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Two Genetic Effects at the IRF5/ TNPO3 Locus are Independently Associated with the Development of Specific Lupus Symptoms

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TWO GENETIC EFFECTS AT THE *IRF5/TNPO3* LOCUS ARE INDEPENDENTLY
ASSOCIATED WITH THE DEVELOPMENT OF SPECIFIC LUPUS SYMPTOMS

A Capstone Experience/Thesis Project

Presented in Partial Fulfillment of the Requirements for

the Degree Bachelor of Science with

Honors College Graduate Distinction at Western Kentucky University

By

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2014

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ABSTRACT

Systemic Lupus Erythematosus (SLE) is an autoimmune disorder that can affect every tissue in the body. Single nucleotide polymorphisms (SNPs) in the *IRF5* and *TNPO3* genes are statistically associated with the development of SLE. My research identified correlations between *IRF5/TNPO3* SNPs and specific lupus symptoms. Logistic regression analyses were conducted using 101 genetic variants in the *IRF5/TNPO3* region that were genotyped in over 6,000 lupus patients of different ethnicities, with admixture covariates applied. Three clinical phenotypes displayed significant correlation ($p < 1.6 \times 10^{-5}$) in subjects of European ancestry. For each of these phenotypes, a step-wise conditional analysis was conducted using two lupus associated single nucleotide polymorphisms (SNPs) at this genetic loci. In Europeans, lupus disease onset ($p\text{-value}_{\text{EU}} = 2.44 \times 10^{-16}$, $\text{OR} = 0.67^*$) and the presence of anti-Ro ($p\text{-value}_{\text{EU}} = 2.09 \times 10^{-7}$, $\text{OR} = 0.67$) and anti-dsDNA ($p\text{-value}_{\text{EU}} = 4.15 \times 10^{-7}$, $\text{OR} = 0.75$) antibodies were associated with SNPs in the *IRF5/TNPO3* genes. SNPs in the *IRF5* promoter and those spanning *IRF5* and *TNPO3* were both associated with disease onset. The presence of anti-Ro and anti-dsDNA antibodies is only associated with SNPs in the *IRF5* promoter. Genetic variants at the *IRF5/TNPO3* locus are associated with lupus disease onset and production of anti-dsDNA and anti-Ro antibodies in lupus patients. SNPs in the promoter region of

IRF5 (associated with rs4728142) and SNPs spanning the *IRF5* and *TNPO3* genes (associated with rs12534421) contribute independently to these symptoms.

Keywords: Lupus, *IRF5*, serology, sub-phenotype, SNP

Dedicated to Derick Strobe, who inspired me to try research in the first place.

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TABLE OF CONTENTS

	<u>Page</u>
Abstract.....	ii
Dedication.....	iv
Acknowledgements.....	v
Vita.....	vi
List of Figures.....	viii
Chapters:	
1. Preface.....	1
2. Introduction.....	9
3. Materials and Methods.....	11
4. Results.....	14
5. Discussion.....	19
References.....	21

LIST OF FIGURES

<u>Figure</u>	<u>Page</u>
1. SLE criteria.....	2
2. SLE case ethnicities.....	3
3. SNPs associated with SLE in the <i>IRF5/TNPO3</i> genes.....	5
4. Age of onset conditional analysis.....	16
5. Anti-Ro conditional analysis.....	17
6. Anti-dsDNA conditional analysis.....	18

CHAPTER 1

PREFACE

During the summer of 2012, I was selected to be one of 120 students involved in a Summer Undergraduate Research Fellowship at Cincinnati Children's Hospital. It was a ten week, paid internship where students conducted research in the extensive research facilities of the third best children's hospital in the nation. Students in this program were placed in laboratories addressing almost every health issue available, from cancer to development to x-ray imaging and cardiac diseases. Because of my prior experience in bioinformatics analysis, I was chosen to analyze the genetic data of lupus patients in the rheumatology department.

Systemic Lupus Erythematosus (SLE or lupus) is a systemic autoimmune disorder that can affect every tissue in the human body. The body's immune system is designed to differentiate between self (cells of the body) and non-self (cells from the outside world, which could possibly be harmful). When functioning correctly, immune cells attack non-self cells while ignoring self cells. However, in an autoimmune disease like SLE, the immune system begins attacking the cells of the body.

Lupus is a heterogenous disease that can look very different in different people. There is no laboratory test for lupus, instead, there are eleven criteria that lead to a clinical diagnosis of lupus. Any four of the eleven must be manifested for a lupus diagnosis according to the American College of Rheumatology. They are: hematologic

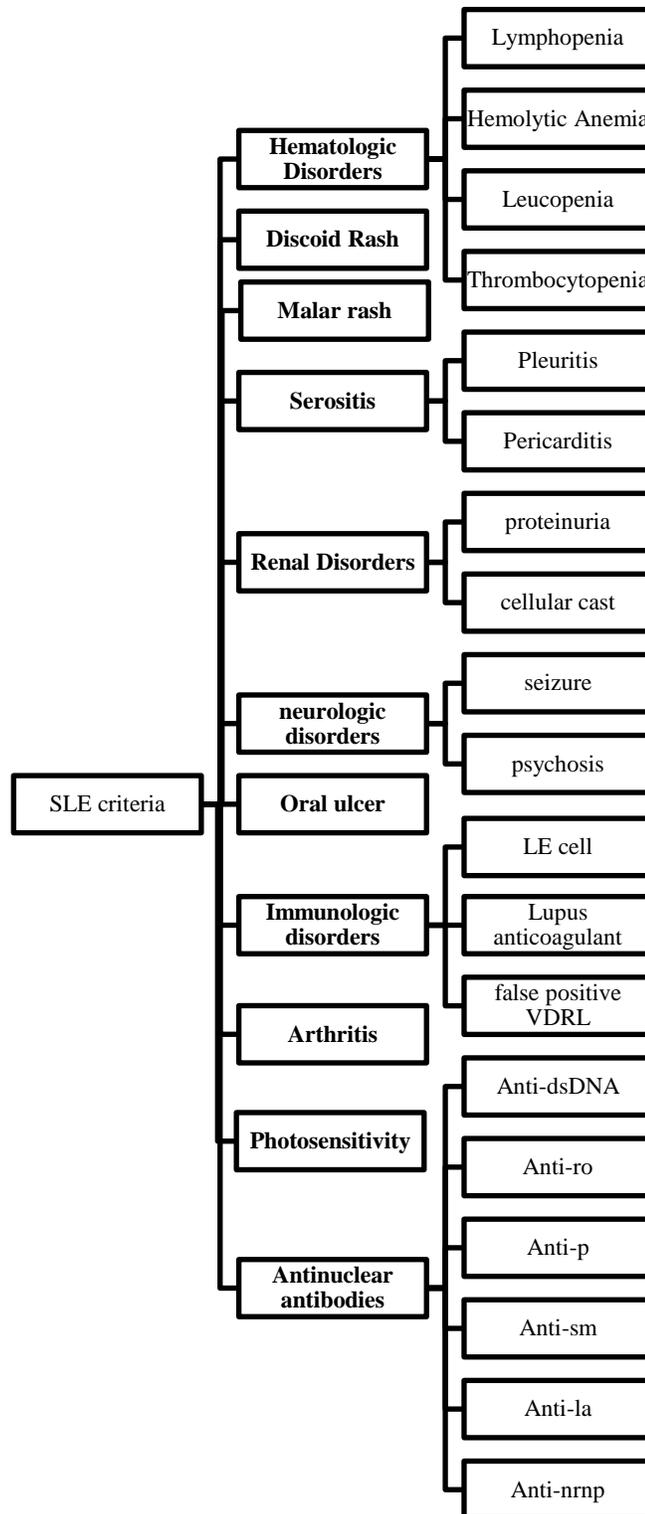


Figure 1. A chart of the thirty phenotypic characteristics of SLE. The bold items are the eleven main criteria defined by the American Rheumatology. In addition to these thirty characteristics, the age of onset of lupus symptoms was also studied.

(blood) disorders (anemia, leukopenia, lymphopenia, or thrombocytopenia), discoid rash, malar rash, serositis (inflammation of the lining around the lungs or heart), photosensitivity, renal (kidney) disorders, arthritis, neurologic disorders, oral ulcers, immunologic disorders (presence of certain autoantibodies, and abnormal antinuclear antibodies). These 11 symptoms have been broken into 30 subgroups, for which clinical data can be collected in lupus cases and controls (Figure 1). To study the genetic determinates of these sub-phenotypes, we used data from the Large Lupus Association Study 2 (LLAS2). Twenty-four different investigators contributed samples of DNA in addition to clinical information. Altogether, the LLAS2 dataset contained genetic and phenotypic data of over 6,000 people with lupus collected by researchers around the globe. Data from subjects of four different ancestral origins was studied: European American, Hispanic, African American, and Asian American (Figure 2). For each ancestry, covariates were calculated to account for admixture. Admixture is the concept

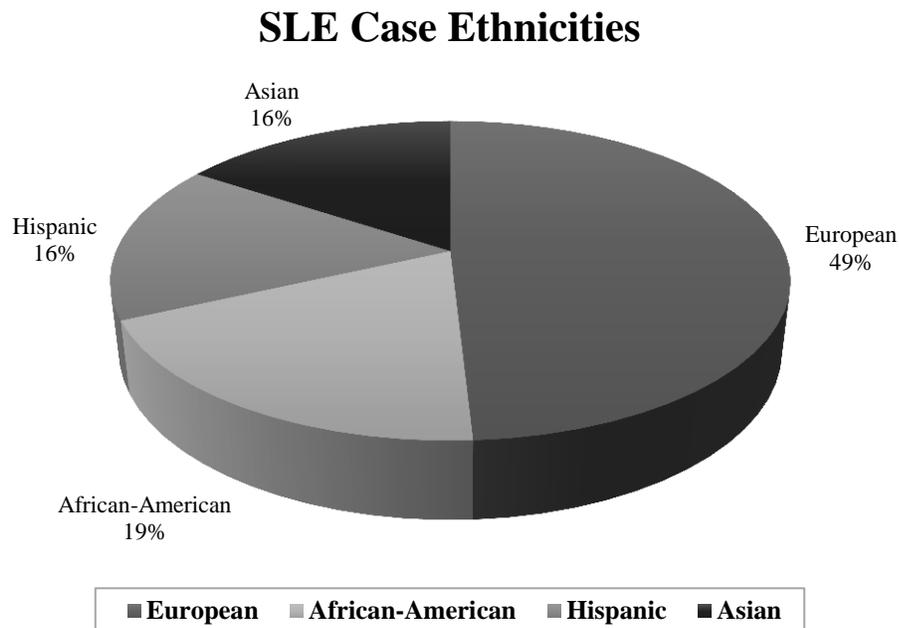


Figure 2. Percentage of cases of different ethnicities analyzed from the LLAS2 data set.

that individuals are rarely ever purely one race, but instead have a genetic history from multiple ancestries. The covariates determine and account for mixed genetics in each individual in the study.

Single Nucleotide Polymorphisms (SNPs) are variations in the genome that occur at a single base pair. These genetic variants are manifested in at least 5% of the population. The variations can be silent, causing no change in the gene's protein structure, or they can change the promoter region, causing the gene to be over or under expressed, or the amino acid sequence, impacting the entire function of the resulting protein.

There is no clearly defined single cause of lupus onset, rather, it is a result of both environmental and genetic causes. SNPs in over 45 genes have been repeatedly associated with lupus development, or etiology. Two of the most commonly associated loci includes the Interferon Regulatory Factor 5 (*IRF5*) gene and the nearby Transportin 3 (*TNPO3*) gene. The *IRF5* gene is especially noteworthy because it regulates chemicals called interferons. Interferons act as signals in the body that activate the immune response to viral infections. In lupus, interferons have been demonstrated to drive the autoimmune response and the pathology of SLE. In the LLAS2 study subjects, 101 genetic variants were genotyped in the *IRF5/TNPO3* gene region. Case-control analysis of these SNPs showed significant association with lupus development. In fact, the group at the Cincinnati Children's Hospital established that there are SNPs that are highly associated with lupus development in the promoter of *IRF5* and in a region spanning the *IRF5* and *TNPO3* genes (p-value of less than 10^{-8}).

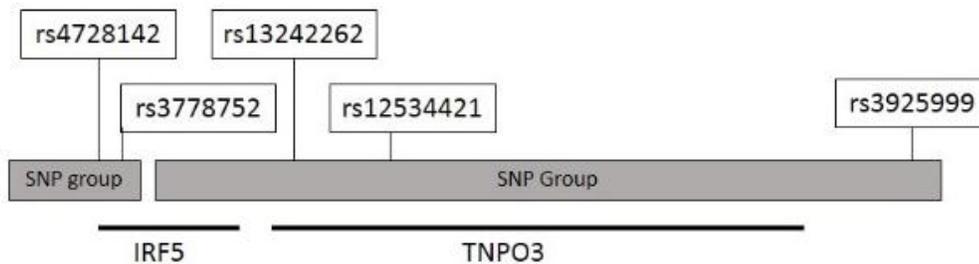


Figure 3. SNP locations in reference to the *IRF5* and *TNPO3* genes. The black bars show the gene locations, and the two gray boxes are two groups of SNPs that are in high linkage within the gray region, but display little association with the other SNP group. The relative locations of SNPs connected to SLE symptoms are shown.

SNPs in a certain area tend to be found together, an occurrence known as linkage disequilibrium (LD). In the case of lupus development, the most associated SNPs are located in the promoter region of *IRF5*, and were closely linked with each other (Figure 3). When the association of the SNP with the lowest p-value (rs4728142, located in the promoter of *IRF5*) was accounted for in a conditional analysis, the only remaining genetic association was found in a group of SNPs that span the *IRF5* and *TNPO3* genes. Upon further conditional analysis, removing the association of the next-most associated SNP (rs12534421) caused all association to be eliminated. This suggested that all significant association with lupus development was linked with two main SNPs in the *IRF5/TNPO3* area.

Although studies have shown the association of SNPs in the *IRF5* locus with lupus development, there has been little analysis of the possible association with specific symptoms in lupus. My research sought to identify correlations between SNPs and the development of lupus sub-phenotypes. I used the statistical software package PLINK version 1.07 to analyze the LLAS2 data. PLINK is designed to perform in-depth analyses of SNP associations, and it enabled me to conduct a sub-phenotypic logistic regression analysis (see Chapter 3) of SNPs in the *IRF5/TNPO3* region, identifying connections

between displayed lupus symptoms and the SNPs present in this gene area. After formatting the data appropriately and including covariates to account for differences in genetic admixture, we determined the p-value for each SNP's association with every clinical phenotype. In a logistic regression, the p-value gives the probability that the frequency of the minor allele of a SNP is the same in the people with a sub-phenotype, such as the people with anti-dsDNA, and the people without the sub-phenotype. The logistic regression analysis was first done on subjects of European ancestry, then on Asians, African Americans, and Hispanics. The accepted alpha error rate is 0.05, but because we performed many independent tests, a multiple testing correction had to be used. This correction takes into account the number of SNPs compared, as well as the number of clinical phenotypes analyzed. Using this correction, a significant p-value was determined to be 1.6×10^{-5} .

In European Americans, the logistic analysis identified three sub-phenotypes that were significantly associated with SNPs in and around the *IRF5/TNPO3* genes (p-value less than 1.6×10^{-5}). These were the age of onset of lupus (how old a person is when they develop lupus), the presence of anti-Ro autoantibodies, and the presence of anti-dsDNA autoantibodies. Anti-Ro autoantibodies target the Ro ribonucleoprotein, which is normally found in the nucleolus of the cell, while anti-dsDNA autoantibodies target double stranded DNA (dsDNA). These autoantibodies are not normally formed in absence of an autoimmune response. In African Americans and Asian Americans, there was a statistically significant association to age of onset, but not to the other symptoms.

A conditional analysis (see Chapter 3) was conducted for each of the three statistically associated symptoms, similar to the conditional analyses that demonstrated

the two independent SNP groups that were associated with SLE development. This analysis revealed an association with specific SNPs in the *IRF5/TNPO3* area. For age of onset of lupus, there was a statistically significant association with the SNP rs12534421. Nearly all phenotype association was removed when the impact of this SNP and all associated variants were removed in the analysis. When the symptom association with the next significant SNP, rs4728142, was removed, no SNP association with the age of onset remained. This demonstrated that all associated SNPs were linked to SNPs rs4728142 and rs12534421.

For the presence of anti-Ro and anti-dsDNA autoantibodies, the conditional analysis showed association to rs4728142, the primary variant associated with SNPs in the promoter region of *IRF5*. After conditioning on (removing the impact of all SNPs associated with) rs4728142, there was still association with a few SNPs spanning *IRF5* and *TNPO3* genes (those variants in linkage disequilibrium with rs12534421), but most of the association was with genetic variants in the promoter.

The fact that different groups of SNPs in the *IRF5/TNPO3* region were statistically associated with the development of different lupus symptoms provides support to the theory that there are two independent groups of variants in this region, and that they play separate roles in the development of SLE. This will allow future studies to specifically focus on the *IRF5/TNPO3* region. My results also support previous studies of these two SNP groups and could refine the study of the biological processes that are impacted by these variants by directing the focus towards each of the SNP groups separately.

Additionally, our work to identify variants associated with the development of specific symptoms in people with lupus has immediate therapeutic implications. Lupus is a relatively rare disease, and doctors are unlikely to prophylactically treat healthy people who are genetically predisposed to lupus. Once people have lupus, however, there are different therapeutic options that vary in their aggressiveness. This study may also contribute to the type of personalized medicine that is the future of health care.

At the end of the summer, I was able to present my research at the University of Cincinnati's Undergraduate Research Symposium, where I earned an honorable mention. In January 2013, I returned to the Rheumatology Department to complete additional data analyses, instruct a new graduate student in programming with PLINK, and assemble cohesive, straightforward instructions for future sub-phenotypic, conditional analysis research in this field.

CHAPTER 2

INTRODUCTION

Systemic Lupus Erythematosus (SLE or lupus) is an autoimmune disorder affecting every organ in the body [1]. Patients must display four of eleven clinical findings for official diagnosis according to the American College of Rheumatology [5, 6]. One in every 5,000 people will be diagnosed with lupus, with 90% of them being female (Figure 3). African Americans and Asians are three to four times more likely to develop lupus than persons of European descent, and African American, Asian, and Hispanic ancestries have a greater mortality rate from this disease [2-4]. Without sophisticated medical care, SLE has a 50% mortality rate [7].

Genetic factors play a significant role in the etiology of lupus [8]. Previous studies have demonstrated the effect of genetic variants on the development of specific symptoms in lupus patients [9-15]. The Interferon Regulatory Factor 5 (*IRF5*) functions within the interferon inflammatory pathway and is critical for lupus pathogenesis [15-19]. Single nucleotide polymorphisms (SNPs) within the *IRF5* and the nearby Transportin 3 (*TNPO3*) genes are highly associated with the etiology of lupus, but genetic variant associations with specific clinical phenotypes of SLE have not yet been identified [20-36]. Prior studies indicate that genetic association occurs through two independent groups of linked SNPs at the *IRF5/TNPO3* locus [37]. Variants in the promoter region are present across ancestries and are accounted for by the rs4728142 SNP, while variants

spanning the *IRF5/TNPO3* region are present only in populations with European admixture and are strongly linked to the SNP rs12534421.

The purpose of this study was to determine if either of these two genetic effects at the *IRF5/TNPO3* locus are statistically associated with specific clinical phenotypes in patients with lupus. The study also investigated how sub-phenotypic associations in *IRF5/TNPO3* vary across different ancestries. Our data indicate that the two effects are independently associated with three different lupus phenotypes in European Americans, but only one effect is evident in African Americans, Asians, and Hispanics.

CHAPTER 3

MATERIALS AND METHODS

Subjects

The study included 3,926 European, 1,257 Asian, 1,287 Hispanic, and 1,524 African-American SLE patients, all of whom met the American College of Rheumatology (ACR) SLE classification criteria. Phenotypic data and patient DNA were collected with informed consent and IRB approval by several institutions around the globe. Thirty-one clinical phenotypes were analyzed, each of which fall into one of the following categories: age of onset of lupus, presence of certain autoantibodies, false positive syphilis test, discoid rash, malar rash, renal disorders, neurologic disorders, oral ulcers, photosensitivity, and hematologic disorders.

Genotyping

Patient DNA was genotyped on an iSCAN array genotyping instrument using the Illumina custom bead system. One hundred and one lupus susceptibility loci in the *IRF5/TNPO3* region were identified for each patient. SNPs were located in a 437,000 base pair region, ranging from 167 kbp upstream of *IRF5* to 61 kbp downstream of *TNPO3*. Admixture markers, which indicate ancestral origins, were genotyped and analyzed for each sample to determine admixture from five ancestries: European American, African American, Asian and Asian American, and Hispanic American [38-41].

Statistical analysis

Two main types of analyses were used in this study. The first was a logistic regression analysis of all SLE symptoms. This analysis compared the presence of different risk alleles with the presence of each symptom, identifying any association. It then determined a p-value, which was the probability that the observed association could randomly occur. The logistic regression served to identify lupus symptoms for which SNPs in the *IRF5/TNPO3* region were significantly associated.

A sub-phenotypic logistic regression analysis was conducted using PLINK version 1.07, a program designed to analyze SNPs and their associations with phenotypic data. Admixture covariates were included in the program to account for variances in ancestry and each ancestry was individually assessed. Using the most stringent Bonferroni multiple testing correction ($p = 0.05/(\text{number of variants} \times \text{number of phenotypes}) = 0.05/(101 \times 31)$), a significant p-value was determined to be 1.6×10^{-5} . Additional label-swapping iterative permutation testing showed that empirically significant p-values for each SNP are actually closer to 10^{-4} . This test swaps the symptom affectedness status (from unaffected to affected, or vice versa) for a random selection of patients, and checks to see if SNP association still exists. It repeats this process several thousand times, and uses the results to calculate the probability of SNP association randomly occurring. The sub phenotypic logistic regression analysis of lupus patients identified three symptoms with significant p-values. The additional permutation testing confirmed that no other symptoms were significantly associated.

Aside from the logistic analysis, the second main test used in this study is a conditional analysis. This test determines how many SNPs are actually associated with a

specific symptom. For a single symptom, this analysis removes the most associated SNP, and all of the SNPs that are linked with it. It is then possible to see if any SNPs not connected with the first SNP are associated with the symptom. For a step-wise conditional analysis, the symptom is “conditioned” (the association is removed) for the most associated SNP, followed by the next remaining SNP, then both SNPs simultaneously, in a series of steps that result in the removal of all significant SNP association. The conditional analysis shows the top two most associated SNPs that are not linked to each other. It could be used to identify more associations, but after the association of the top two are removed, very little SNP association remains.

A conditional analysis was conducted in PLINK v 1.07 to determine which SNPs were statistically associated with these three phenotypes [42]. Phenotypic associations were conditioned step-wise using the SNPs that account for the two linked SNP groups in the *IRF5/TNPO3* area: the SNP rs4728142, which is associated with genetic variants in the promoter region of *IRF5*, and the SNP rs12534421, which is associated with variants spanning *IRF5* and *TNPO3*. In cases where the SNPs most associated with lupus development differed from those most associated with the specific symptoms, the SNPs most associated with the symptoms were used for the conditional analysis. This was the case for anti-Ro and anti-dsDNA. In these cases, conditional analyses were conducted with the two main SNPs for lupus development in addition to the two most associated symptomatic SNPs.

CHAPTER 4

RESULTS

The three clinical phenotypes that demonstrate statistically significant association with variants in *IRF5* and *TNPO3* are: age of onset of lupus (p value_{EU} = 2.44x10⁻¹⁶, Odds Ratio = 0.67*), the presence of anti-Ro antibodies (p value_{EU} = 2.09x10⁻⁷, Odds Ratio = 0.67), and the presence of anti-dsDNA antibodies (p value_{EU} = 4.15x10⁻⁷, Odds Ratio = 0.75). Of the three phenotypes, age of onset of lupus was the only one that was significantly associated across all three ethnicities (European American, African American, and Asian). Testing revealed no genetic association with any symptom in Hispanics. The presence of anti-Ro antibodies was associated with variants in Europeans only, and the presence of anti-dsDNA antibodies displayed SNP association in Europeans and African Americans. In Europeans, the SNP rs3778752 had the lowest p value for the presence of both anti-Ro and anti-dsDNA antibodies. For age of onset of lupus, the SNP rs4728142 was most significantly associated in both African Americans and Asians, but not in Europeans.

For all three phenotypes, genetic variant association was no longer significant when the phenotypic association resulting from the two most associated SNPs was removed. With age of onset, the group of SNPs spanning *IRF5/TNPO3* (closely linked to the SNP rs12534421) and the group of genetic variants in the promoter region of *IRF5* (closely linked with the SNP rs4728142) have significant association in Europeans, with

variants linked to rs12534421 having the lowest p values (Figure 4). This is shown by the sharp decline in statistical significance (-log p value) when each SNP is conditioned separately. For the presence of anti-Ro and anti-dsDNA antibodies, the promoter group (rs4728142 and associated SNPs) had the greatest effect (Figures 5-6).

Although rs4728142 and rs12534421 are most closely associated with the development of lupus and the two genetic effects in the *IRF5/TNPO3* region, rs3778752 was most closely linked to the presence of anti-Ro and anti-dsDNA antibodies. The rs3778752 risk allele is a part of the SNP group in the promoter region of IRF5. In association studies, rs3778752 had lower p-values than rs4728142 in both anti-dsDNA ($p_{rs3778752} = 4.154 \times 10^{-7}$, $p_{rs4728142} = 5.85 \times 10^{-6}$) and anti-Ro ($p_{rs3778752} = 2.09 \times 10^{-7}$, $p_{rs4728142} = 9.37 \times 10^{-7}$). We identified chromosomes in European Americans in which the two SNPs segregate (n = 1992) and the subjects have either anti-dsDNA or anti-Ro antibodies (n = 624). Our results show that subjects with anti-Ro or anti-dsDNA antibodies are 133% more likely to have the rs3778752 risk allele than the rs4728142 risk allele.

Age of Onset

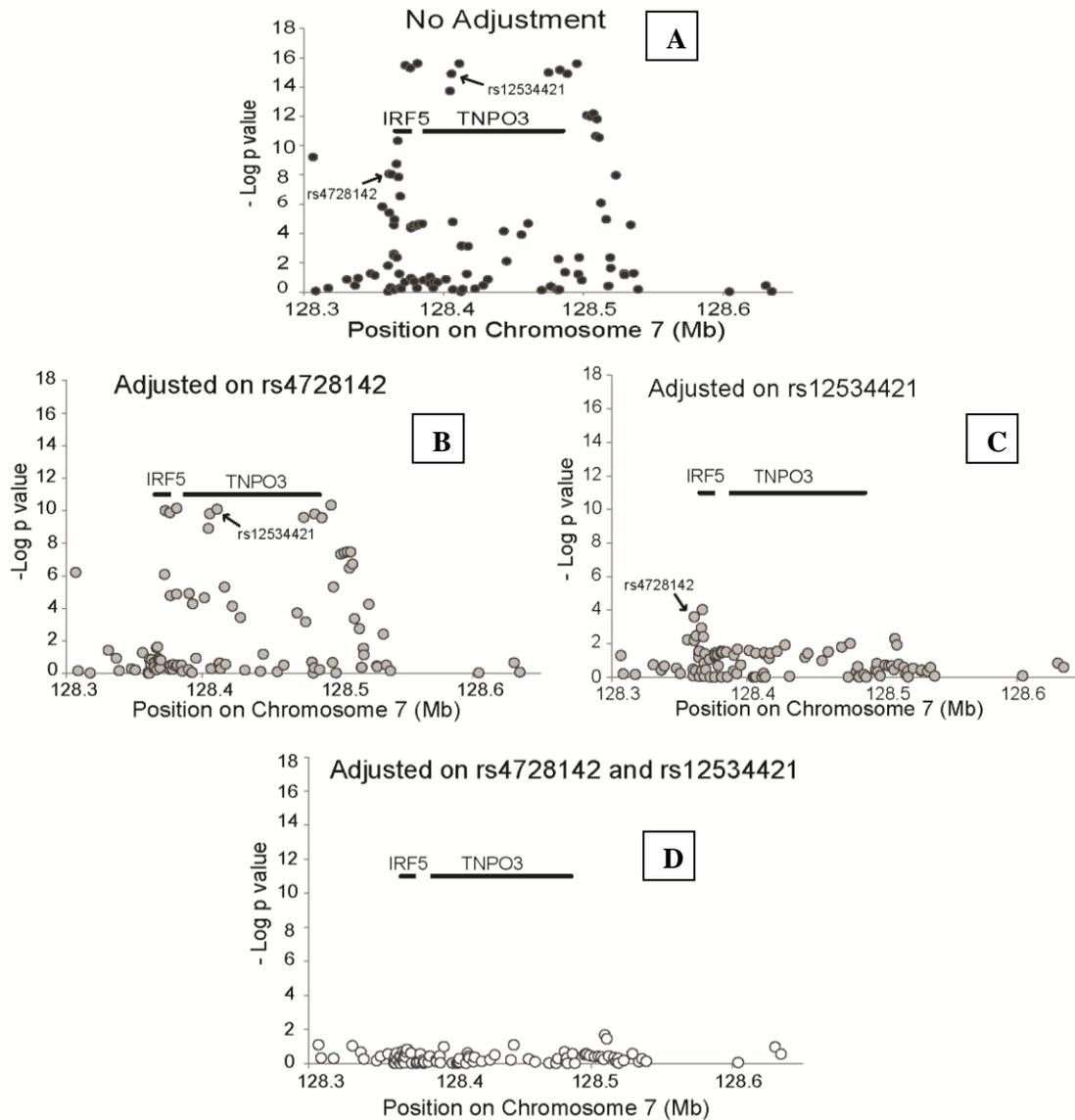


Figure 4. Conditional analysis of age-of-onset phenotype. The horizontal bars show the position on chromosome 7 of *IRF5* and *TNPO3*. The most associated SNPs are identified in A, B, and C. Graph A shows the statistical significance ($-\log_{10}[p\text{-value}]$) of each SNP in the *IRF5/TNPO3* region. For graphs B and C, we removed each of the top two most associated SNPs. Graph D removes the association of both SNPs. From this, we conclude that rs12534421 (the second group of linked SNPs) is responsible for most of the statistical association between genetic variants and the age of onset of lupus. When the contribution of both SNPs is removed, no association remains $p < 0.01$ (D).

Anti-Ro

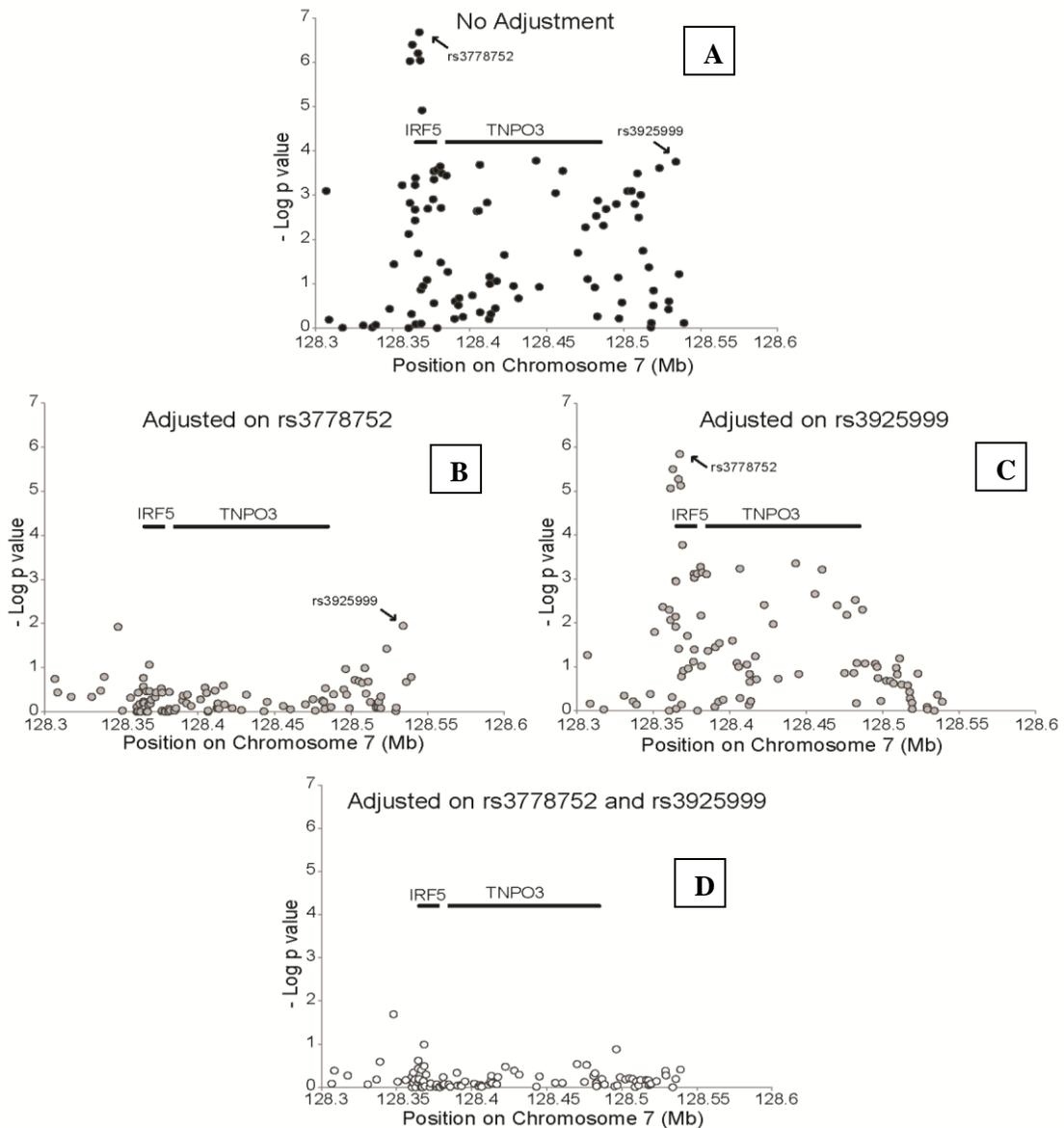


Figure 5. Conditional analysis of the presence of anti-Ro antibodies. Graph A shows the statistical significance ($-\log_{10}[\text{p-value}]$) of the association of each SNP in the *IRF5/TNPO3* region with the presence of anti-Ro antibodies. For graphs B and C, we removed the association of the two most significant SNPs (which did not include rs4728142 or rs12534421) separately. The bottom graph removes the association of both SNPs. From this, we can conclude that rs3778752 (the first SNP group) is responsible for most of the statistical association of genetic variants with the presence of anti-Ro antibodies.

Anti-dsDNA

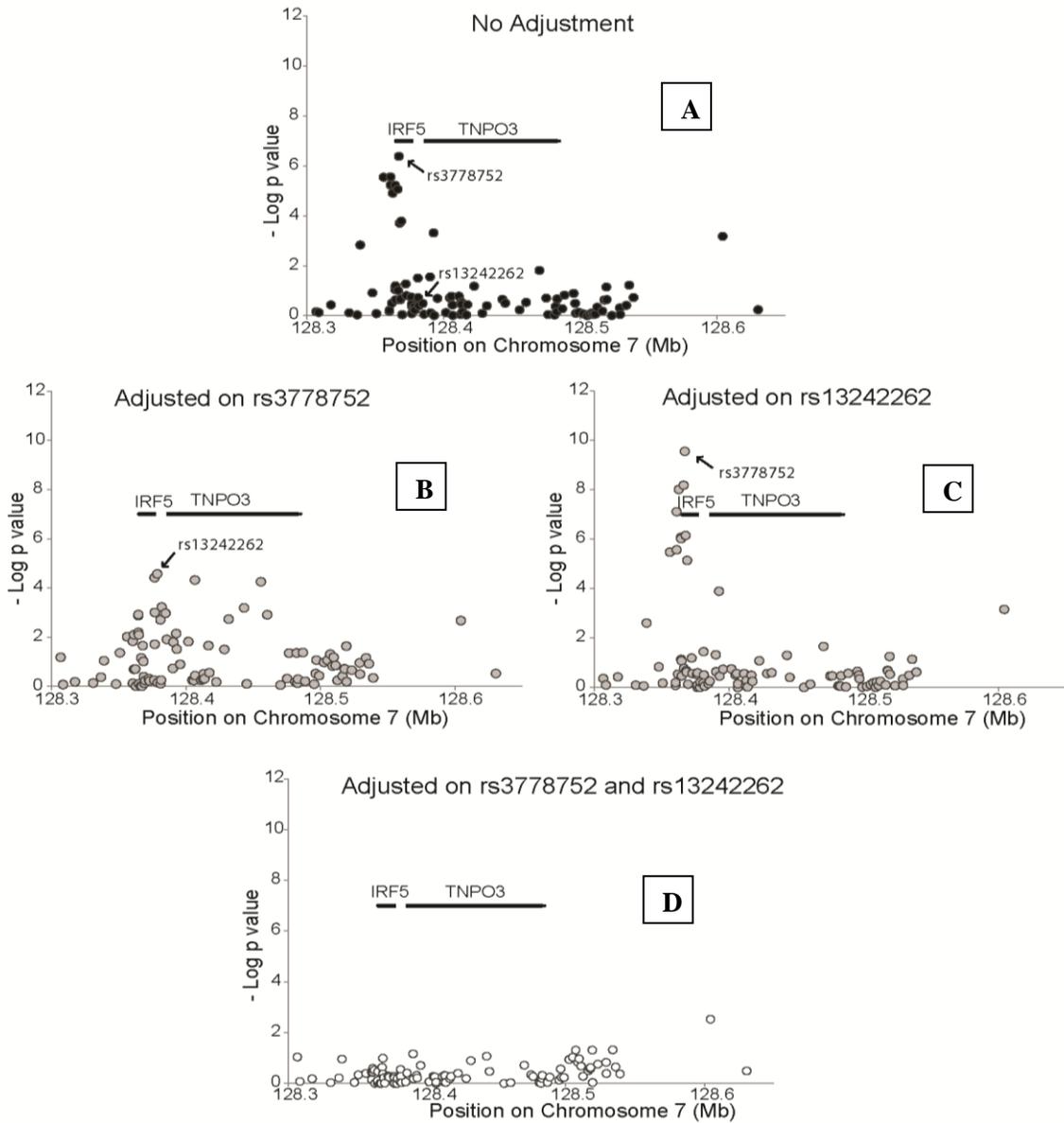


Figure 6. Conditional analysis of the presence of anti-dsDNA antibodies. Graph A shows the significance ($-\log_{10}[p\text{-value}]$) of the association of each SNP in the *IRF5/TNPO3* region with the presence of anti-dsDNA antibodies. For graphs B and C, we conditioned separately on the two most closely associated SNPs. Graph D adjusts for the association of both SNPs. From this, we can conclude that rs3778752 (the first SNP group) is responsible for most of the statistical association of genetic variants with the presence of anti-dsDNA antibodies.

CHAPTER 5

DISCUSSION

Genetic Variant Association

Defined connections between genetic variants and lupus sub-phenotypes may enable increased understanding of the etiology of lupus. These connections may also allow clinical practitioners to predict a patient's risk of developing specific symptoms. In this study, variants in *IRF5* and *TNPO3* that are already known to be statistically associated with the development of lupus were shown to be connected with specific sub phenotypes including age of onset of lupus and the production of anti-Ro or anti-dsDNA antibodies. Association was found largely in European American subjects but was also present in African Americans and Asians to a lesser degree.

Two Independent Genetic Effects

Although the two groups of linked SNPs in *IRF5* and *TNPO3* are highly associated with the development of lupus, genetic variants in the promoter of *IRF5* (linked to the SNP rs4728142) and genetic variants spanning *IRF5* and *TNPO3* (linked to the SNP rs12534421) are independently associated with specific symptoms of lupus. This supports the hypothesis that these are indeed two separate SNP groups which play different roles in SLE. The group spanning *IRF5/TNPO3* only displays significance in

European Americans, while the promoter group plays a role in all ethnicities. This could signify that SNPs in the promoter of *IRF5* are part of an ancient set of variants, while the group of associated SNPs spanning *IRF5* and *TNPO3* are the result of more recent variation.

SNP Association Differences

The rs3778752 risk allele shows 133% more association with the presence of anti-Ro and anti-dsDNA antibodies than the rs4728142 risk allele. Our results suggest that although rs4728142 is one of the most significant indicators of lupus risk, rs3778752 seems to be far more effective in predicting the production of anti-Ro and anti-dsDNA in the body.

Conclusion

In conclusion, our study shows that genetic variants in the *IRF5/TNPO3* genes are associated with specific clinical phenotypes of lupus. The two independent SNP groups in this region function separately in the different symptoms as well as in the different ethnicities. Our data support prior findings that the two etiological effects are associated with different ancestries, and indicate that genetic variant groups in *IRF5/TNPO3* function differently in the development of certain lupus phenotypes.

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