; CLR = Conditional Logistic Regression.

\* Minor/Major alleles are listed.

† INFO is the metric about imputation quality provided by IMPUTE2.

‡ CLR was applied to imputed SNP genotype data to identify SNPs with significant association (P < 5×10-8) with LAM.

**Table 3. Gene-based analyses of SNP association with LAM.** Three protein-coding genes were found on chromosome 15 from 94.2 Mb to 98.2 Mb, the 2 Mb region surrounding the GWAS-SNPs, and gene-based analysis for association with LAM was performed using SKAT-O.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene | CHR | Start\* | End† | Number of SNPs | P-value |
| *NR2F2* | 15 | 96869157 | 96883492 | 5 | 0.0307 |
| *MCTP2* | 15 | 94774767 | 95027181 | 4 | 0.3579 |
| *SPATA8* | 15 | 97326619 | 97328845 | 3 | 0.5250 |

Definition of abbreviations: SNP= Single-Nucleotide Polymorphism; LAM = Lymphangioleiomyomatosis; GWAS = Genome-Wide Association Study; CHR = Chromosome

\* Start position of the corresponding gene.

† End position of the corresponding gene.