

The Role of Chromosomal Region 16p13.13 in Type 1 Diabetes

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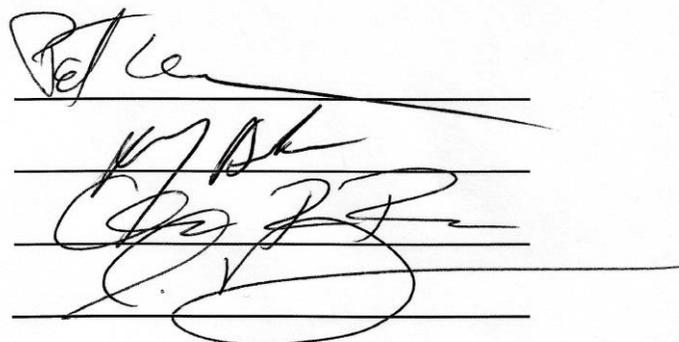
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Advisor: Patrick Concannon Ph.D.

Abstract

Type 1 diabetes most frequently results from the autoimmune destruction of the insulin producing pancreatic *Beta* cells, resulting in dependence on exogenous insulin. The disease is complex and arises due to the effects of both genetic and environmental factors. With the advent of genome-wide association studies (GWAS) over 40 additional loci have been identified that confer low to moderate risks of developing type 1 diabetes (Odds Ratios, OR, ≤ 1.3). One of these regions identified is located at chromosome 16p13.13 and is associated with type 1 diabetes and several other autoimmune disorders. The specific region of interest on chromosomal region 16p13.13 implicated in autoimmunity spans approximately 530 KB from 10,937,499-11,467,499 base position (bp) (build Hg19) and encompasses four major genes: *CIITA*, *DEXI*, *CLEC16A* and *SOCS1*.

In order to identify specific risk variants for type 1 diabetes in this region and understand the mechanism of their action, we re-sequenced the entire region in 192 individuals (128 patients and 64 controls) identifying 93 novel variants. A panel of 939 SNPs, that included 46 of these novel variants, was genotyped in 3,070 multiplex families with type 1 diabetes to identify potential risk variants. After correcting for multiple testing, 48 SNPs provided statistically significant evidence of association with type 1

diabetes (most significant SNP rs34306440 $P = 5.74 \times 10^{-6}$), conditioning on the top SNP found no further significant associations.

The panel of SNPs used for fine mapping was also tested for association with variation in the transcript levels of each reported isoform of all genes in the region. Significant associations were observed only for transcript levels of *DEXI*, a gene originally reported to be unregulated by dexamethasone but whose function is unknown. We also tested novel unreported isoforms of *CIITA* in our study, but found no association.

We examined the relationship between the odds ratio for type 1 diabetes and the magnitude of the effect of *DEXI* transcript levels for each SNP in the region. Among SNPs significantly associated with type 1 diabetes, the common allele conferred an increased risk for disease, and corresponded to lower *DEXI* expression. Our results suggest that the primary mechanism by which genetic variation at *CLEC16A* contributes to risk for type 1 diabetes is through reduced expression of *DEXI*.

Dissertation Overview

The dissertation is divided into five chapters. Chapter 1 (Type 1 Diabetes) focuses on a review of our current knowledge of type 1 diabetes. Chapter 2 (Brief History of Diabetes) examines the magnitude and impact diabetes has had on our society and some of the major historical events that led up to our current understanding of the disease. Chapter 3 (Genetics of Type 1 Diabetes) encompasses a compressive review of the current genetic understanding of type 1 diabetes and the contextual placement of the dissertation project in this rapidly advancing field. Chapter 4 (Chromosome 16p13.13 and Its Role in Type 1 Diabetes) is the main focus of the dissertation and explores the overall project. Chapter 5 (Future Directions) expands upon future experiments of this project and overall future directions of type 1 diabetes research.

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Chapter 1

Type 1 Diabetes in Today's World

Introduction

Type 1 diabetes most frequently results from the autoimmune destruction of the insulin producing pancreatic β cells, ultimately resulting in the affected individual requiring exogenous insulin for survival. Type 1 diabetes is considered a complex disease that arises due to the effects of both genetic and environmental factors evident by the incomplete concordance of 30-70% between monozygotic twins (1-6). For dizygotic twins the concordance rate is estimated to be around 5-15% (2-4,6). Type 1 diabetes was previously known as insulin-dependent diabetes mellitus (IDDM), or juvenile onset diabetes, because it was originally recognized to occur in young children, but these terms are no longer widely used. Type 1 diabetes can occur at any age and it has been found that over 50% of new cases of type 1 diabetes occur in adults (7).

The initial symptoms of type 1 diabetes are excessive thirst, urination, and hunger. These symptoms occur because the body is producing insufficient amounts of insulin resulting in chronic hyperglycemia: a condition which if not treated can result in death (8). Type 1 diabetes has two sub-types; 1A and 1B. Type 1 diabetes 1A refers to the auto-immune driven form of the disease, which is evident by the development of autoantibodies. Type 1 diabetes 1B, also called "idiopathic diabetes," is a form of diabetes with no auto-antibodies present even though the insulin levels are drastically reduced similar to type 1A. Type 1 diabetes 1B mainly occurs in Africans or Asians and the exact mechanism of the disease is poorly understood (8). Type 1 diabetes 1B will not be discussed further here and for simplicity, type 1 diabetes will refer to the sub-type 1A hereafter.

Incident Rates

Based on the Center for Disease Control and Prevention (CDC), approximately 13,000 young people are diagnosed with type 1 diabetes each year. The most recent CDC reports put the prevalence of type 1 diabetes at 1.7 per 1000 people age 0-19 in the United States (9). Type 1 diabetes is predominantly a disease that affects Europeans or populations of European descent. The highest incidence rates (age 0-14) were found in Finland and Sardinia (37/100,000), the USA rate was 16.1/100,000 and the lowest rates of <1/100,000 were found in China and Venezuela (10,11). Globally the rates of type 1 diabetes have been increasing, and the USA has seen a yearly increase of 5.3% (12). A study in Europe has predicted that by 2020 the prevalence of type 1 diabetes among individuals 15 years and younger will increase by 70% (13). Clearly the epidemic of type 1 diabetes is exacerbating and research into the underlying mechanisms is essential in understanding the disease and to help prevent future cases.

General Features of Diabetes

In all forms of diabetes, the key identifying trait is hyperglycemia; a condition where there is a high glucose level in the blood stream that can cause very serious medical conditions such as ketoacidosis, kidney failure, heart disease, stroke, and blindness. Hyperglycemia occurs in all four of the classified forms of diabetes: type 1 diabetes, type 2 diabetes, gestational diabetes, and "other" (14). The World Health Organization (WHO) currently estimates that 347 million people in the world have diabetes. In 2004, ~3.4 million people died from hyperglycemia (15). The three other

types of diabetes will be briefly mentioned for contextual understanding. Type 2 diabetes is now the major form of diabetes; it encompasses 90% of all cases and occurs when an individual develops insulin resistance, further risk augments with age and obesity. Generally individuals do not need exogenous insulin for survival and disease can be controlled by diet, exercise and medications (9,16). Gestational diabetes is a form of diabetes that affects pregnant women and usually subsides after pregnancy. However, if the condition persists after pregnancy, the diabetes type needs to be re-classified and treated accordingly. The "other" category of diabetes refers to an underlying identifiable defect in the way the body responds to insulin; it is not related to autoimmune destruction of β -cells (8).

Type 1 Diabetes Environmental Variables

There has been much investigation into "unknown environment factor/factors" that trigger the autoimmune response to type 1 diabetes. More children are diagnosed with diabetes during the winter "cold season" and less during the summer. A plausible explanation for this observation is on the account of the winter season bringing people in closer contact, thus increasing the exposure to viral infections (17,18). No definitive triggering virus strain has been found; however, some evidence hints at the genus of an enterovirus, specifically Coxsackievirus involvement in the development of type 1 diabetes (19-21). It has been reported that when migrants move from a low incidence region for type 1 diabetes to a region of higher risk their incidence rate increases as well (22,23). Various other environmental triggers have also been investigated such as

bacterial gut composition and consumption of certain foods and nutrients (12,24), or lack of exposure to immunogens as postulated in the "hygiene hypothesis". The hygiene hypothesis states that as countries become more developed (cleaner living environments), individuals are exposed to less pathogens and the immune system begins to malfunction due to the "lack of challenge," resulting in autoimmune diseases and allergies (25).

Evidence for this argument is seen in the model organisms for type 1 diabetes such as the non-obese diabetic (NOD) mouse and the inbred BioBreeding (BB) rat, which develop diabetes at a higher rate when animals are kept in a pathogen-free environment (26,27).

Further evidence for this hypothesis (as previously mentioned) is seen by the increased incidence of type 1 diabetes among migrants to a region of high incidence (22,23).

However, all these detailed studies have found no conclusive evidence of the causative factor in humans. Ongoing collaborative studies such as The Environmental Determinants of Diabetes in the Young (TEDDY) (28) and Diabetes Autoimmunity Study in the Young (DAISY) (29) aim to determine environmental triggers for type 1 diabetes in children who are at risk based on genetics.

Pathogenesis of Type 1 Diabetes (What is known)

It is predicted that type 1 diabetes occurs due to an accumulation of multiple immune responses that ultimately result in the destruction of the insulin producing β -cells. Type 1 diabetes will occur when 70-90% of the β -cell mass is destroyed. This cascade of immune response can occur very quickly (e.g. juvenile onset of disease) or take years to develop (12,30). Deciphering what events precede diagnosis of type 1

diabetes in humans is very complicated due to the "unknown trigger" and difficulty in examining the pancreas in living individuals. Based on examinations of pancreas from cadavers from long term type 1 diabetes patients, it appears that β -cell destruction in the pancreas is very slow and incomplete (31). Studies also found that during insulinitis, macrophages and $CD8^+$ T-cells were the most abundant cell types present, $CD4^+$ T-cells were present as well but at a lower rate (32,33). Due to the difficulty in examining the pathogenesis in humans, we turn to genetic studies to shed light on biochemical pathways leading to type 1 diabetes that can be tested in animal models such as the NOD mouse (34) and BB rat (35).

In the NOD mouse model there are four stages of disease progression; pre-insulinitis, peri-insulinitis, intra-insular insulinitis and finally complete islet destruction (30). In pre-insulinitis no damage or immune response is evident in the pancreatic islets. $CD11c^+$ dendritic cells and $ER-MP23^+$ macrophages are the first cells that invade the pancreas in three week old mice (30). Around the same time (or shortly after) pathogenic T-cells, majority $CD4^+$ T-cells, $CD8^+$ T-cells, and other immune cells are also present and have been identified surrounding the pancreas. This period of development is referred to as peri-insulinitis (34). It is postulated that these T-cells react to β -cells' antigens based on the high turnover of β -cells in the mouse islet (36). At this point, lymphocytes invade the islets in the stage referred to as intra-insular insulinitis, resulting in more inflammation preempting total islet destruction. In comparison to the animal models, the amount of insulinitis that occurs in humans is much less and incomplete (30,31,37)

In the NOD mouse, it has been found both CD4⁺ and CD8⁺ T-cells are needed for the development of diabetes (34). For example, when the NOD mouse does not have a functional β_2 -microglobulin (β_2M), resulting in a non-functional MHC class I molecules (CD8⁺ T cells absent in periphery); they do not develop diabetes (38-40). When the MHC class II molecule is not expressed as in the CIITA knockout mouse (CD4⁺ T cells absent), islet infiltration in the NOD mouse occurs but diabetes does not develop (41). However, if an autoaggressive CD8⁺ T cell clone is introduced into NOD CIITA knockout or NOD SCID mice, diabetes will develop in the absence of CD4⁺ T cells (41,42). Based on these findings both MHC class I & II molecules are needed in the development of diabetes. The absence of either will inhibit diabetes, but with a slightly greater emphasis on the requirement for CD8⁺ T-cells as key to initial development.

It has also been determined that developing self-antigens of insulin is essential in developing diabetes. This finding was based on observations of antibodies against insulin appearing first in young children that develop type 1 diabetes (43,44). Mice have two insulin genes that express proteins differing by two amino acids, at position B9 and B27 (45,46). In insulin 1 knockout NOD mice diabetes was prevented, but in insulin 2 knockout NOD mice diabetes was accelerated.(46,47). The specific epitope triggering the autoimmune reaction in the NOD mice was narrowed down to amino acid sequence B9-B23 in insulin 1 (48-50).

After examining human and animal cases of type 1 diabetes, a pathway of pathogenesis of diabetes can be postulated. Some "unknown trigger" or lack thereof causes the development of autoreactive T-cells (CD4⁺ and CD8⁺). It can be speculated

that CD8⁺ T-cells are recruited first to pancreas and then after this initial wave of attack CD4⁺ T-cells are activated. However, the end result is that T-cells invade the islets and cause β -cell destruction. Over time this causes more inflammation and even greater destruction which destroys an individual's ability to produce insulin and ultimately results in diabetes.

Important Research Tool- Islet Cell Autoantibodies (ICA)

In type 1 diabetes, the development of autoantibodies is indicative of an autoimmune response occurring. The targets of some of the autoantibodies are insulin, glutamate decarboxylase (GAD65), insulinoma-associated antigen-2 (IA2), islet cells, and zinc transporter 8 (ZNT8) (43,51-53). The presence of one of these autoantibodies does not necessarily indicate an individual will develop diabetes because levels of autoantibodies have been found to fluctuate (43). An individual's risk for developing type 1 diabetes does increase as the number of autoantibodies increases rather than the titre of autoantibodies (43,51,52). Also antibodies appear to develop in a sequential order and as previously mentioned antibodies against insulin appear first (43,44). Autoantibodies are important for diabetes research due to the fact they are an easily measurable quantity for investigators that can be indicative of a pending autoimmune or occurring autoimmune destruction of β -cells in the pancreas (44). However, antibodies are not the only specific epitope targeting mechanism in the immune system and it was recently found that cytotoxic T-cells from a type 1 diabetes patient were targeting β -cells through a glucose regulated preproinsulin epitope (54). Future testing to determine an individual's risk for

type 1 diabetes should also include T-cells screening, although they are more difficult to measure.

Conclusion

Type 1 diabetes is a complex disease that is influenced by many different factors, some known and many unknown. Currently, why diabetes occurs (destruction of insulin producing β -cells) is known, but what triggers it and exactly what leads up to this final precipitating event is unknown. Researchers and doctors have a few tools to try to identify the pathogenesis of diabetes by examining the presence of autoantibodies and the genetics of an individual. There are certain combinations of genetic risk factors that greatly increase an individual's likelihood of developing diabetes. But, in order to better understand the present direction of research, understanding the past history of the disease is important.

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Chapter 2

Brief History of Diabetes:

Introduction

Diabetes is a disease that has been documented for thousands of years. Many of the big breakthroughs for understanding diabetes did not occur until the last one hundred years, but there were numerous small steps that led up to these important discoveries. To understand what led up to the current Genome Wide Association Studies (GWAS) that have revolutionized the field, understanding the discoveries that came before is essential to fully appreciate the state of the field today.

Ancient Times---"To Pass Through"

In the Ebers Papyrus, an ancient Egyptian text from ~1500 B.C.E., a disease (presumed to be diabetes) is referenced that causes "great emptying of the urine" (1) and excessive thirst (2). The term "diabetes," a literal translation from Greek as "to pass through," was first used by the Apolonius of Memphis (230 B.C.E.) (1). The naming most likely referred to the continuous urination and wasting away of affected individuals (3). The Greek physician Aretaeus (from 80-138 A.C.E. Cappadocia) noted the sweet taste of diabetic urine (2) in his work "On the Causes and Indications of Acute and Chronic Diseases," (1) an exhaustive analysis of the disease.

Diabetes is a dreadful affliction, not very frequent among men, being a melting down of the flesh and limbs into urine. The patients never stop making water and the flow is incessant, like the opening of the aqueducts...The patients are affected by nausea, restlessness and burning thirst, and within a short time they expire. (1,4)

Numerous allusions to diabetes are referenced in cultures of India, China and Middle East (1,3); for instance in 5th century India, physicians Sushruta and Charaka noted the appearance of two types of diabetes: one afflicting younger individuals and the other

affecting the heavier and older (1). Furthermore in 7th century China, physician Li Hsuan observed the susceptibility of diabetic patients to boils and lung infections. Although misleadingly concluding as treatment, an abstinence from sex and wine (1,3), these original observations lay the foundation for the discoveries of the 18th and 19th century.

Diabetes "Mellitus"

In 1670 Thomas Willis re-discovered the “sweet” tasting of urine in affected individuals (1). This “sweet” tasting compound was identified as sugar in 1776 by Matthew Dobson. This was deduced by procuring urine from a diabetic patient and performing various experiments on it: letting sit, boiling, evaporating and mixing with mineral acids.

Two quarts of this urine were, by a gentle, evaporated to dryness...There remained, after the evaporation, a white cake which weighed 3iv. 3ij. and ʒij. This cake was granulated, and broke easily between the fingers ; it smelled sweet like brown sugar. (5)

Matthew Dobson also noted that the level of glucose was elevated in the urine of patients with the disease and that the blood of patients was sweeter too (1,5). In 1788 Thomas Cawley, a surgeon, suggested there was connection between diabetes and the pancreas after he noted individuals that sustained pancreatic injuries developed diabetes (6,7).

John Rollo (1749-1809), a surgeon general in the British Army, was the first person to use the phrase diabetes “mellitus,” (Latin and Greek for "honey") when referring to diabetes. This was done to differentiate the two types of “diabetes” identified at the time; diabetes mellitus (sweet) and diabetes insipidus (tasteless) (1,3). Diabetes insipidus refers to a disease that manifests itself as excessive urination due to hormonal imbalance of vasopressin and is not at all related to diabetes mellitus (8). John Rollo with

assistance from William Cruickshank monitored the amount of sugar excreted by a Captain Meredith who had diabetes and severe glycosuria (sugary urine) (4). They monitored the amount of sugar in his urine by boiling it and weighing the sugar residue leftover. They also meticulously recorded the types of foods he ate. They noticed that breads, grains and fruits increased the sugar content in the urine and meats lowered it. After these observations they concluded the stomach was overproducing sugar from certain foods and recommended a diet low in carbohydrates and high in fat and protein. (4,9). This recommendation became the standard for future treatments of diabetes until the discovery of insulin (4). It should be noted for the treatment of type 2 diabetes this method worked well, but for type 1 diabetes it was lethal due to starvation (1).

Discovery of Insulin

The next big breakthrough in diabetes did not come until 1889 when Joseph von Mering and Oskar Minkowski found that by removing the pancreas of dogs they could trigger a diabetic state (excessive urination, intense thirst, hunger and weight lost), resulting in death of the dogs. However, their attempts to isolate this pancreatic compound failed (2,7). Jean de Meyer in 1910 postulated that this pancreatic chemical that was not being produced in diabetic patients be called "insulin." The term was derived from "insula" which means island in Latin referencing to its origin in the "islets of Langerhans" (10).

Diabetes

Ligate pancreatic ducts of the dog. Keep dog alive till acini degenerate leaving Islets. Try to isolate the internal secretions of these to relieve glycosurea

Frederick Grant Banting's lab notebook October 31, 1920, University of Toronto, Canada (1,11)

In 1921 Frederick Banting and graduate student Charles Best, utilizing John MacLeod's laboratory, began experiments into extracting pancreatic hormones from dogs with ligated pancreas and re-injecting the extract into dogs with removed pancreas (diabetic dogs). Banting and Best's experiments were effective in relieving diabetic symptoms, prolonging the diabetic dogs' lives. Later experiments used pancreas from fetal calves (no proteolytic enzymes present and were more readily available) and later adult bovines' pancreas when extraction techniques improved (12). The finding that from these pancreas extracts prolonged a diabetic dog's life from fourteen days to seventy days and prompted further experimentation. Banting enlisted James Collip, a biochemist, to help further purify the compound they called "isletin" (1,4,12). The compound "isletin" was later renamed by MacLeod to "insulin" to recognize de Meyer's original naming, which was not known at the time (1).

Human diabetic patients were first tested in January 1922, with this compound called "insulin" with very positive results: immediate effects on lowering blood glucose levels (12). Leonard Thompson, a fourteen year old boy, was the first diabetic patient tested and his life was prolonged 13 years with ongoing insulin therapy. He died at the age of 27 from pneumonia (1).

Interestingly, the group then had difficulties isolating the compound again, but with assistance from a small company named Eli Lilly, the compound was successfully

isolated and produced on a large scale. The breakthrough in large scale production came from the observation of a chemist, George Walden, at Eli Lilly who noticed maintaining insulin at its isoelectric point (no charge) could allow for maximum isolation and extraction from beef or pork pancreas (4,13). In 1923 Banting and Macleod received the Nobel Prize for discovering insulin. (4).

Insulin immediately became a "wonder" drug, drastically changing the lives of diabetics who would have certainly faced premature deaths without treatment (4,14). In the years following the discovery of insulin, breakthroughs occurred in improved production, knowledge of its structure and variations in the types used (4). Even though a successful treatment for diabetes was found, a reclassification of the disease itself was needed to better understand and study the mechanism underlying diabetes.

Two Diseases: Type 1 and Type 2

Over the course of years after insulin was discovered various classification schemes were adopted to describe diabetes. Prior to 1976 the classification of diabetes was based on phenomenological observations and was extremely confusing (15). The terms juvenile onset and maturity onset diabetes were also in popular usage. These terms would be replaced by insulin dependent diabetes (IDDM) and non-insulin-dependent diabetes mellitus to make the classification less dependent on age at onset and more representative of the disease mechanism (15). In 1976 Andrew Cudworth reintroduced the terms type 1 and type 2 diabetes (John Lister had previously used these designations in 1951) (15,16). This time the designations caught on and in 1979 these terms were

officially adopted and standardized by the National Diabetes Data Group Committee to the present day usage: type 1 diabetes (previously IDDM or juvenile onset diabetes) and type 2 diabetes (NIDDM or adult onset diabetes) (4). Interestingly H.P Himsworth originally postulated in 1939 that diabetes had two types: lack of insulin or the resistance to insulin, however it took 40 years for this idea to finally catch on (4).

1970 - Present

Since 1979 there have been updates to the official classification of diabetes to include rarer forms (4). As diabetes was in the midst of re-classification, the scientific field was changing rapidly as well, laying the foundation for a better understanding of type 1 diabetes. The first genetic locus identified to be involved in type 1 diabetes was the HLA region in 1973 in a candidate gene study through serotyping (17). This was followed by a candidate gene association study that identified insulin in 1984(18), a linkage study identifying *CTLA-4* in 1996 (19) and in more recent years *PTPN22* (20) and *IL2RA* (21) were identified in candidate gene association studies.

In the 1990's and early 2000's genome wide linkage studies were performed using microsatellite markers. These relatively infrequent markers were statistically underpowered for detecting new genes affecting type 1 diabetes and only could re-validate known regions (22). Microsatellite markers were replaced with single nucleotide polymorphisms (SNPs) to investigate disease association with much deeper coverage on a greater genomic scale (although at moderate effect sizes) (23-25). The first comprehensive Genome Wide Association Study (GWAS) for type 1 diabetes using

SNPs was reported in 2007 and completely changed the field (26,27). The major genetic findings from these studies for type 1 diabetes will be discussed to a greater extent in chapter three.

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Chapter 3

The Genetics of Type 1 Diabetes

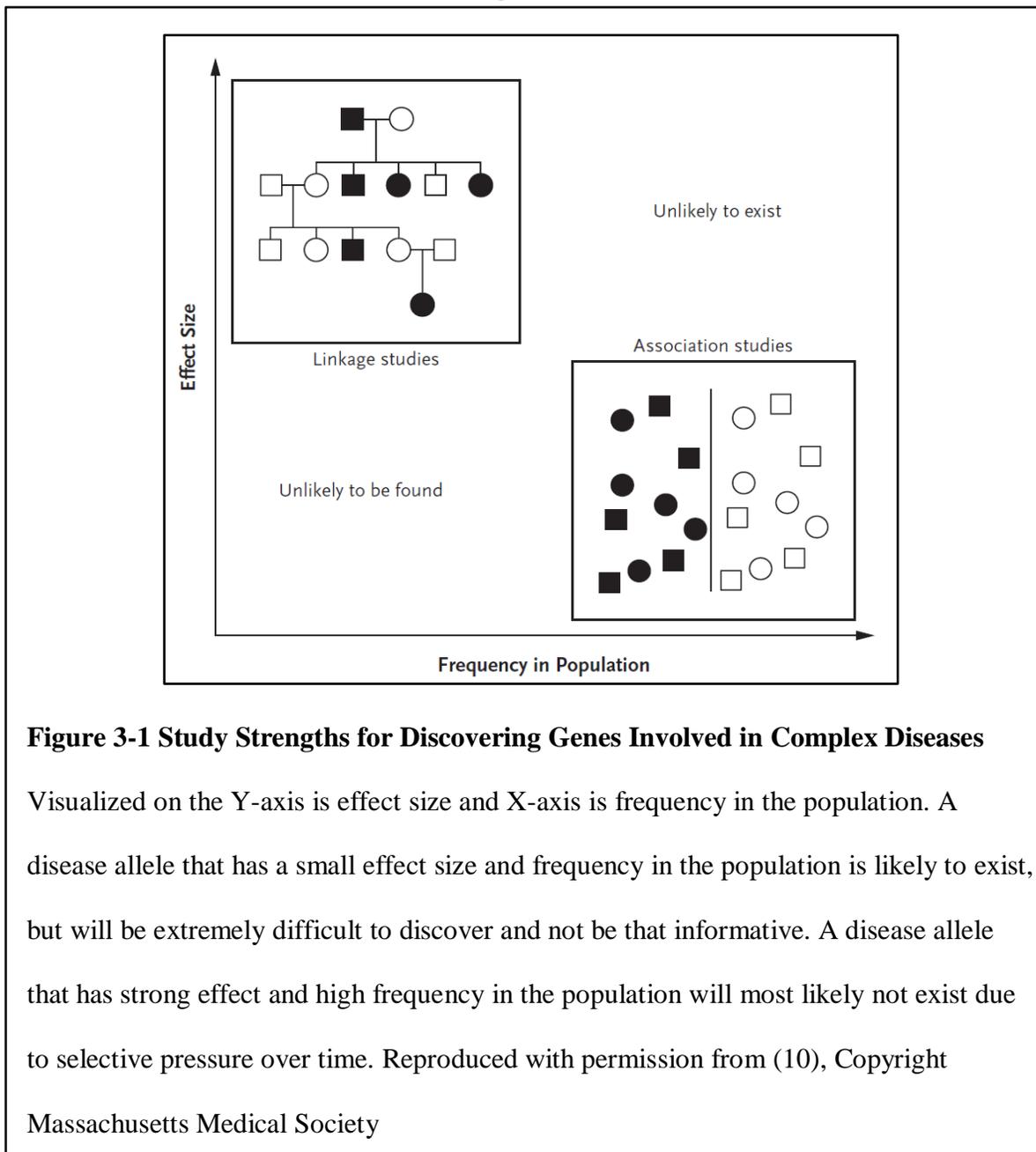
Introduction

Type 1 diabetes is considered a complex disease that arises due to the effects of both genetic and environmental factors evident by <100% concordance between monozygotic twins (1-6). The most prevalent form of type 1 diabetes is thought to occur due the interaction of multiple genes (polygenic) and does not appear to show any clear pattern of inheritance though it does aggregate in families (6,7). It should be noted there are less common forms of type 1 diabetes that are monogenic and are immune-mediated, but these types will not be discussed further (8,9). Due to the ambiguity about the pathogenesis of type 1 diabetes and the exact genes involved, genetic studies have been performed that make few assumptions about the disease (model-free). Two study approaches that are commonly utilized in studying type 1 diabetes are linkage studies and association studies (10).

In linkage studies, affected related individuals (such as siblings) are investigated for identical chromosomal regions that are shared more frequently than expected by Mendelian inheritance. Linkage of the marker and the locus that confers susceptibility for the disease is identified by the accumulation of data across numerous families investigated. In general, linkage studies work well when the overall effect of the risk allele is large and the overall frequency of the allele is low in a population (Figure 3-1). However, linkage studies implicate regions of DNA that are many megabases long, which then require intensive investigation using fine mapping techniques to identify the causative risk variant (10,11). In association studies, case (affected) and control (unaffected or general population) groups are compared based on frequencies of specific

marker alleles within candidate genes, pathways or chromosomal regions. Association studies work well at discovering alleles that have a moderate to high frequency in the population, even if they have a small effect size (Figure 3-1) (10). An issue with association studies is carefully matching the control population for comparison; however, this can be avoided by utilizing the transmission disequilibrium test (TDT) and an affected sib-pair population. The TDT test investigates the number of times a marker allele is transmitted and not transmitted in the cases population (11,12). Association studies take advantage of linkage disequilibrium (LD) in the human genome, exploiting the situation where an allele (testable polymorphic marker) is in linkage disequilibrium with a causative variant. LD is the situation where specific allelic combinations that are relatively close to each other are recombined at a lower frequency than would be predicted (11). Linkage disequilibrium can span from a few hundred bases up to a few hundred kilobases, making identification of the causative variant much simpler than linkage study. (10).

Figure 3-1



Genetic Linkage Studies

The first genome wide genetic linkage study for type 1 diabetes was performed in 1994 (13). This study reported linkage with human leukocyte antigen (HLA), insulin and 18 other regions. This was followed up with other genome wide linkage studies in different populations in 1998 (14,15), 2001 (16) and ultimately ended with a comprehensive study that combined all prior studies in 2005 (17). These linkage studies further validated the HLA region as being the major risk locus for type 1 diabetes (10). Many of the other regions identified in linkage studies have been inconsistently seen because they are either false positives or when combining many different families, population heterogeneity is masking the true effects (10). However, a small scale candidate gene linkage study did identify *CTLA-4* gene in 1996 as a risk for type 1 diabetes (18).

Candidate-Gene Association Studies

As previously mentioned, the first gene region identified to be involved with type 1 diabetes was HLA in 1973 (19) through a candidate gene study using serotyping. The next couple of genes discovered were *INS* insulin in 1984 (20), *PTPN22* in 2004 (21) and *IL2RA* in 2005 (22). However, candidate gene association studies require prior knowledge about a gene or region. The field of association studies was completely revolutionized by the development of genome wide association studies (GWAS) which utilized tagging single nucleotide polymorphisms (SNPs) for high-throughput screening of the entire genome and requiring no prior knowledge of a region to implicate it (23-25).

GWAS became feasible due to the availability of fine resolution SNP maps of the whole genome. In addition, knowledge of the linkage disequilibrium patterns in human populations decreased the number of SNPs that needed to be genotyped in order to cover the genome.

GWAS

One of the first GWAS was performed in 2005 on patients with age related macular degeneration (AMD) (26). The first type 1 diabetes GWAS, performed in 2006 using non-synonymous SNPs, identified *IFIH1* in association, however SNP coverage and statistical power was very poor (27). The first comprehensive GWAS that interrogated the entire human genome for type 1 diabetes was performed in 2007 (28). Since that initial study another GWAS was performed with much greater SNP coverage (29) along with a comprehensive meta-analyses (30,31) and numerous follow-up studies that interrogated the identified regions more thoroughly (32-34). GWAS studies have greatly increased the number of type 1 diabetes loci to over fifty reported loci that confer low to high risks. In Figure 3-2, the odds ratios for forty-nine of these loci that are most significantly associated with type 1 diabetes are graphed (note: HLA is excluded but confers an odds ratio of 6.8) (10,35). An odds ratio of one means the event can occur with equal likelihood in both the affected group and controls. An odds ratio greater than one means the event has a greater likelihood to occur in the affected group (36). An odds ratio less than one means the event is less likely to occur in the affected group. When

analyzing alleles (major/minor) switching to the risk allele allows for correction of the odds ratio, so that all values are greater than one.

Figure 3-2

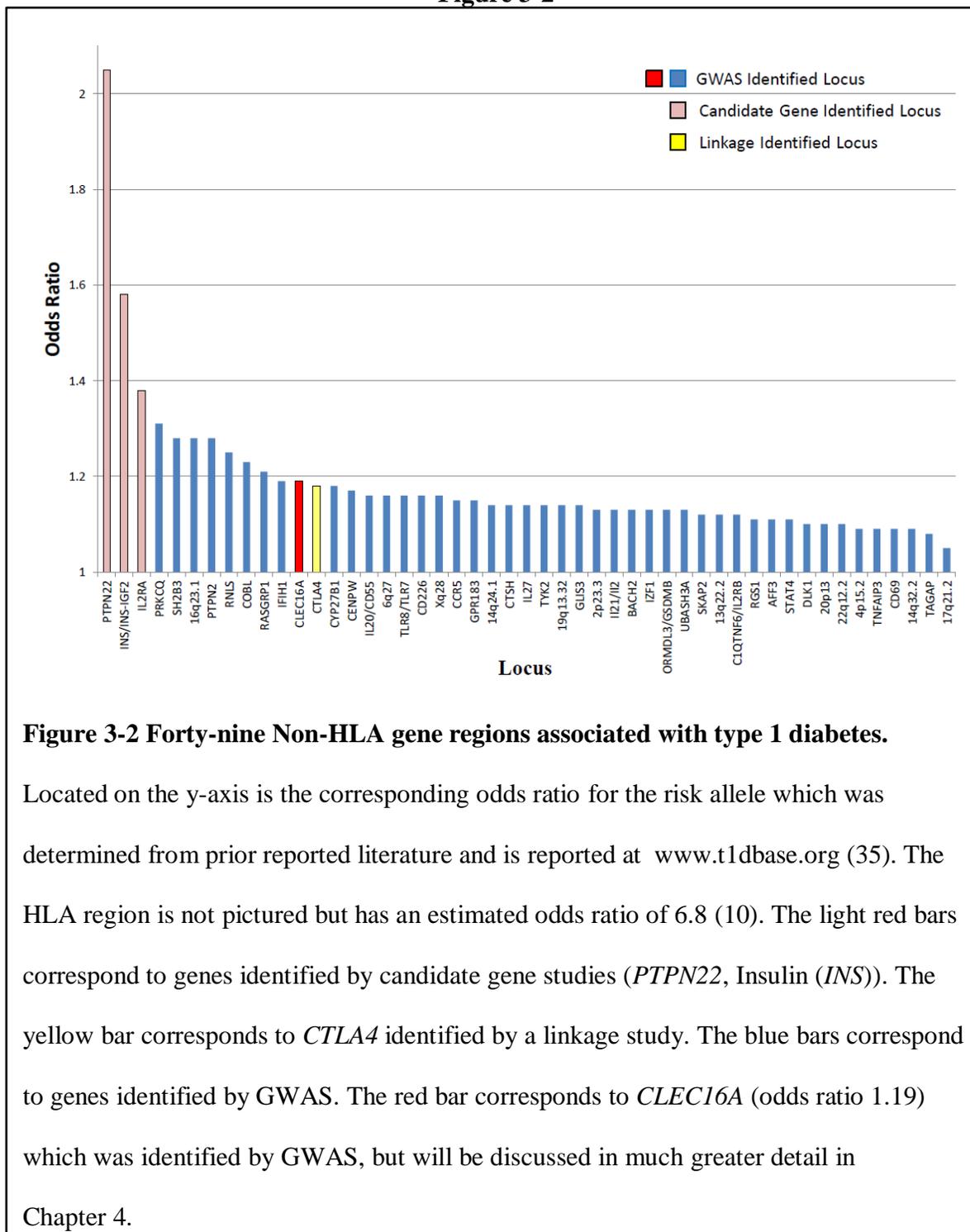


Figure 3-2 Forty-nine Non-HLA gene regions associated with type 1 diabetes.

Located on the y-axis is the corresponding odds ratio for the risk allele which was determined from prior reported literature and is reported at www.t1dbase.org (35). The HLA region is not pictured but has an estimated odds ratio of 6.8 (10). The light red bars correspond to genes identified by candidate gene studies (*PTPN22*, Insulin (*INS*)). The yellow bar corresponds to *CTLA4* identified by a linkage study. The blue bars correspond to genes identified by GWAS. The red bar corresponds to *CLEC16A* (odds ratio 1.19) which was identified by GWAS, but will be discussed in much greater detail in Chapter 4.

GWAS have helped re-confirm known loci such as *HLA*, *INS*, *PTPN22*, *CTLA4* and *IL2RA* whose specific genetic involvement in type 1 diabetes has been elucidated to some extent by prior studies. The current dilemma is that instead of having a shortage of additional loci to investigate (problem in the 1990's), there are now a multitude of possible candidate regions. To better focus time and resources, loci that are involved in specific biochemical pathways or shown to overlap with other autoimmune disorders are currently being prioritized for further interrogation.

For example, the initial non-synonymous GWAS study identified *IFIH1* gene in association with type 1 diabetes (27,34). *IFIH1* codes for the protein melanoma differentiation-associated gene 5 (*mda5*), which is involved in the recognition of double stranded RNA (dsRNA) from picornaviruses (37,38). This feature of *mda5* is exciting because, as previously mentioned, one of the possible environmental triggers of type 1 diabetes is suspected to be a virus. Specifically, it has been hypothesized that the Coxsackievirus B4, a virus in the picornavirus family, is involved in type 1 diabetes (39-41). The SNP rs1990760 in *IFIH1* codes for a non-synonymous mutation of an alanine to threonine (A946T) (27). Recently it was found that the SNP was associated with different frequencies of enterovirus RNA in the blood of healthy children, with heterozygous individuals having the highest amount (42).

Another way to investigate these new loci is to determine whether any of these regions overlap with other autoimmune related disease associated regions, which may hint at a common pathogenic mechanism. For example SNPs in the *CLEC16A* region were identified in association with both type 1 diabetes (28) and multiple sclerosis (43).

The association with type 1 diabetes risk maps to a locus that is composed of four genes; *CIITA*, *DEXI*, *CLEC16A* and *SOCS1*. Two of these genes are good candidates for an immune related disorder; *CIITA* is a positive regulator of MHC class II molecules (44) and *SOCS1* is involved in the negative regulation of cytokines (45). The other two genes in this region; *DEXI* and *CLEC16A* currently have unknown functions, making this region even more perplexing and important to decipher. Further exploration of this entire region will be the focus of chapter 4.

Clearly understanding which of these loci truly affect type 1 diabetes is important in understanding the disease. The next section explores how *HLA*, insulin, *CTLA-4*, *PTPN22* and *IL2RA* confer genetic risk in the disease.

HLA (IDDM1)

The Human Leukocyte Antigen (HLA) region was the first region identified in association with type 1 diabetes and confers the largest risk. As shown in Figure 3-2, the odds ratio for the association of the HLA region with type 1 diabetes is 6.8, which is significantly larger than any other locus (odds ratios usually between 1.2 - 1.3, excluding *PTPN22* and insulin) (10). The HLA region located on chromosome 6 at the region 6p21.1-21.3 codes for three classes of major histocompatibility complex (MHC) molecules (MHC class I, MHC class II, and MHC class III), with each class consisting of several genes (Figure 3-3). MHC class I molecules are expressed on all nucleated cells and present antigens derived from the cytoplasmic proteins and activate CD8⁺ T cells against abnormal cells. MHC class II molecules are expressed on certain antigen

presenting cells (APC), such as macrophages and dendritic cells that present external antigens to CD4⁺ T cells. CD4⁺ T cells activated by specific peptides in the context of APCs are involved in B cell proliferation and antibody production. MHC class II molecules are also involved in antigen processing such as tapasin, DM, DO and proteasome. MHC class III molecules code for molecules involved in other immune related processes like complement, cytokines and heat shock proteins (46).

Figure 3-3

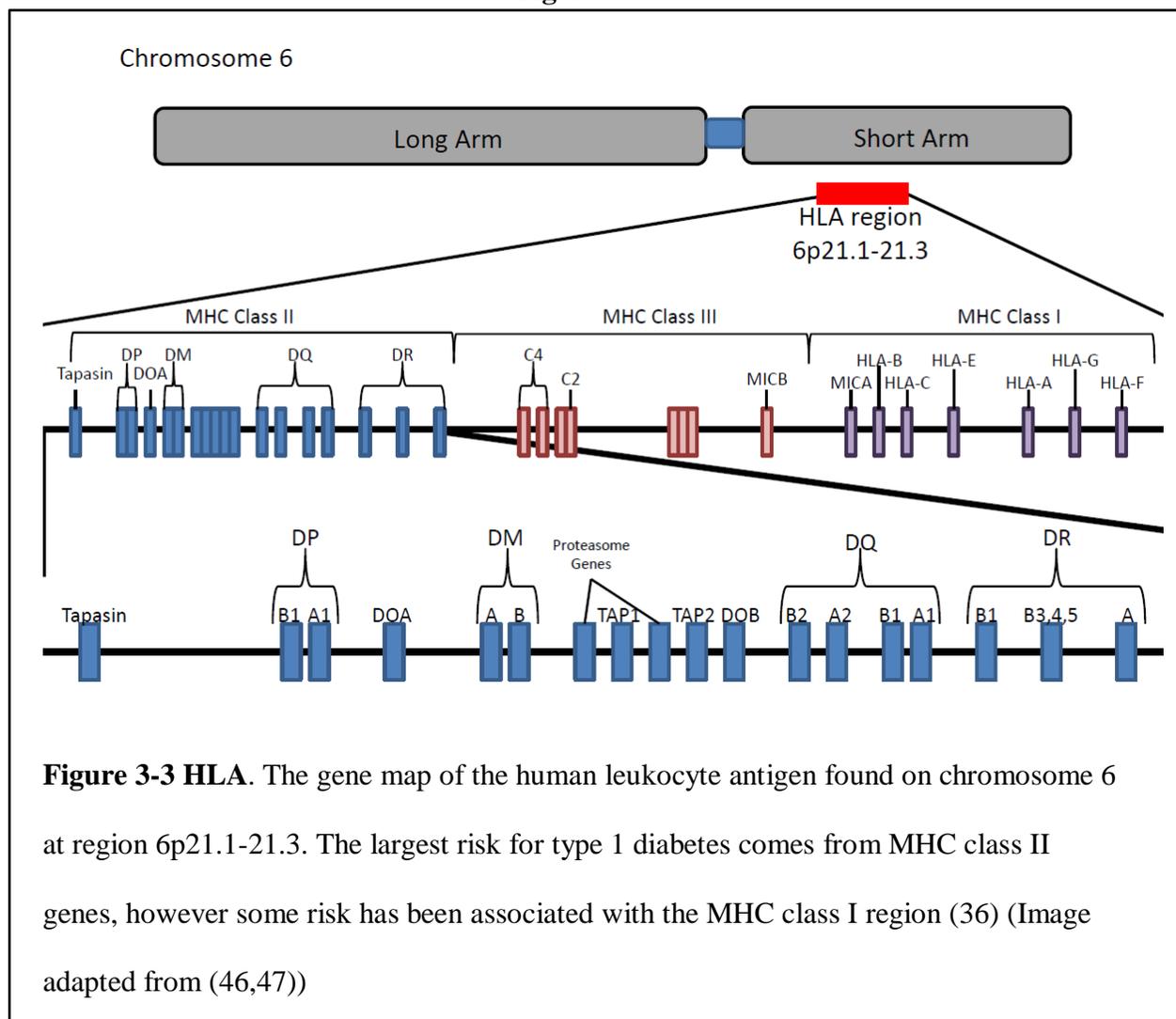


Figure 3-3 HLA. The gene map of the human leukocyte antigen found on chromosome 6 at region 6p21.1-21.3. The largest risk for type 1 diabetes comes from MHC class II genes, however some risk has been associated with the MHC class I region (36) (Image adapted from (46,47))

The nomenclature for the region starts with a four character alphanumeric code which refers to the locus, followed by an asterisk and four digits which refer to the allele at the locus. For example in DQB1*0302, the 0302 refers to the allele at the highly polymorphic locus DQB1 which is located in MHC class II (48).

The HLA region was first implicated in association with type 1 diabetes in the 1970's through a candidate gene study that was based on prior studies implicating HLA in autoimmune disorders. Originally the MHC class I antigens (B8 and B15) were reported to be in association with type 1 diabetes (19,49,50). Much stronger associations were then found with the MHC class II molecules HLA-DR and HLA-DQ (36,51-56). The prior association with B8 and B15 was detected due to high linkage disequilibrium among MHC molecules (B8 and DR3, and B15 and DR4) (51,57,58). However, MHC class I molecules do confer some risk in type 1 diabetes (discussed later).

Since the original association of MHC class II with type 1 diabetes was discovered, studies have shown a hierarchy of gene/haplotype combinations within MHC II that range from protective to high risk for development of type 1 diabetes (59,60), differing slightly among different ethnicities (61-65). For example in Caucasians of European descent the haplotype DRB1*1501-DQA1*0102-DQB1*0602 was found to be strongly protective and occurring in ~20% of the population, but is only seen in ~1% of diabetes patients (60). The highest susceptibility for type 1 diabetes in Caucasians is found in individuals who are heterozygous for the haplotypes DR3/DR4-DQ8 (note: this can also be written as DR3/DR4-DQ2/DQ8 or DR3/DR4) (36,60,66). Currently 30-50% of new type 1 diabetes cases have the DR3/DR4-DQ8 genotype, which only occurs in

2.4% of the general population (67). One hypothesis for the increased risk from the haplotypes is that slight changes in the amino acid codes change how the MHC II molecules present antigen peptides that favor T-cell activation and result in the attack against self antigens in the pancreatic β cells (60,66).

It would appear MHC class II molecules confer the largest risk in development of type 1 diabetes, however the MHC class I molecules have been re-implicated in association with type 1 diabetes, but to a much lesser extent than MHC class II molecules (68-73). After adjusting for the strong association of MHC class II molecules, MHC class I molecules HLA-B and HLA-A genes were identified to confer a risk in disease (74). The HLA-B and HLA-A genes appear to modify the severity of an individual's disease risk; with certain alleles being associated with age of diagnosis and overall risk of developing type 1 diabetes (67,75-79).

On the functional side there is evidence that $CD8^+$ T-cells, which are activated by APC presenting MHC class I molecules, drive the progression of the β -cell destruction in the pancreas (80,81). This finding was supported by studies showing that MHC I molecules (allele HLA-A*02) loaded with beta cell antigens react strongly with $CD8^+$ cytotoxic T-cells (CTLs) from type 1 diabetes patients' peripheral blood (82-84). The selection of HLA-A*02 allele (also written as HLA-A2 allele) was based on the fact that it is found in >60% of type 1 diabetes patients (67,69). This allele is also correlated with increased risk of developing type 1 diabetes when found in individuals with the high risk haplotype DR3/DR4-DQ8 (67,69). In transgenic NOD mice (mouse model of type 1 diabetes) expressing HLA-A*02, the onset of diabetes was accelerated (85). These

studies support a role for MHC class I molecules in risk of type 1 diabetes, adding to the risk conferred by MHC class II molecules (36).

Insulin (*INS*) (IDDM2)

In 1984 a polymorphism located in the 5' region of the insulin gene was identified in a candidate gene study to be associated with type 1 diabetes in a Caucasian population (20). The association was with a "variable number of tandem repeats" (VNTR) region located in the promoter of insulin (86-89). The VNTR region could be classified into three different groups based on the size of the VNTR region (20,90,91). Individuals with the shortest VNTR (class I) were found to be at the highest risk for type 1 diabetes and individuals with the longest VNTR (class III) were protected from type 1 diabetes (20,92,93). The medium length VNTR (class II) rarely occurs in Caucasians (20,91). It was found that the short VNTR (class I) risk allele decreased expression of insulin in the thymus and increased expression in the peripheral tissue, while the protective, longest VNTR (class III) showed higher expression in the thymus and lower expression in the peripheral tissue (66,86,93-95). It is hypothesized that individuals with the risk associated "short" class I VNTR have less expression of insulin in the thymus and therefore negative selection of autoreactive T cells for insulin is less efficient. Whereas in the "long" class III VNTR individuals the selection is more efficient, preventing the production of autoreactive T-cells for insulin (94,95).

CTLA-4 (IDDM12)

Cytotoxic T lymphocyte-associated protein 4 (*CTLA-4*) gene was first identified as a susceptibility locus for type 1 diabetes in a 1996 linkage study (18) and was confirmed in a multi-ethnic association study in 1997 (96). *CTLA-4* is involved in negative regulation of T-cells. The exact mechanism of how it regulates T-cells is unknown, but it is speculated that it functions by directly binding B7 (on APC cells) and competitively blocking CD28 from binding, or it binds B7 and sends an inhibitory signal (phosphatases) damping the TCR and CD28 signal, blocking T-cell activation (46,97). When the *CTLA-4* gene was knocked out in a mouse it resulted in severe lymphoproliferation (over production of immune cells) that resulted in early lethality (98). This finding hints that *CTLA-4* is an essential molecule in the negative regulation of the immune system. The risk associated with *CTLA-4* has also been replicated in other autoimmune related diseases like multiple sclerosis (MS) (99), systemic lupus erythematosus (SLE) (100), rheumatoid arthritis (101), Grave's disease (102) and Addison's Disease (103). Currently three polymorphism types have been reported that could influence *CTLA-4*: SNPs in the promoter of *CTLA-4*, a non-synonymous SNP in exon 1, and microsatellite repeats in the 3'UTR (97,104-106). All three polymorphisms are in linkage disequilibrium with each other and deciphering the true causative variant is difficult because the three variants almost always co-occur (107), though a meta-analysis from 2005 suggests the SNP in exon 1 is the true risk variant (108). One of the SNPs in the promoter region of *CTLA-4* (318 C→T) was found to increase promoter activity and increase *CTLA-4* expression (104). The exon 1 polymorphism (SNP rs231775 49A→G)

results in a non-synonymous amino acid change from threonine to alanine at residue 17 (T17A). In-vitro, the non-synonymous variant, resulted in CTLA-4 being processed incorrectly in the endoplasmic reticulum resulting in less surface expression of the protein (105). In a study of myasthenia gravis patients (autoimmune neuromuscular disease) the 3'UTR polymorphism (longer AT)_n) was found to affect mRNA stability and reduced CTLA-4 expression (106). The risk variants appear to reduce the amount of CTLA-4 expressed (either through reduced mRNA expression or reduction of final protein expression) increasing T-cell activation and increasing the risk of autoimmunity. However, further investigation is necessary due to conflicting reports for both effects on expression and for association with autoimmune disease.

PTPN22

A SNP (rs2476601) in the *PTPN22* gene, which produces the lymphoid protein tyrosine phosphatase (LYP), was originally identified in a candidate gene study in 2004 to be associated with type 1 diabetes (21,109). *PTPN22* (LYP) forms a complex with C-terminal Src kinase (CSK) to negatively regulate the T-cell receptor (TCR) (110). LYP functions by dephosphorylating the proteins involved in the TCR signaling cascade like Lck (Src family kinase), the ITAMs of TCR ζ /CD3 complex, Zap70, Vav and valosin (111).

The SNP (rs2476601) is located in a coding exon (1858C→T) and results in non-synonymous amino acid change (arginine to tryptophan) at residue 620 in the LYP protein (R620W) (21,29). This same SNP has also been confirmed to be associated with

numerous other autoimmune diseases like rheumatoid arthritis and systemic lupus erythematosus (110,112,113). It has been found that the variant allele disrupts the interaction of LYP and CSK (21). Currently there are two theories (loss of function/gain of function) that predict how the mutations could affect function of a T-cell with evidence that supports both models (36). If the mutation causes a loss of function, it could mean that autoreactive T-cell in the periphery could become more active (hyperactivity) and cause more damage. This loss of function hypothesis is consistent with a mouse model where the mouse orthologue of LYP, PEST-enriched tyrosine phosphatase (PEP) (110), was knocked out and an expanded T-cell population occurs (114). If the mutation causes a gain of function, it could mean that T-cell activation is reduced which could allow autoreactive T-cells to escape negative selection in the thymus (110). This gain of function model was seen in T cells from heterozygous carriers of the allele who had less phosphorylated proteins targeted by LYP and also showed less T-cell signaling (115,116). Interestingly, there also appears to be a dose dependent factor with the *PTPN22*'s SNP rs2476601 risk allele (T) in some autoimmune diseases, meaning the number of copies determines overall risk (10,109,117,118). Also, the polymorphism R620W appears to affect B cells. The polymorphism affected B cell receptor (BCR) signaling (signal reduction) and also favored production of autoreactive B cells and antibodies (66,116,119,120).

IL2RA

The interleukin (IL)-2 receptor α gene (*IL2RA*) was identified in type 1 diabetes candidate gene association studies in 2005 (22) and was re-confirmed and fine-mapped in numerous follow up studies (28,121,122). The region has also been found in association with multiple sclerosis (123). The *IL2RA*, also known as CD25, is one of three non-covalently associated proteins that make up the interleukin-2 receptor. The interleukin-2 receptor is composed of *IL2RA*, *IL-2/15R β* and γ_c (46). *IL2RA* is the only subunit that is unique to the interleukin-2 receptor, the other two subunits are found in other cytokine receptors.

When cytokine interleukin-2 (IL-2) is released by a T cell, it binds to the *IL-2R $\alpha\beta\gamma_c$* complex and signal transduction occurs through *IL-2/15R β* and γ_c to activate the Jak3-STAT5 signal transduction pathway (46,124). All three subunits are required for high affinity binding of interleukin-2 (124). Interleukin-2 is important for T-cell proliferation and survival and is essential for Tregs (T regulatory cells) to survive (124). Multiple sclerosis patients have an increased amount of soluble *IL2RA* (s*IL2RA*) in circulation (125). The levels of s*IL2RA* in multiple sclerosis patients correlate with certain SNP variants and disease severity (122,123,126). An explanation for this observation is that s*IL2RA* can bind to circulating IL-2 and impair Treg function and disease variants in multiple sclerosis appear to increase s*IL2RA* levels (36). However, in type 1 diabetes patients the risk variants correlate with lower levels of s*IL2RA* (122,123). This lower level of s*IL2RA* in type 1 diabetes patients was also reported in in-vitro stimulated peripheral blood mononuclear cells (PBMCs) (127). Interestingly, normal

levels of Tregs can be found in type 1 diabetes patients (128), however, their ability to suppress effector T-cells is inhibited(129). A possible explanation is a risk polymorphism in the IL2RA receptor causes a defective receptor causing lower expression of the receptor and/or poorer IL-2 signaling in Tregs, which ultimately results in inhibited Treg function. Supporting this idea are two different studies performed in healthy individuals. In one study individuals with the risk haplotype have lower IL2RA levels (130). Whereas in another study they found individuals with the risk haplotype have reduced interleukin-2 signaling in memory T cells and Tregs and a reduction in Treg ability to suppress effector T-cells (131). Clearly, *IL2RA* is important in T-cell regulation and different autoimmune disease loci affect *IL2RA* in different ways. However, both pathways appear to result in less interleukin-2 being recognized by T-cells (defective production of IL2RA or higher levels of sIL2RA) which drastically affects Tregs and inhibits their ability to function properly (36).

Conclusion

Deciphering the risks involved in type 1 diabetes will take time and resources. In the last couple of years, major strides have been made in identifying multiple genetic risk regions in addition to those identified prior to GWAS. The challenge is to understand how these loci contribute to the risk of type 1 diabetes and other autoimmune disorders.

To understand all these novel gene regions we begin by fine mapping the regions to locate the true causative gene variant. GWAS help to narrow the risk region down to a linkage disequilibrium block that could contain many genes. In the type 1 diabetes

associated loci identified by GWAS, the average number is 8.5 protein-coding genes per region (132). The tagging SNP could be in linkage with the true causative variant and so fine mapping with greater coverage (sequencing to identify additional SNPs in the region) is needed. After locating the variant(s) most significantly associated with risk, deciphering its role in a gene will be important in determining whether it is causative to disease risk: does it influence the protein directly, or does it influence neighboring genes? Risk associated SNPs can be assessed for effects on expression of the gene or neighboring genes. The next step would be determining how the change in expression of these genes increases risk for type 1 diabetes. Such a study as described above will be the focus of Chapter 4 where we investigated chromosomal region 16p13.13 and its role in type 1 diabetes.

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Accessed 7-04-2013

Chapter 4:

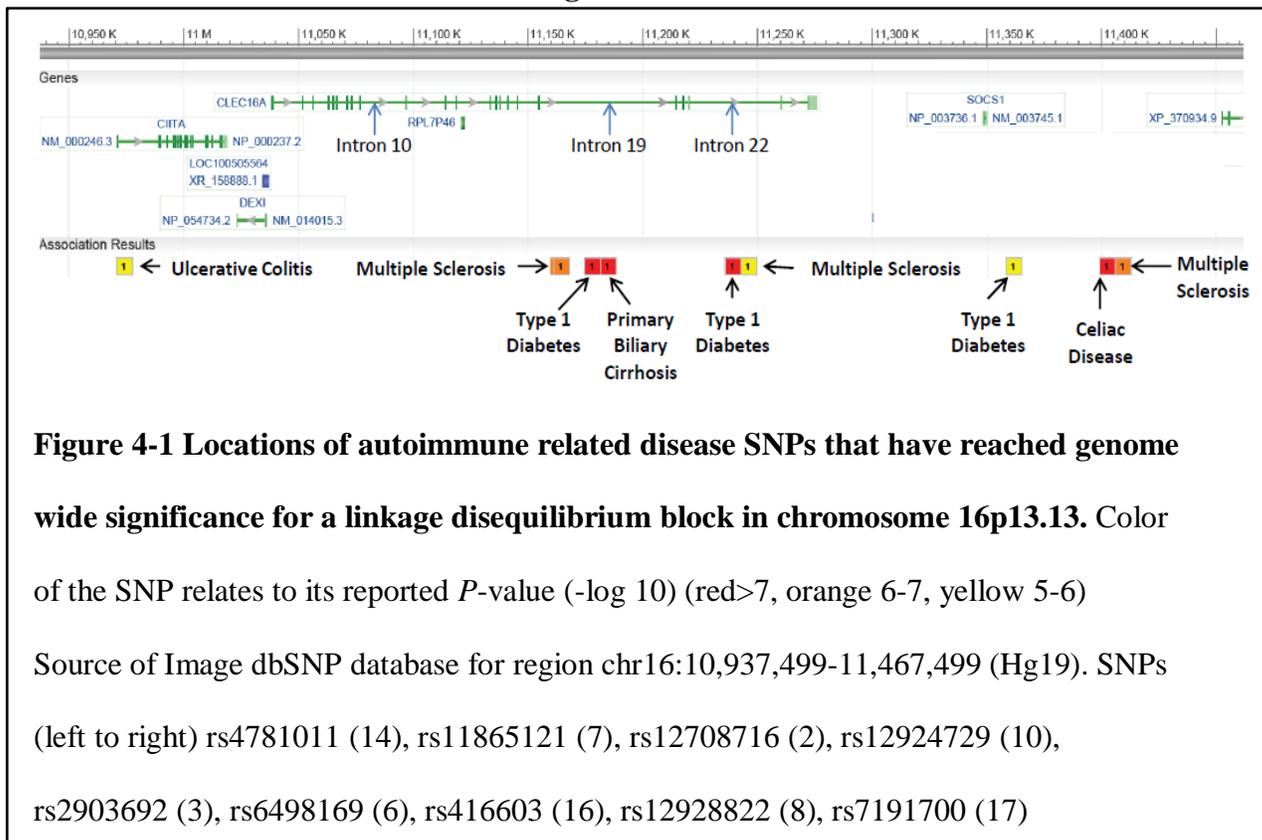
Chromosome 16p13.13 and Its Role in Type 1 Diabetes

Introduction

Background Information

As mentioned in previous chapters prior to 2007, a small number of genetic loci that contributed to type 1 diabetes risk were identified through linkage and candidate gene studies including *HLA*, *INS*, *IL2RA*, *CTLA4* and *PTPN22* (1). With the advent of genome-wide association studies (GWAS) over 40 additional loci have been identified that confer low to moderate risks of developing type 1 diabetes (Odds Ratios, OR, ≤ 1.3)(2). One of these regions is located at chromosome 16p13.13 and is associated with type 1 diabetes and several other autoimmune disorders, including Multiple Sclerosis (MS), celiac disease, Primary Biliary Cirrhosis (PBC), Systemic Lupus Erythematosus, Crohn's Disease, Ulcerative Colitis and primary adrenal insufficiency (Figure 4-1) (3-15).

Figure 4-1



The specific region on chromosomal region 16p13.13 implicated in autoimmunity spans approximately 530 KB from position 10,937,499-11,467,499 (build Hg19) (Figure 4-2). The most significant evidence of association with type 1 diabetes was with two SNPs, rs12708716 and rs2903692, located in the different introns of a gene of only inferred function, *CLECI16A*, previously known as *KIAA0350* (2,3). Complicating the interpretation of these results is the fact that neighboring genes appear to be stronger candidates for playing a role in type 1 diabetes pathogenesis based on their known functions. The region contains 4 genes *CIITA*, *DEXI*, *CLECI16A* and *SOCS1*.

Figure 4-2

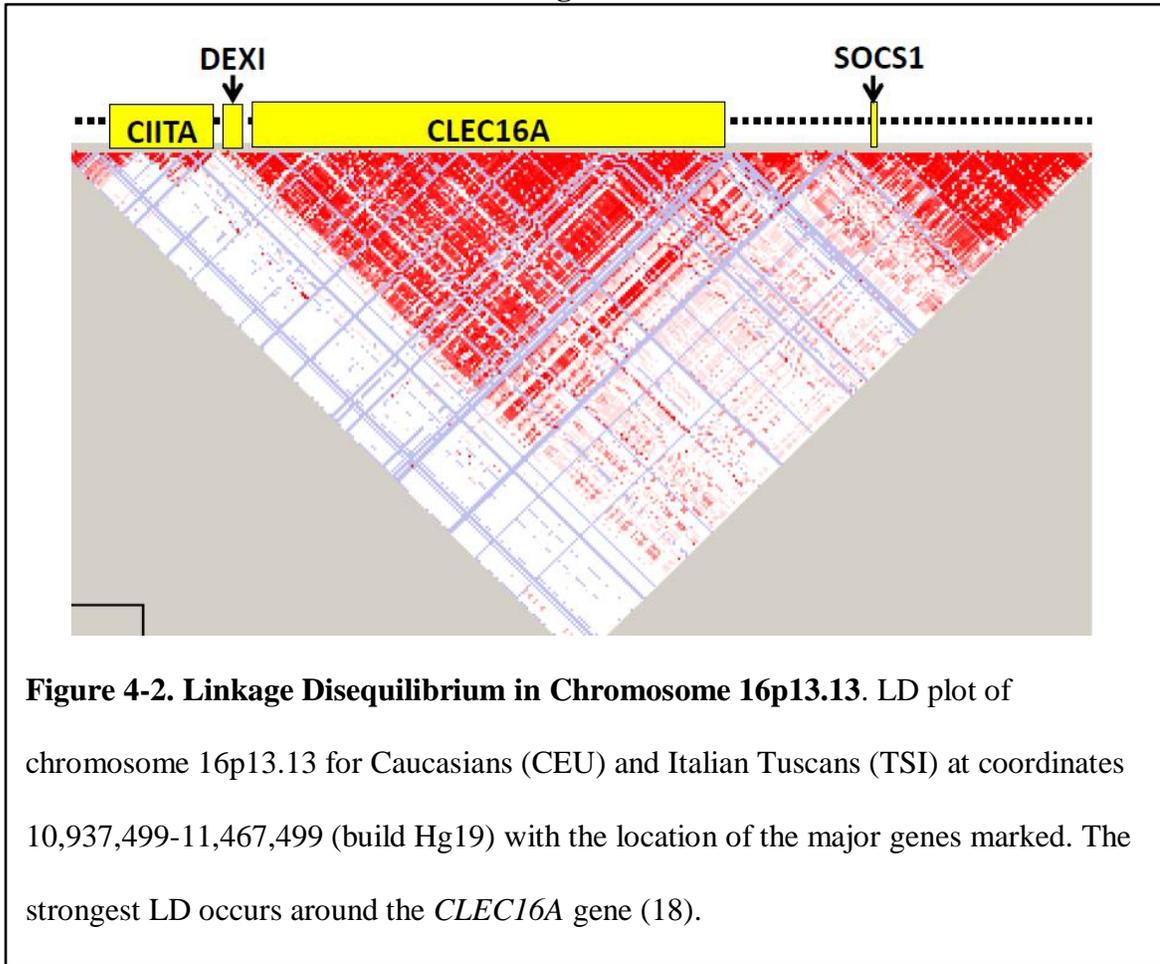
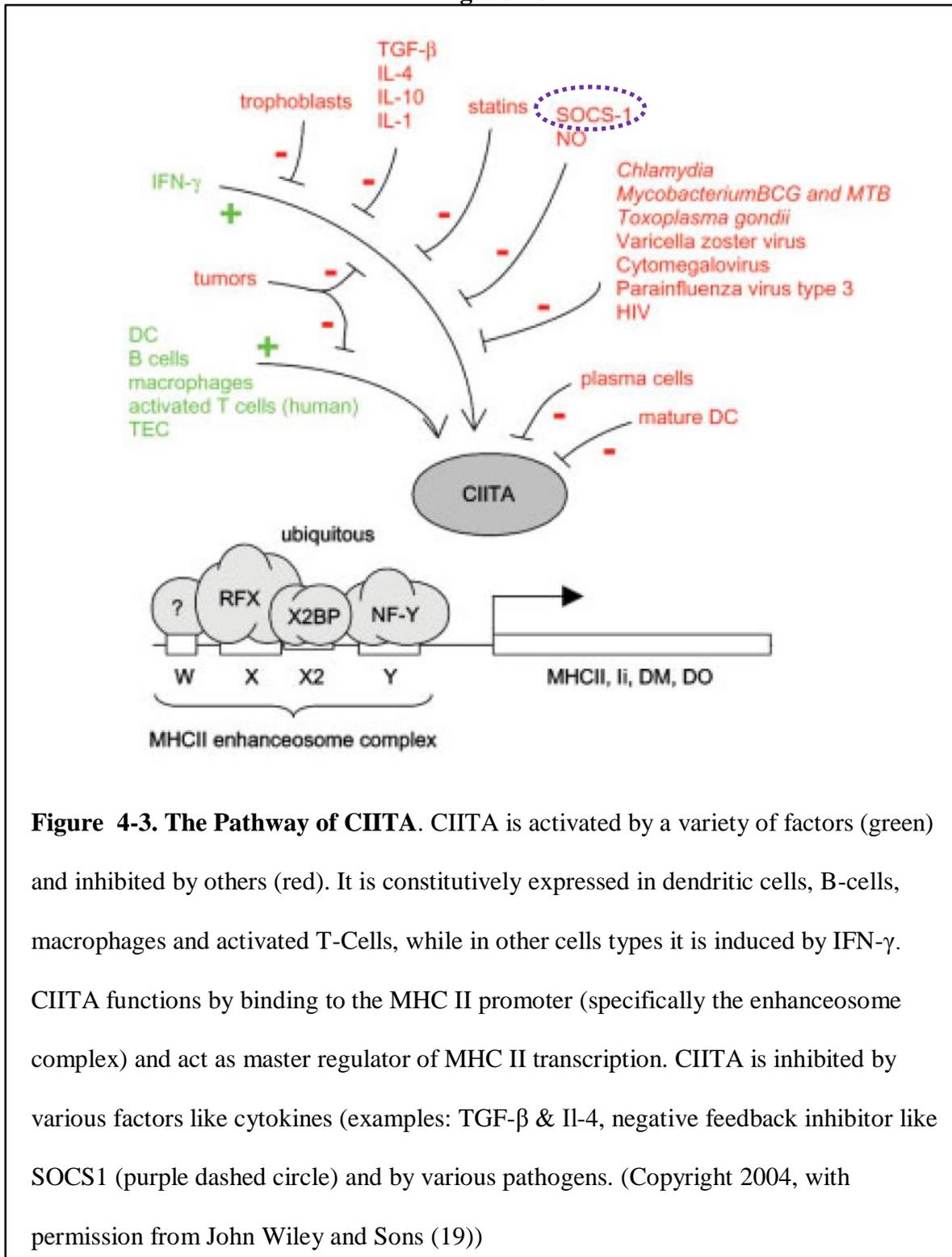


Figure 4-2. Linkage Disequilibrium in Chromosome 16p13.13. LD plot of chromosome 16p13.13 for Caucasians (CEU) and Italian Tuscans (TSI) at coordinates 10,937,499-11,467,499 (build Hg19) with the location of the major genes marked. The strongest LD occurs around the *CLEC16A* gene (18).

CIITA

CIITA is a ~48 KB gene that is controlled by four different promoters (pI-IV) that produce three isoforms of *CIITA* (pII promoter function is currently unknown). The three isoforms of *CIITA* are cell type specific: isoform I is found in myeloid cells, isoform III is found in lymphoid cells and isoform IV in cells from non-hematopoietic origin. *CIITA* is involved in the regulation of HLA class II gene transcription and has been extensively studied due to its important immunological role (19). Mutations in the *CIITA* regulation pathway can cause bare lymphocyte syndrome, a severe immune deficiency disease (20). SNPs specifically in *CIITA* have been found to increase susceptibility for multiple sclerosis, arthritis and myocardial infarction (21). Down regulation of *CIITA* has also been implicated in various forms cancer (22). *CIITA* is constitutively expressed in dendritic cells (DC), B cells, macrophages and activated T Cells, while in other cell types it is induced by IFN- γ . *CIITA* functions by binding to the MHC II enhanceosome complex promoter and acts as master regulator of the MHC II transcription complex (Figure 4-3). It is inhibited by various cytokines (examples: TGF- β & IL-4), negative feedback inhibitor (SOCS1) and by various pathogens (19). In an interesting development it was found that regulation of *CIITA* also occurs through chromatin remodeling that regulates distal enhancer sites. One of these distal enhancer sites is located in the intronic region of adjacent gene *DEXI* (23,24).

Figure 4-3



DEXI

DEXI is a 14 KB gene that is transcribed in the opposite direction to *CIITA* and *CLEC16A*. *DEXI* is composed of two exons (only 1 coding) and codes for a protein 95 amino acids long (25). *DEXI* is up-regulated by dexamethasone, a glucocorticoid (a steroidal hormone) but little is known about its function. Protein analyses have identified a central transmembrane domain, carboxy-terminal leucine zipper motif and a negatively charged carboxy-terminal. It is speculated that *DEXI* could be a membrane protein and not a nuclear protein because of the central transmembrane domain. It is found to be highly expressed in the heart, brain and liver (26). In a yeast two-hybrid screen *DEXI* was found to interact with Golgi membrane protein 1 (*GOLM1*) and tubulin-specific chaperone D protein (*TBCD*) (27). *GOLM1*, also known as GP73, has been found to be up-regulated in a viral infection (28), implicating *DEXI* in a possible immune response mechanism. Whereas *TBCD* is a protein involved in helping beta-tubulin fold correctly and seems like a unlikely target for an auto-immune disease (29).

CLEC16A

CLEC16A also referred to as *KIAA0350*, is a possible C-type lectin that is ~240 KB with mostly unknown function. C-type lectins normally function as cell surface receptors in the immune system. Based on available cDNA, there are three predicted isoforms of *CLEC16A* that vary greatly in size. Their specific genomic location, size, exons and number of amino acids can be seen in Figure 4-4. There also appears to be an ITAM sequence located in the middle region of the protein (4). ITAM sequences function

as targets in tyrosine phosphorylation and in the transmission of cell surface signals (30). CLEC16A is highly expressed in immune cells like T cells, B cells and NK cells (31). However, in a more recent study with *Drosophila* orthologue of CLEC16A - *ema* - was reported to be involved in late endosomal maturation (Figure 4-5) (32).

Figure 4-4

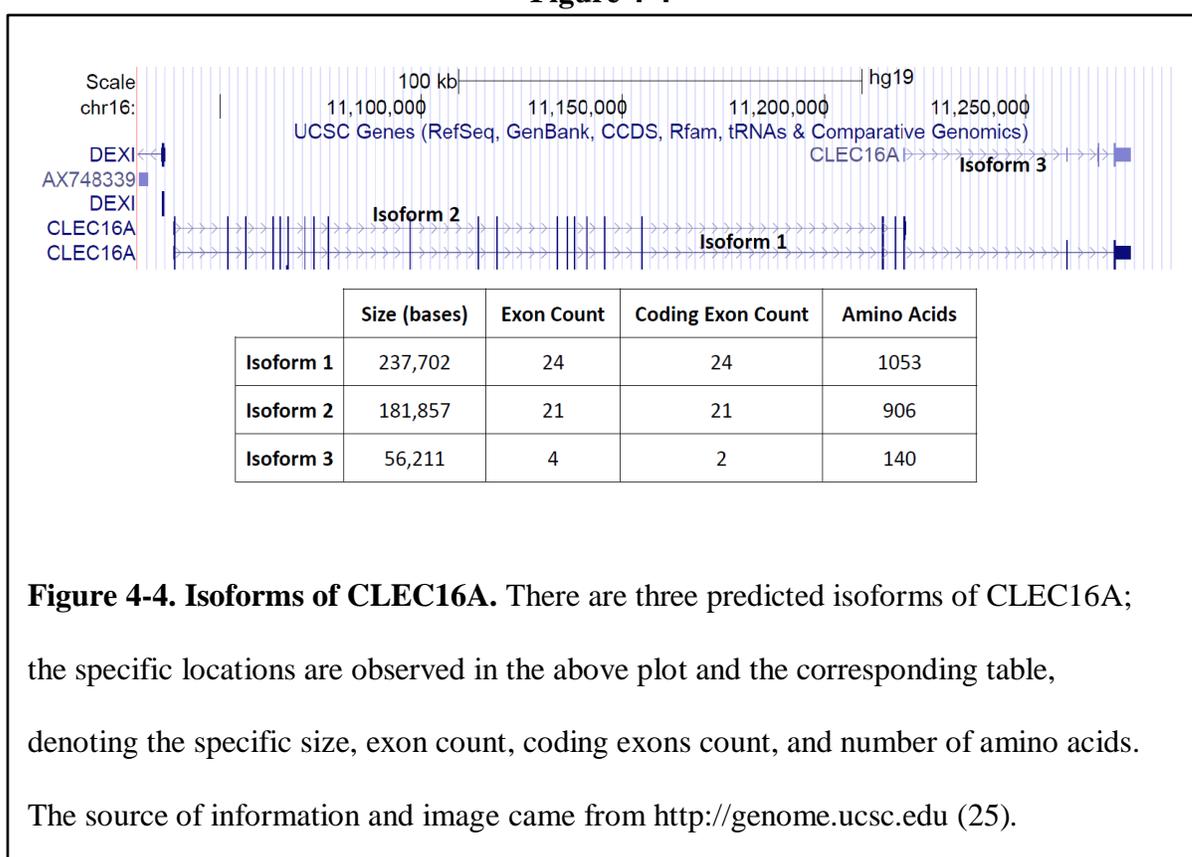
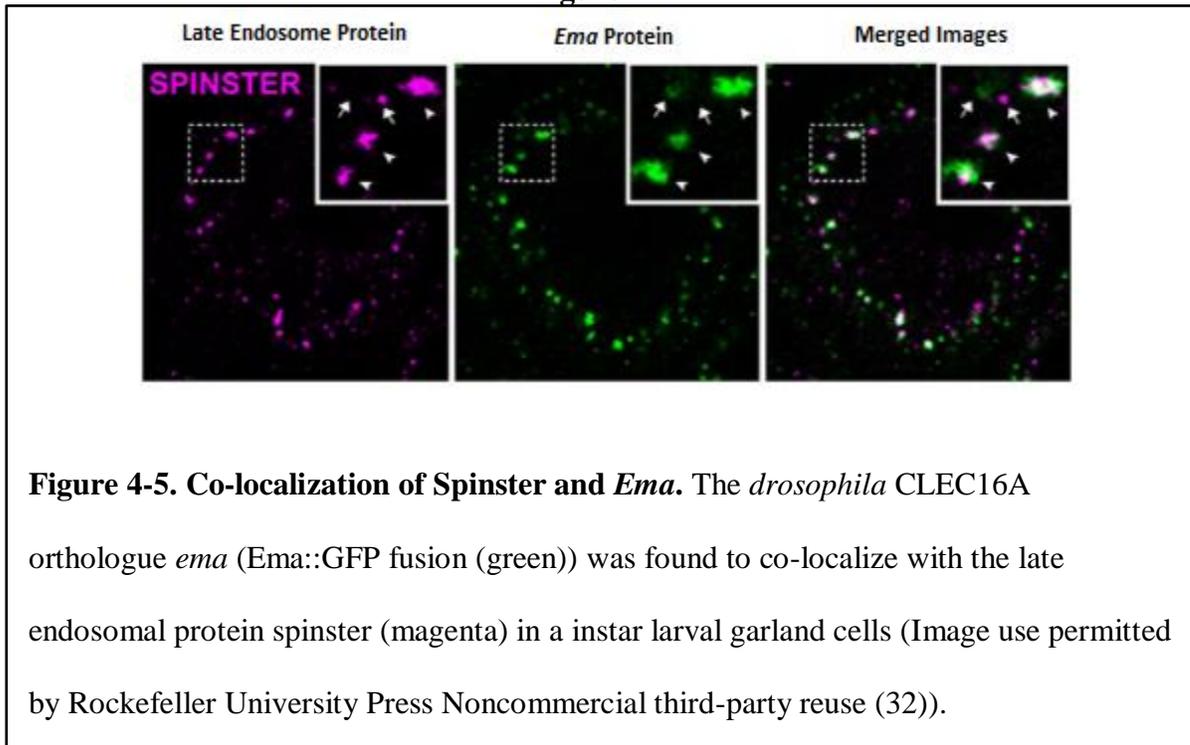


Figure 4-5

SOCS1

The last important gene in the region is *SOCS1*, a small gene located ~80 KB downstream from *CLEC16A*. *SOCS1*, a negative feedback regulator of cytokine signaling and is <1 KB. It is part of the family of suppressors of cytokine signaling (SOCS) family that is made up of eight proteins SOCS1-7 and CIS. All SOCS family proteins have a Src homology 2 (SH2) domain, C-terminal motif referred to as the SOCS box and a variable N-terminal region. When cytokines are received by a cell, they induce transcription of genes for survival, proliferation, and functional activation; however, they also induce *SOCS* genes. *SOCS* genes function to dampen/turn off the signaling in a negative feedback loop; SOCS1 specifically binds to JAK and inhibits its kinase activity (Figure 4-6) (33,34). When *SOCS1* is completely knocked out in mice, neonatal lethality occurs (35-37) and when over expressed results in increased apoptosis of peripheral T-cells (38). *SOCS1* is clearly an essential gene for proper cytokine regulation and is important in T-cell development (33,34). In an interesting "diabetes" connection, *SOCS1*, *SOCS3* and *SOCS6* were found to block insulin signaling, causing insulin resistance, however this finding maybe be more relevant to type 2 diabetes (39,40).

Figure 4-6

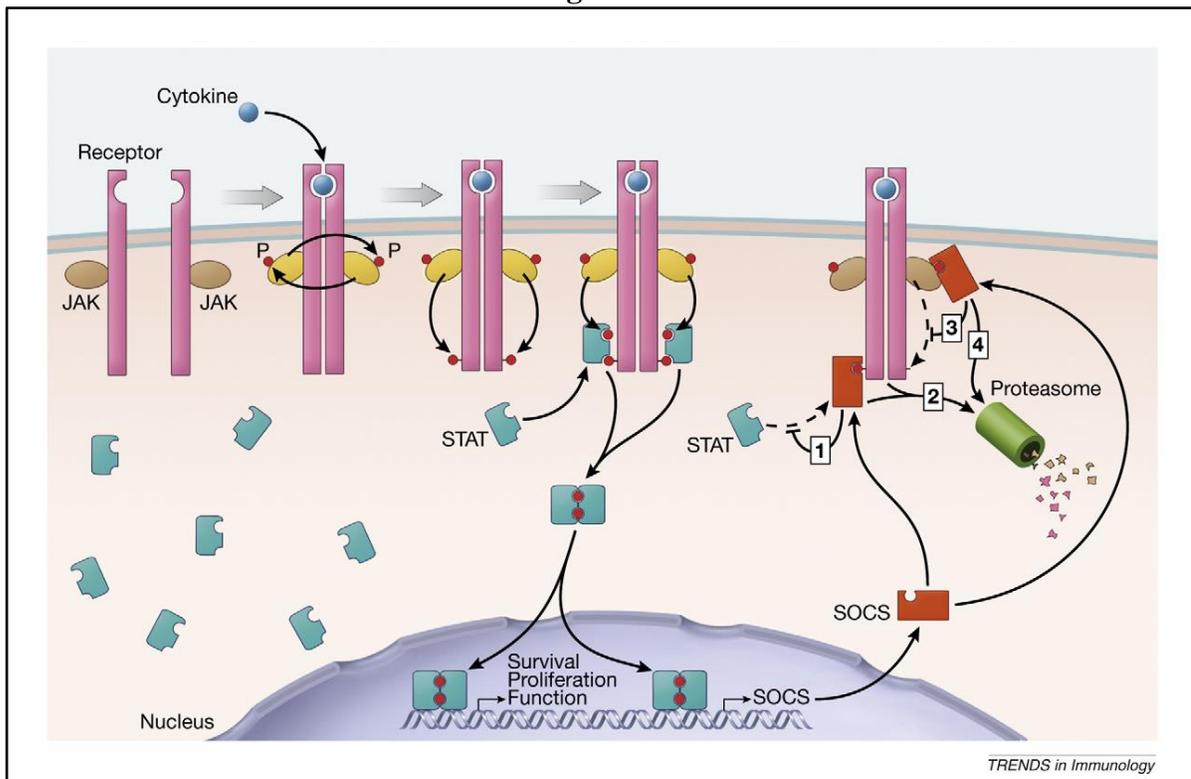


Figure 4-6. The SOCS Activation Pathway (negative feedback inhibition). A cytokine signal is received by the cell and causes dimerization of two receptors. Attached JAK molecules become active and phosphorylate the receptors' cytoplasmic tails allowing for the STAT molecules to bind. These STAT molecules become phosphorylated by JAKs, dimerize and translocate into the nucleus to promote genes involved in survival, proliferation, and functional activation of immune related genes like the SOCS. SOCS genes can inhibit cytokine by: **(1)** blocking STATs binding to the cytokine receptor, **(2)** causing the receptor to be degraded by the proteasome, **(3)** binding to the JAK receptor and preventing kinase activity, and **(4)** causing JAKs to be degraded by the proteasome. Specifically, SOCS1 functions through option **(3)**, binding directly to JAK and inhibiting its kinase activity. (Copyright 2009, with permission from Elsevier (33))

Project Purpose

Several GWAS studies (3-5) identified the chromosome 16p13.13 region as associated with type 1 diabetes and these reported associations were replicated in several follow up studies (16,18,41-44). While these replication studies clearly confirm a role for the 16p13.13 region in conferring risk for type 1 diabetes, they do not clearly delineate which specific genes or SNPs are responsible for this effect. There is, however, complementary functional data suggesting a possible model for how SNPs in this region might act. Most of the variants most strongly associated with type 1 diabetes in this region occur within introns of the *CLEC16A* gene. It has been reported that intronic regions of *CLEC16A* can physically interact with the putative promoter region of *DEXI* and thereby modulate *DEXI* expression in monocytes and in Epstein Barr Virus (EBV) transformed lymphoblastoid cell lines (45-47). As previously mentioned, the intronic region of *DEXI* then works as a distal enhancer for *CIITA* (23,24). These functional findings provide a potential mechanism for variation at intronic sites in *CLEC16A* affecting neighboring genes expression. However they do not clearly resolve the causative variants or whether this mechanism is the actual mode of action of these variants with regards to modulating risk of type 1 diabetes. In the current study, in order to refine the type 1 diabetes association at 16p13.13 and identify the relevant risk variants and genes, a 455 KB segment of the region was re-sequenced in 128 type 1 diabetes patients and 64 controls. Both the newly identified SNPs from the sequencing and the prior reported SNPs from HapMap (48) and 1000 Genomes (49) were tested for an association with type 1 diabetes and with mRNA transcript levels for genes located in the

region. A group of highly correlated SNPs were found to be both significantly associated with type 1 diabetes and with the expression of DEXI.

Research Design and Methods

Subjects

This study was reviewed and approved by the Institutional Review Board at the University of Virginia. DNA from anonymous type 1 diabetes cases and controls were obtained from Virginia Mason Medical Center and Puget Sound Blood Center (Seattle, WA, USA), respectively. DNA from affected sib-pair families (ASP) was obtained from the Type 1 Diabetes Consortium (T1DGC) (50) and Human Biological Data Interchange Repository (HBDI) (51).

Sequencing of Region to Identify SNPs

We targeted a 455 kb region (10,943,936 - 11,399,037 (Hg19)) on 16p13.13 for deep sequencing, which encompassed the four genes (*CIITA*, *DEXI*, *CLEC16A*, and *SOCS1*) and all SNPs previously reported to be significantly associated with type 1 diabetes. The region was tiled with ~10 kb PCR fragments with ~0.5 kb overlaps. Amplifications were carried out in 48 pools that each contained DNA from 4 individuals (128 type 1 diabetes patients and 64 controls). Amplified PCR fragments were pooled in equimolar amounts to create DNA libraries. DNA libraries were prepared for sequencing using Illumina's Paired-End Sample Preparation Kit (Illumina Inc.). Sequencing was performed on an Illumina Genome AnalyzerIIx (Illumina Inc) using 63 base paired-end reads. Sequencing reads were assembled using Burrows-Wheeler Aligner (BWA) tool (52). SAMtools (53) was used for conversion, indexing, and aligning of the data to the reference genome (Hg18 ver. 36) (25,54) as well as for identifying SNPs.

SNP Filtering and Selection

Putative SNPs identified from sequencing were filtered to limit false positives caused by strand bias by including only minor alleles with a frequency rate $\geq 0.1\%$, for which the proportion of forward reads was not statistically different from the proportion of reverse reads. The two proportions were only declared not statistically different if the absolute value of the t-statistic for the proportions test was less than one. The SNP list was then parsed into two groups: annotated SNPs and novel unreported SNPs (defined as lacking a dbSNP ID).

SNPs annotated in dbSNP were excluded from analysis if they had a minor allele frequency (MAF) $< 5\%$ (except exonic SNPs) or had < 50 mapped reads. The annotated SNP list was further filtered to exclude SNPs that had previously been genotyped by the HapMap project (48), leaving a total of 355 annotated SNPs.

Novel variants, were filtered to exclude those with a MAF $< 5\%$ (for exonic SNPs exclusion was for MAF $< 1\%$) or the combination of < 50 aligning reads and $> 20\%$ non-aligning reads, which left a total of 93 novel SNPs.

Genotyping

We designed two custom GoldenGate genotyping assays (Illumina, CA). The first panel consisted of 123 SNPs which were selected as tagging SNPs ($r^2 = 0.9$) to capture information on the 505 reported SNPs in the CEU HapMap population using Haploview 4.2 (18). The second panel consisted of SNPs identified through sequencing. The compiled SNP lists were verified for design-ability using Illumina's GoldenGate Panel

Design software (www.illumina.com). Genotyping was performed on a total of 413 SNPs on 1850 HBDI and 1750 TIDGC samples. Data were examined in GenomeStudio (Illumina Inc.) and exported in PLINK (55) format.

The following quality control steps were applied to the SNP genotyping data. Signal cloud graphs were manually reviewed for all of the SNPs and those with poor clustering were excluded. SNPs with >5 Mendelian transmission errors were identified and excluded from further analyses. SNPs genotyped in duplicate were examined for concordance using PLINK; those with $\geq 5\%$ discordance were excluded. SNPs with significant deviations from Hardy-Weinberg equilibrium, >5% missingness or <1% MAF.

For sample quality control in GenomeStudio, DNA samples with a genotype call rate of <90% were removed from further analyses. Subjects with >5 Mendelian transmission errors were identified with PLINK (55) and excluded from the analyses. All remaining Mendelian transmission errors were identified and problematic genotypes removed with PEDCHECK (56).

ImmunoChip Dataset

Genotypes from 1,734 SNPs in the 16p13.13 region obtained from 10,796 individuals were extracted from the ImmunoChip dataset (data release Feb 2012) (57). Quality control included the exclusion of SNPs with significant deviations from Hardy-Weinberg equilibrium or >5% missingness. PEDCHECK was used to identify Mendelian

errors and remove conflicting genotypes. Finally, the data was filtered to remove all duplicate SNPs and SNPs with <1% MAF.

Imputation

After quality control, the data set that was derived from targeted sequencing included 319 SNPs with genotypes from 749 families containing 3370 individuals. The ImmunoChip dataset included 1040 SNPs with genotypes from 2689 families containing 10,746 individuals. There were 252 SNPs and 1581 individuals in common between the two datasets.

The two datasets were merged and missing genotypes were filled in by imputation. A reference haplotype population (same individuals from both panels) was generated using MACH (58) and data from 481 parental Caucasian founders whose ethnicity was confirmed using KING (59). Imputation was performed using MACH and the reference population. SNPs with $r^2 \leq 0.5$ (values generated by MACH) were removed. The same quality control steps as applied to the originally generated genotype data were applied to the imputed data.

Association Testing

The final merged datasets was tested for association with type 1 diabetes using the TDT option in PLINK and results were visualized using LocusZoom (60). Test for residual evidence of disease association after conditioning on the SNP with the most significant association with type 1 diabetes were carried out using UNPHASED (61).

Statistical significance for association was determined by the conservative Bonferroni correction based on the number of SNPs tested ($P \leq [0.05 / (\text{Number of SNPs tested})]$) (62,63)

RT-PCR

RNA was isolated from the 33 HapMap B lymphoblastoid cell lines (Coriell Institute for Medical Research, Camden NJ) using TRIzol (Invitrogen Inc.) followed by a DNase treatment (Applied Biosystems). RNA was reverse transcribed using random primers (Invitrogen Inc.) and Superscript II (Invitrogen Inc.) following manufacturer's protocol. The cDNA samples and standards were then plated in triplicate using a Beckman FX-Robotic workstation and air dried (24-48 hours). PCR primers were designed using cDNA transcripts from the NCBI database and Primer3 (64) (Table 4-1). Amplifications were carried out on an Applied Biosystems Inc. 7900 [95C for 10 minutes, (95°C for 15 seconds, (60°-61°C) for 30 seconds, 72°C for 30 seconds) for 35-40 cycles, followed by a dissociation curve]. The data was examined using ABI's SDS 2.3 software, and CT (threshold cycle) and baseline adjusted for each PCR run.

Table 4-1

Primer Sequences used for the expression quantitative trait loci (eQTL) analysis of the genes and isoforms in LD block 16p13.13

NCBI Ref Seq	Gene	Forward Primer	Reverse Primer	Size (bp)
BQ221200	<i>CIITA III*</i>	ggggaagctgagggcacg	gaagctccaggtagccaccttcta	182
BM147267	<i>CIITA IV *</i>	gcggccccagagctgg	gaagctccaggtagccaccttcta	125
NM_015226.2	<i>CLEC16A Iso I</i>	cgcataagatgcagagaat	ggtggcgactgtgaggac	257
BC112897.1	<i>CLEC16A Iso II</i>	ctctgtggagcctgtgtgag	tgtttaatcttgcgctgtgc	102
AK126771.1	<i>CLEC16A Iso III</i>	acagcccagagtccagca	actcatggggcatctgaat	157
NM_014015.3	<i>DEXI †</i>	agtagggctcgcactgctgttc	acctctctgtggcacgaag	192
NM_003745.1	<i>SOCS</i>	gccccctctgtaggatggta	ggaggaagaggaggaagggtt	104
NM_002046.3	<i>GAPDH</i>	cagccgagccacatcgc	catgggtggaatcatattggaaca	186
Novel Transcript	<i>CIITA V</i>	acctgcaacaacaggattcac	caccaacacctcagacttcac	105
Novel Transcript	<i>CIITA VI</i>	agctcgctgccagccttc	ggattctcgctgtccctgt	159

**CIITA III* and *CIITA IV* primers were originally designed by Hornell 2003 (65)

†There are two intron-less *DEXI* pseudogenes (retro-*DEXI*) located on chromosome 15 at coordinates (Hg19) (29,033,933-29,035,470) and (23,157,046-23,158,548) whose genomic DNA matches almost exactly the cDNA for *DEXI*. The forward primer has one nucleotide difference at the 3' end (**bold**) that differ from the pseudogenes.

Expression Quantitative Trait Loci (eQTL) Analysis

Amplification efficiencies were calculated per transcript and compared to that for the control *GAPDH* gene. Median CT values were determined from the raw triplicate CT values. The $\Delta\Delta\text{CT}$ values were calculated correcting for primer efficiencies and were quantile normalized. The quantile normalized $\Delta\Delta\text{CT}$ were merged with genotyping data on the 33 HapMap cell lines to create a PLINK PED file. An eQTL analysis (linear model with quantitative trait) was then performed in PLINK using the normalized expression data. The eQTL results from the custom and ImmunoChip panels were merged together. The dataset was filtered to remove SNPs with a MAF <5% as well as all duplicate SNPs. The final SNP dataset was visualized using LocusZoom. To correct for limited sample size, instead of using stringent Bonferroni corrected *P*-values (63), a program was designed to calculate the total number of independent tests. The program examined the correlations (r^2) for all 915 SNPs by examining each SNPs genotyping pattern, determining how many SNPs had the same pattern, versus how many unique patterns and represented independent tests. The number of independent tests performed was $N = 366$ with a corrected *P*-value of $0.05 / 366 = 1.37 \times 10^{-4}$.

Results

Re-sequencing of the 16p13.13 Region Identifies Novel SNPs

A region of 455 kb from 16p13.13 was amplified in 192 individuals (128 T1D patients and 64 control individuals) and sequenced to an average depth of coverage of 35X. When aligned to the human reference sequence, there were two gaps at coordinates (Hg19) (11,028,710-11,083,336) and (11,340,104-11,350,943) from which no sequence was obtained that passed quality control. When compared to the human reference genome, 962 SNPs were identified, of which 93 had no prior annotation. A genotyping panel spanning the region was designed containing both tagging SNPs selected from HapMap, and novel SNPs identified from our re-sequencing (60 of the 93 SNPs were designable and included in the panel).

Fine Mapping Identifies Statistically Significant Associations with Type 1 Diabetes

Custom Panel

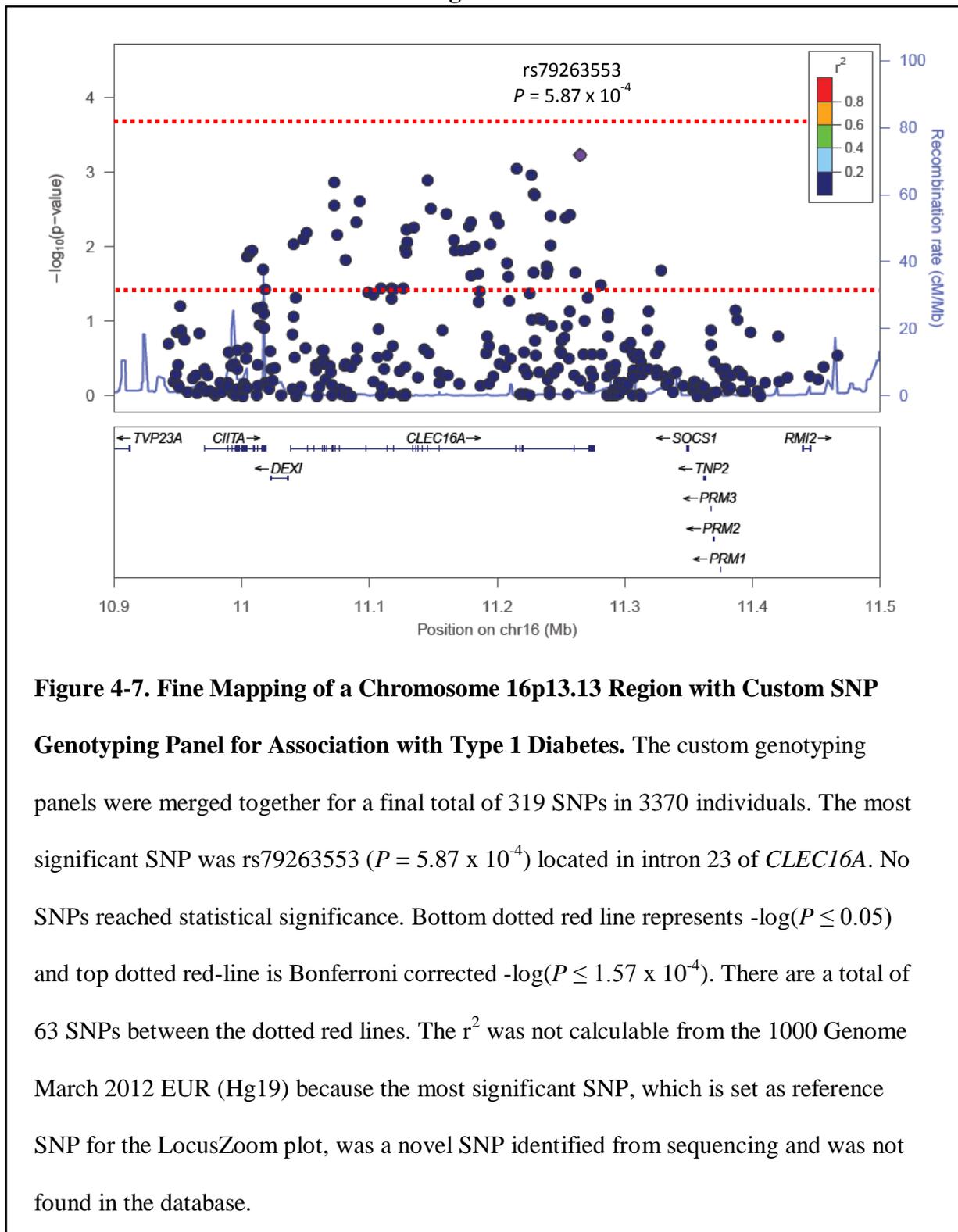
A total of 413 SNPs were genotyped on 3600 individuals from the HBDI and T1DGC. After data cleaning and merging, the custom panel contained 319 SNPs (MAF >1%) genotyped on 3370 individuals from 749 families (Table 4-2 and Figure 4-7). The data was analyzed by the TDT test using PLINK

Table 4-2
Functional Annotation of SNPs on Custom Panel

Type of SNP	Combined
Exonic-coding synonymous	6
Exonic-coding missense	4
Near 5' UTR	4
3' UTR	9
Intron	191
Intergenic	105
Total	319

Function was determined from UCSC Genome Table Browser (25)

Figure 4-7



ImmunoChip

In order to increase the statistical power of the study, the data were merged with the ImmunoChip affected sib-pair dataset using imputation to fill in the missing genotypes. The ImmunoChip dataset originally contained 1,734 SNPs genotyped on 10,796 individuals. After quality control steps described in the methods section, the final numbers were filtered down to 1,040 SNPs (MAF >1%) and 10,746 individuals (Figure 4-8). In the ImmunoChip a total of 30 SNPs were identified to have alleles significantly associated with disease. The ImmunoChip dataset was then merged with the custom genotyping panels.

Figure 4-8

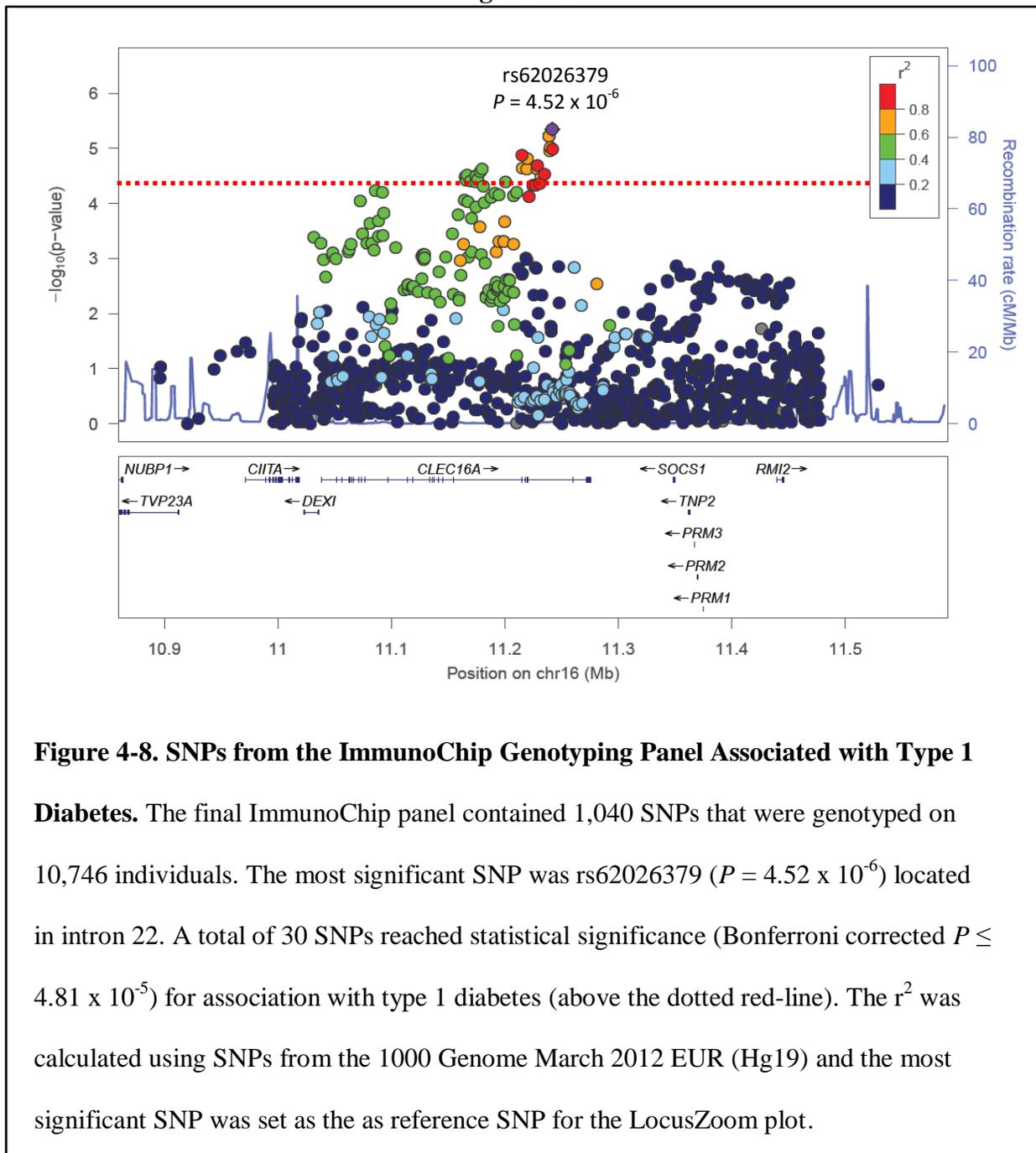


Figure 4-8. SNPs from the ImmunoChip Genotyping Panel Associated with Type 1 Diabetes. The final ImmunoChip panel contained 1,040 SNPs that were genotyped on 10,746 individuals. The most significant SNP was rs62026379 ($P = 4.52 \times 10^{-6}$) located in intron 22. A total of 30 SNPs reached statistical significance (Bonferroni corrected $P \leq 4.81 \times 10^{-5}$) for association with type 1 diabetes (above the dotted red-line). The r^2 was calculated using SNPs from the 1000 Genome March 2012 EUR (Hg19) and the most significant SNP was set as the as reference SNP for the LocusZoom plot.

Final Merged Dataset

The merged dataset, after imputation, contained genotypes for 939 SNPs on 12,485 individuals (4,057 ASP). A breakdown of the type of SNPs can be found in Table 4-3. The combined panel contained 26 SNPs from the Custom Genotyping panel, 661 SNPs from the ImmunoChip and 252 SNPs that were genotyped on both panels (Figure 4-9). The family based TDT (66) was used to test for association of alleles at these SNPs with type 1 diabetes (Figure 4-10). A total of forty eight statistically significant SNPs were identified (Bonferroni corrected $P \leq 5.32 \times 10^{-5}$) (Table 4-4). A magnified plot of the forty-eight statistically significant SNPs can be seen in Figure 4-11. The strongest evidence for association was obtained at rs34306440 located in intron 20 of *CLEC16A* (OR = 0.838 (0.776-0.904), $P = 5.74 \times 10^{-6}$).

Table 4-3

Functional Annotation of SNPs on Final Panel (939 SNPs)

Type of SNP	Count
Exonic-coding synonymous	9
Exonic-coding missense	3
Near 5' UTR	31
3' UTR	15
Intron	555
Intergenic	326
Total	939

Function was determined from UCSC Genome Table Browser (25)

Figure 4-9

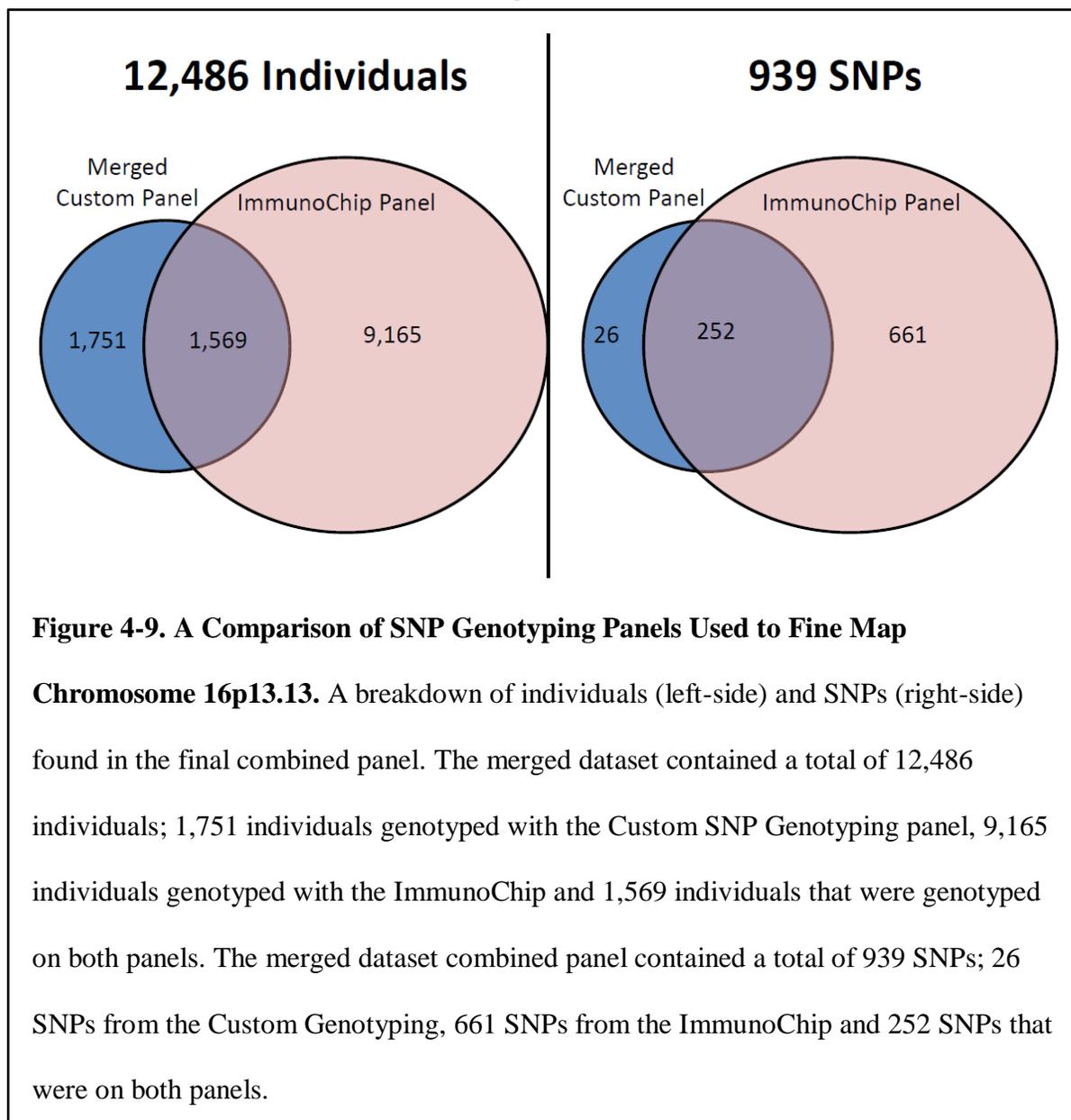


Figure 4-10

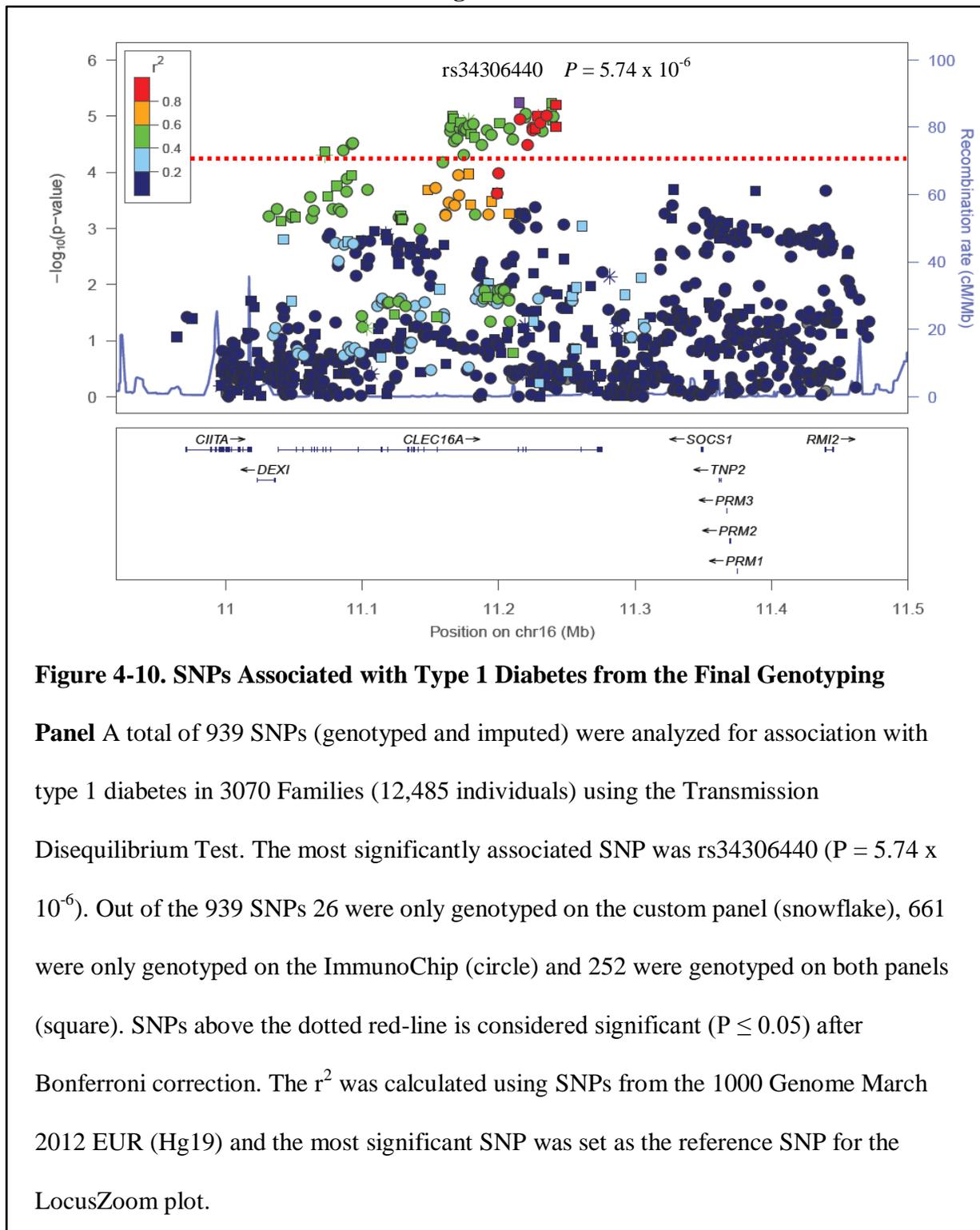


Figure 4-11

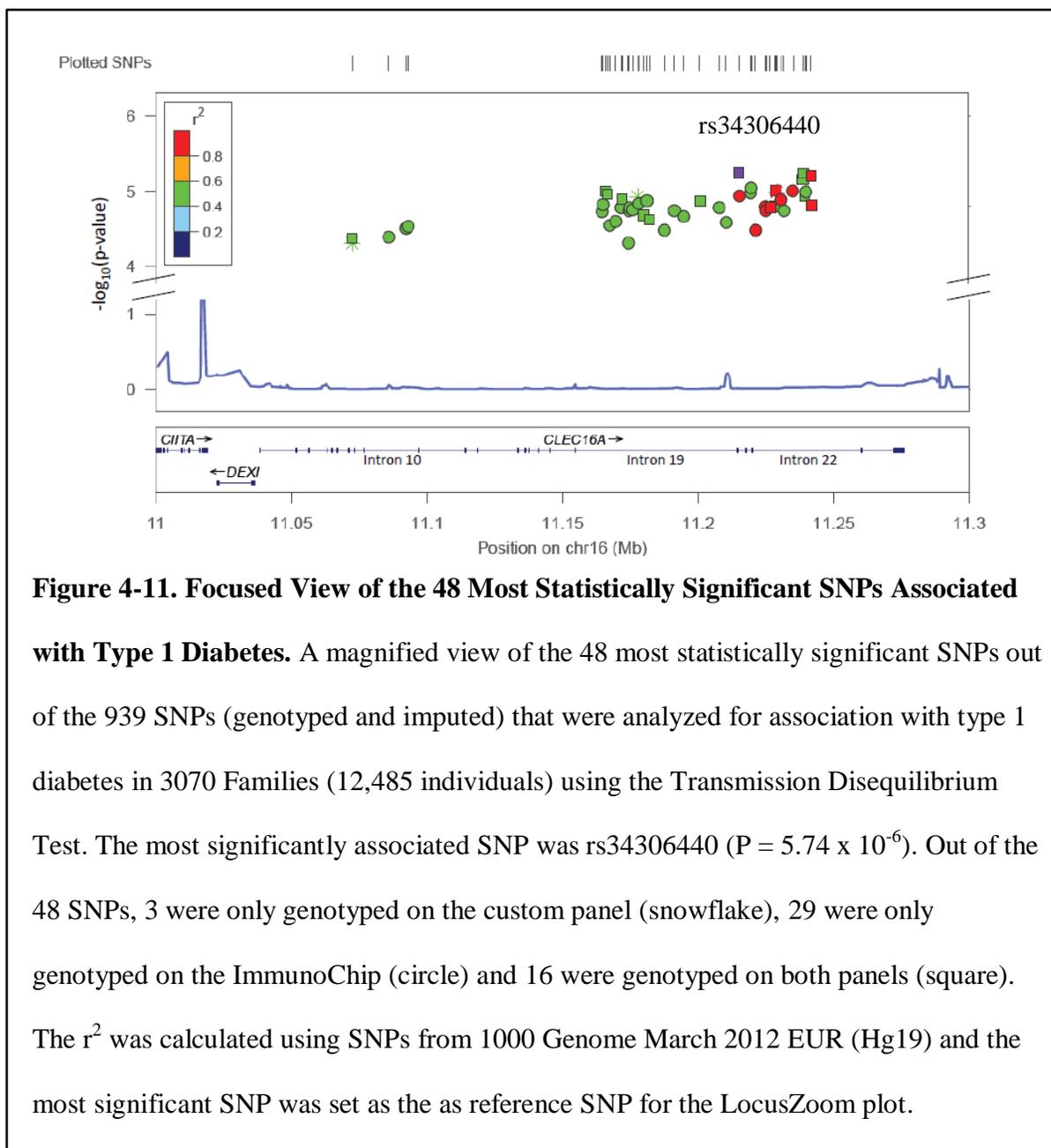


Table 4-4

SNPs in *CLEC16A* most strongly associated with type 1 diabetes (total 48) from TDT analysis sorted in order of base position.

SNP Name	Position (Hg19)	MAF*	Minor Allele	Major Allele	Transmitted Minor Allele Count	Untransmitted Minor Allele Count	TDT P-value†	Odds Ratio†	Location ‡
rs12708713	11072459	0.167	T	C	1045	1239	4.92E-05	0.843 (0.777-0.916)	Intron 8
rs12708714	11072525	0.168	C	T	1048	1244	4.24E-05	0.842 (0.776-0.915)	Intron 8
rs7403919	11085968	0.341	C	T	1691	1938	4.13E-05	0.873 (0.818-0.931)	Intron 10
rs8062322	11092319	0.289	A	C	1529	1768	3.15E-05	0.865 (0.808-0.926)	Intron 10
rs9926367	11093179	0.288	C	T	1520	1759	3.00E-05	0.864 (0.807-0.926)	Intron 10
rs7200940	11164567	0.307	G	C	1556	1804	1.88E-05	0.863 (0.806-0.923)	Intron 19
rs11860603	11165017	0.305	C	T	1546	1796	1.53E-05	0.861 (0.804-0.921)	Intron 19
rs9934969	11166002	0.303	A	G	1540	1795	1.01E-05	0.858 (0.802-0.918)	Intron 19
rs11865121§	11166688	0.304	A	C	1544	1798	1.11E-05	0.859 (0.802-0.919)	Intron 19
rs7198621	11167458	0.304	G	C	1538	1779	2.86E-05	0.865 (0.808-0.926)	Intron 19
rs725613	11169683	0.336	C	A	1625	1874	2.56E-05	0.867 (0.811-0.927)	Intron 19
rs12925642	11171602	0.304	G	A	1548	1797	1.67E-05	0.861 (0.805-0.922)	Intron 19
rs2058531	11172109	0.305	G	A	1554	1807	1.28E-05	0.860 (0.804-0.920)	Intron 19
rs9652601	11174365	0.306	A	G	1557	1792	4.89E-05	0.869 (0.812-0.93)	Intron 19
rs9652582	11174564	0.300	A	G	1536	1783	1.81E-05	0.862 (0.805-0.922)	Intron 19
rs2041670	11174652	0.300	T	C	1537	1785	1.69E-05	0.861 (0.804-0.922)	Intron 19
rs11648679	11175984	0.335	G	A	1623	1877	1.76E-05	0.865 (0.809-0.924)	Intron 19
rs12708715	11177824	0.301	T	C	1542	1795	1.19E-05	0.859 (0.803-0.92)	Intron 19
rs9929994	11178245	0.336	G	A	1617	1873	1.47E-05	0.863 (0.808-0.923)	Intron 19
rs12708716	11179873	0.333	G	A	1615	1866	2.10E-05	0.866 (0.810-0.925)	Intron 19
rs9888908	11181244	0.300	A	C	1539	1790	1.36E-05	0.860 (0.803-0.92)	Intron 19
rs7203793	11182134	0.335	G	C	1626	1876	2.39E-05	0.867 (0.811-0.926)	Intron 19
rs12924729¶	11187783	0.305	A	G	1565	1806	3.31E-05	0.867 (0.810-0.927)	Intron 19
rs12928537	11191400	0.303	A	G	1550	1798	1.82E-05	0.862 (0.806-0.923)	Intron 19
rs12927355	11194771	0.302	T	C	1556	1802	2.18E-05	0.864 (0.807-0.924)	Intron 19
rs741172	11200798	0.300	T	C	1551	1803	1.35E-05	0.860 (0.804-0.921)	Intron 19
rs9746695	11207894	0.302	C	T	1550	1799	1.69E-05	0.862 (0.805-0.922)	Intron 19
rs12935413	11210447	0.333	A	G	1617	1865	2.64E-05	0.867 (0.811-0.927)	Intron 19
rs34306440#	11215035	0.209	G	A	1203	1436	5.74E-06	0.838 (0.776-0.904)	Intron 20
rs35032408	11215424	0.208	G	T	1204	1429	1.16E-05	0.843 (0.780-0.910)	Intron 20
rs8064154	11219419	0.338	G	A	1610	1870	1.05E-05	0.861 (0.806-0.920)	Intron 21
rs12924112	11219720	0.336	G	T	1589	1849	9.24E-06	0.859 (0.804-0.919)	Intron 21
rs34540843	11221287	0.242	G	A	1332	1555	3.32E-05	0.857 (0.796-0.922)	Intron 22
rs36045143	11224966	0.242	G	A	1332	1564	1.62E-05	0.852 (0.792-0.916)	Intron 22
rs2241099	11225064	0.241	G	C	1325	1555	1.82E-05	0.852 (0.792-0.917)	Intron 22

SNP Names	Position (Hg19)	MAF*	Minor Allele	Major Allele	Transmitted Minor Allele Count	Untransmitted Minor Allele Count	TDT P-value†	Odds Ratio†	Location ‡
rs12919828	11226779	0.243	G	A	1335	1567	1.66E-05	0.852 (0.792-0.917)	Intron 22
rs35732840	11228355	0.336	G	T	1606	1860	1.60E-05	0.863 (0.808-0.923)	Intron 22
rs62026376	11228712	0.243	T	C	1331	1569	9.89E-06	0.848 (0.789-0.913)	Intron 22
rs62026377	11229128	0.243	T	G	1327	1564	1.04E-05	0.849 (0.789-0.913)	Intron 22
rs7203459	11230703	0.242	C	T	1324	1558	1.31E-05	0.850 (0.790-0.914)	Intron 22
rs2867880	11231857	0.334	A	G	1604	1856	1.84E-05	0.864 (0.808-0.924)	Intron 22
rs12919732	11235123	0.244	G	A	1321	1558	1.00E-05	0.848 (0.788-0.912)	Intron 22
rs2903692	11238783	0.330	A	G	1581	1844	6.99E-06	0.857 (0.802-0.917)	Intron 22
rs4322688	11238991	0.332	G	C	1590	1856	5.86E-06	0.857 (0.801-0.916)	Intron 22
rs12930373	11239599	0.331	A	G	1590	1847	1.17E-05	0.861 (0.805-0.921)	Intron 22
rs12917893	11239978	0.331	T	A	1584	1842	1.04E-05	0.860 (0.804-0.92)	Intron 22
rs62026379	11241806	0.241	A	G	1314	1556	6.27E-06	0.845 (0.785-0.909)	Intron 22
rs17673553	11241906	0.242	G	A	1326	1558	1.56E-05	0.851 (0.791-0.916)	Intron 22

*MAF was calculated from the founders (4,655 individuals).

†TDT P-values and Odds Ratio were calculated from the 3,070 multiplex families (12,485 individuals).

‡ Intronic regions were based on Ensembl (CLEC16A - 001 ENST00000409790) (67).

§GWAS reported SNP in association with multiple sclerosis (7). || GWAS reported SNPs in association with type 1 diabetes (2,3).

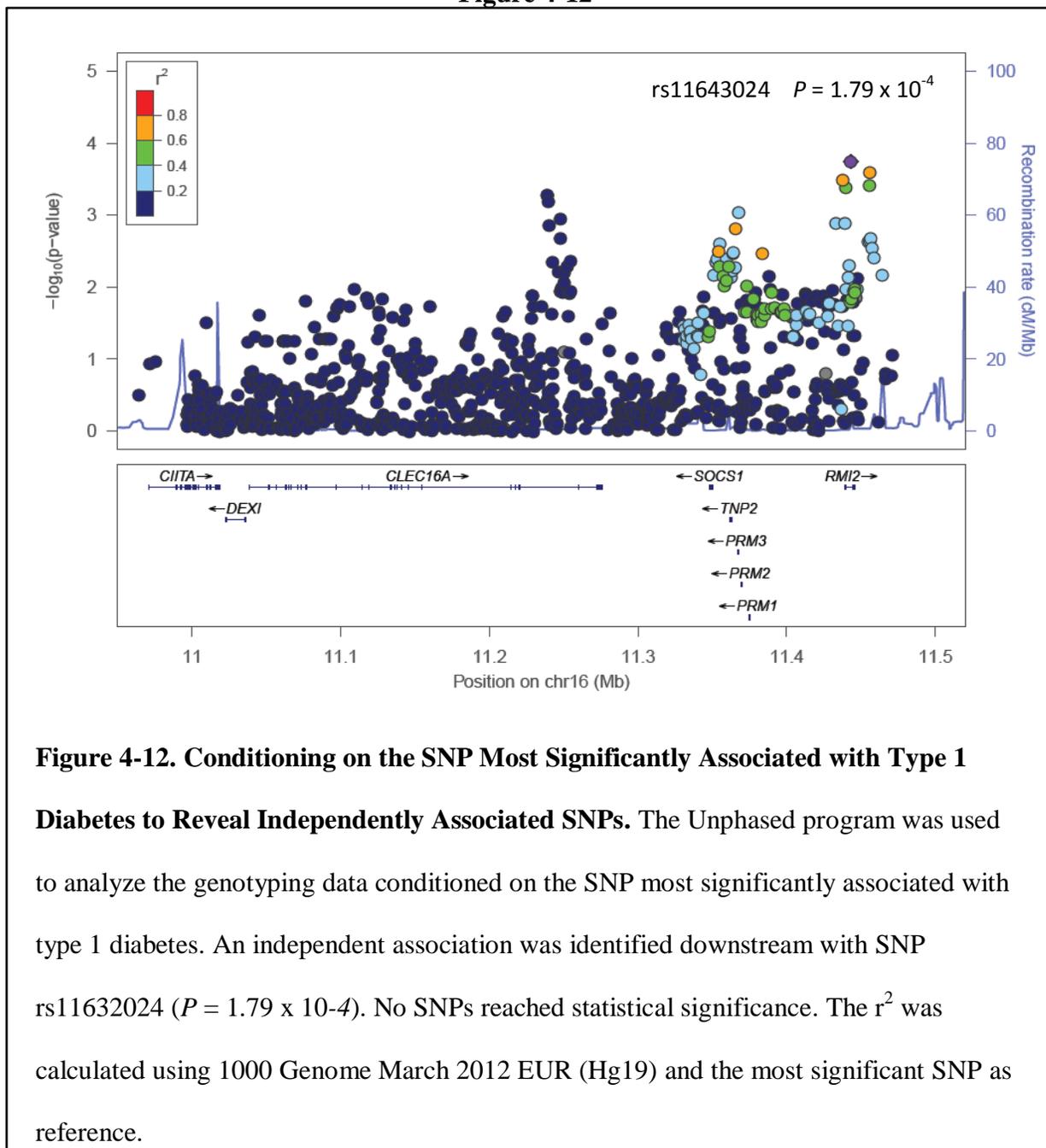
¶GWAS reported SNP previously reported in association with primary biliary cirrhosis (10).GWAS reported SNPs were limited to the dbGAP NHGRI GWAS catalog.

#Most significant SNP associated with type 1 diabetes. MAF, minor allele frequency.

Conditioning on Top SNP

In order to determine whether any other SNPs were independently associated with type 1 diabetes in this region, the data was reanalyzed conditioning on the most significantly associated SNP using Unphased (61). An independent, but not statistically significant association was found downstream of *CLECI6A* at SNP rs11643024 ($P = 1.79 \times 10^{-4}$) (Figure 4-12). After identifying the most significant SNPs associated with type 1 diabetes, we investigated whether any of these SNPs showed correlation with mRNA expression level changes for any of the genes in the region. Prior to assessing expression levels, we catalogued alternative splice forms of genes in the region.

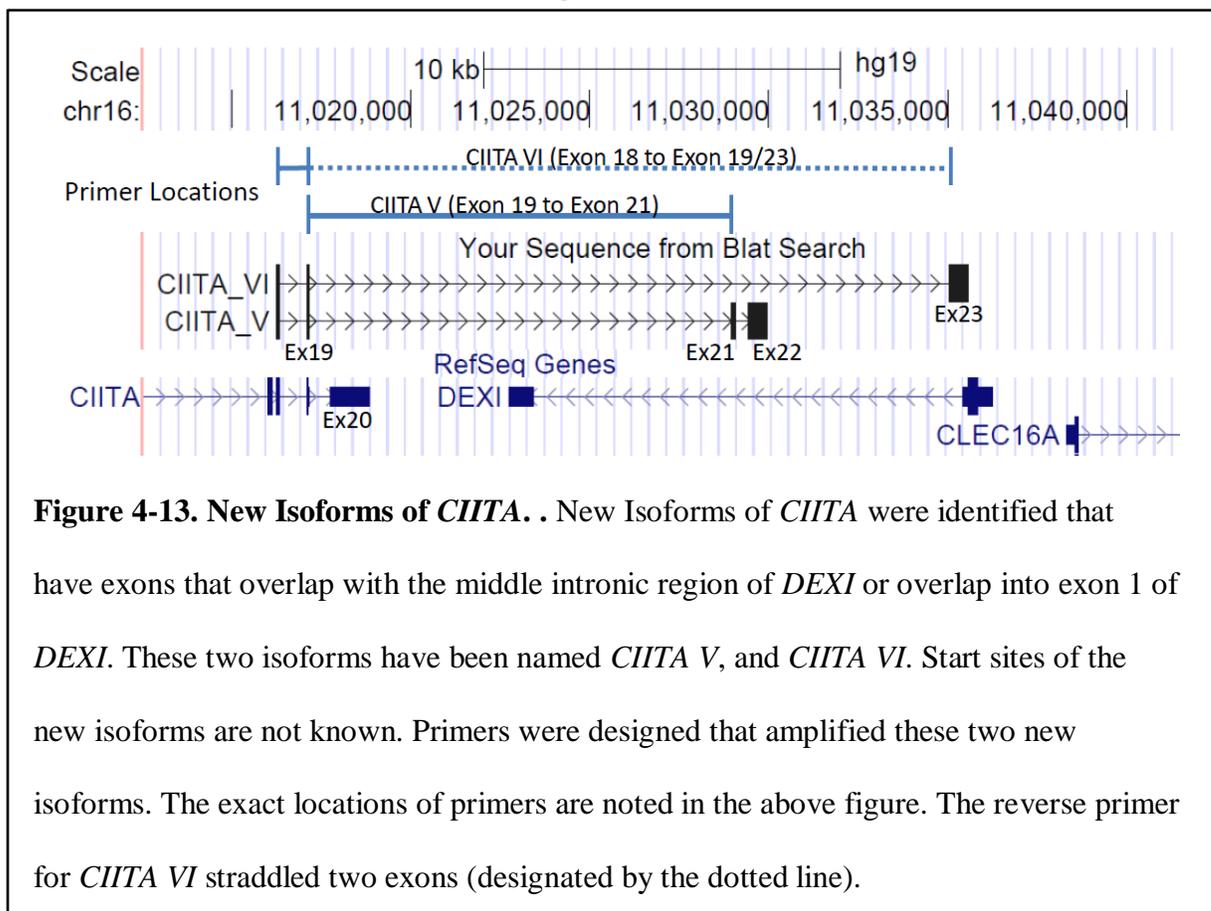
Figure 4-12



Identification of Novel Splicing Isoforms of *CIITA* Created by Alternative Splicing

Examination of RNA-Seq data from the Human BodyMap 2.0 project (Illumina Inc.) (data available at (<http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-513/novel>)) at coordinates (Hg19 chr16:11,010,386,-11,039,093) revealed evidence of infrequent transcripts that included sequences from both *CIITA* and *DEXI*, which are neighboring genes that are transcribed in opposite directions (Figure 4-13). This observation raised the possibility that these genes could exert some regulatory role on each other via anti-sense inhibition. The transcripts were validated and characterized by amplification and Sanger sequencing. Two types of novel isoforms of *CIITA* were identified that overlap with the *DEXI* transcript. One isoform that ends in the intronic region of *DEXI*, referred to here as *CIITA V* and another isoform that overlaps with exon 1 of *DEXI*, referred to as *CIITA VI* (Fig. 4-13). The novel isoforms of *CIITA* have the same stop codon as other *CIITA* isoforms, but differ in the 3'UTR. Real time PCR primers were designed that amplified the two isoforms found and are noted in Figure 4-13.

Figure 4-13



SNPs in *CLECI6A* are Associated with Variation in Expression Level of *DEXI*

Given that one of the significant associations with type 1 diabetes were observed at SNPs located within a coding region, and previous reports suggested that sequences in the 16p13.13 region could act at a distance (*cis*) to regulate the expression of genes in the region, an expression quantitative trait locus analysis (eQTL) was performed using the expression levels of *CIITA*, *DEXI*, *CLECI6A* and *SOCSI* in B-cell lines as phenotypes. Primers that specifically amplified each of the common reported alternative spliced transcripts for the target genes were designed and used to assess transcript levels by quantitative RT-PCR. The full panel of SNPs ($N = 915$) from the region were then tested for association with quantitative variation in the levels of each of the transcripts. The only significant associations were observed for *DEXI* transcripts and a number of SNPs spanning the *CLECI6A* gene, many of which had alleles that were modestly correlated ($r^2 > 0.6$) (Figure 4-14). The most statistically significant association was observed at rs7403919 ($P = 1.24 \times 10^{-4}$). A second independent biological replicate focusing on *DEXI* expression yielded similar results (rs7403919, $P = 5.45 \times 10^{-5}$). A full breakdown of the forty-eight type disease associated SNPs and their correlation (r^2) with SNP rs7403919 can be found Table 4-5. All other SNPs tested as eQTL for other genes in the region (*CIITA Isoforms III-VI*, *CLECI6 Isoforms 1-3*, and *SOCS*) did not show statistically significant association with expression levels. The most significant SNP for each gene eQTL test and corresponding P -value can be found in Table 4-6. Note: *CIITA I* was not measured because it is myeloid dependent (19).

Figure 4-14

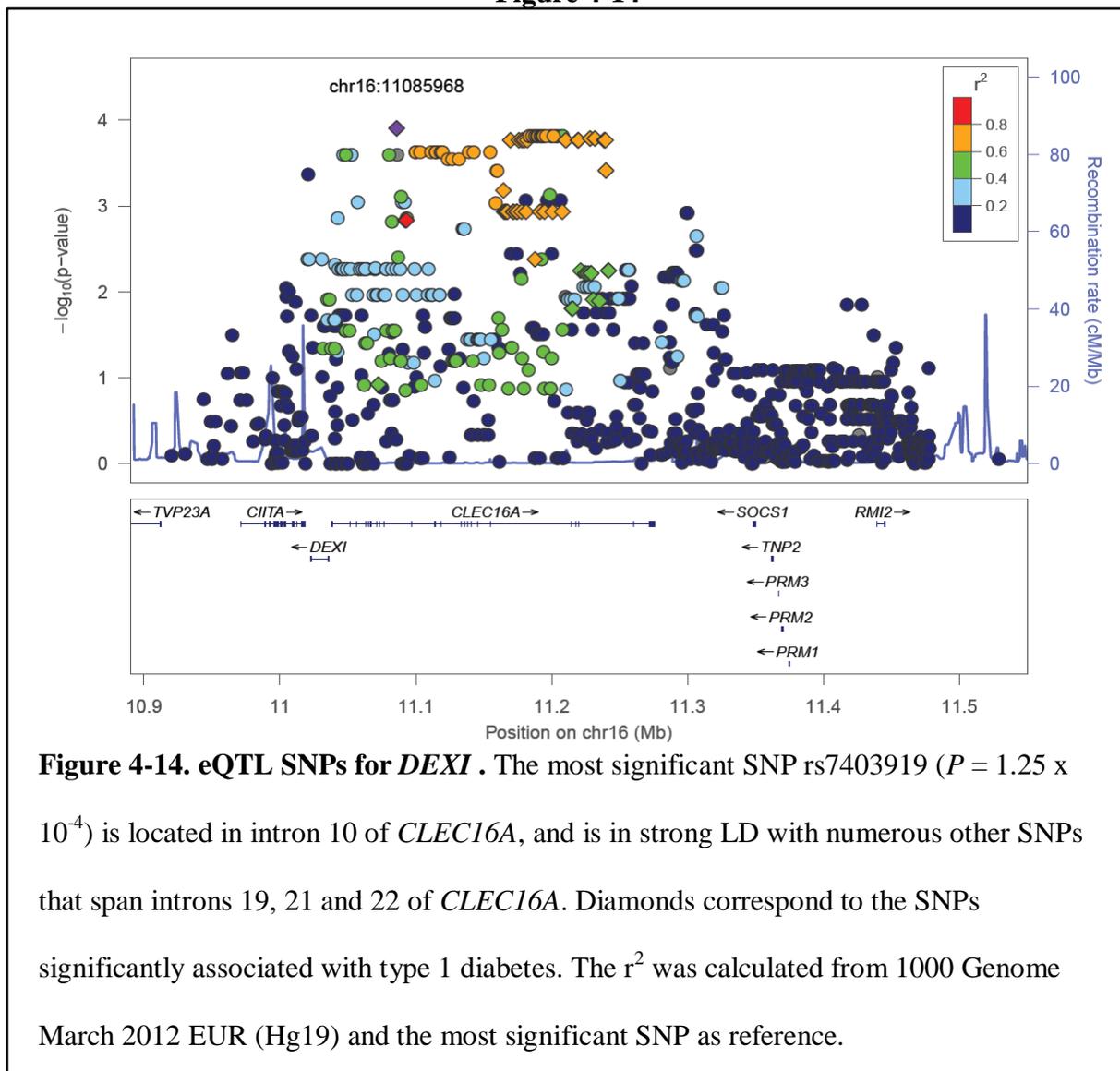


Figure 4-14. eQTL SNPs for *DEXI*. The most significant SNP rs7403919 ($P = 1.25 \times 10^{-4}$) is located in intron 10 of *CLEC16A*, and is in strong LD with numerous other SNPs that span introns 19, 21 and 22 of *CLEC16A*. Diamonds correspond to the SNPs significantly associated with type 1 diabetes. The r^2 was calculated from 1000 Genome March 2012 EUR (Hg19) and the most significant SNP as reference.

Table 4-5
 SNPs Significantly Associated with Type 1 Diabetes with their Corresponding eQTL
 Results for *DEXI*

SNP	Position (Hg19)	Minor Allele	β^*	STAT*	P-value*	r^2 rs7403919†	r^2 rs34306440†	Location‡
rs7403919	11085968	C	0.9029	4.404	1.25E-04	1.000	0.533	Intron 10
rs725613	11169683	C	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs11648679	11175984	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs9929994	11178245	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs12708716	11179873	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs7203793	11182134	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs12935413	11210447	A	0.8884	4.289	1.72E-04	0.940	0.501	Intron 19
rs8064154	11219419	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 21
rs12924112	11219720	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 21
rs4322688	11238991	G	0.8884	4.289	1.72E-04	0.940	0.501	Intron 22
rs12930373	11239599	A	0.8884	4.289	1.72E-04	0.940	0.501	Intron 22
rs2903692	11238783	A	0.8884	4.289	1.72E-04	0.940	0.529	Intron 22
rs35732840	11228355	G	0.8934	4.306	1.64E-04	0.875	0.467	Intron 22
rs2867880	11231857	A	0.8934	4.306	1.64E-04	0.875	0.467	Intron 22
rs12917893	11239978	T	0.8518	3.994	3.88E-04	0.875	0.467	Intron 22
rs7200940	11164567	G	0.7586	3.799	6.61E-04	0.844	0.645	Intron 19
rs8062322	11092319	A	0.7974	3.502	1.47E-03	0.834	0.578	Intron 10
rs9926367	11093179	C	0.7974	3.502	1.47E-03	0.834	0.578	Intron 10
rs11860603	11165017	C	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs9934969	11166002	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs11865121	11166688	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs7198621	11167458	G	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs12925642	11171602	G	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs2058531	11172109	G	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs9652601	11174365	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs9652582	11174564	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs2041670	11174652	T	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs12708715	11177824	T	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs9888908	11181244	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs12928537	11191400	A	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs12927355	11194771	T	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs741172	11200798	T	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs9746695	11207894	C	0.7596	3.586	1.17E-03	0.790	0.622	Intron 19
rs12924729	11187783	A	0.6429	3.1	4.19E-03	0.737	0.511	Intron 19

SNP	Position (Hg19)	Minor Allele	β^*	STAT*	P-value*	r^2 rs7403919†	r^2 rs34306440†	Location‡
rs34540843	11221287	G	0.9382	2.98	5.67E-03	0.600	0.680	Intron 22
rs62026379	11241806	A	0.9382	2.98	5.67E-03	0.600	0.680	Intron 22
rs17673553	11241906	G	0.9382	2.98	5.67E-03	0.600	0.680	Intron 22
rs34306440§	11215035	G	0.8521	2.561	1.57E-02	0.533	1.000	Intron 20
rs35032408	11215424	G	0.8521	2.561	1.57E-02	0.533	1.000	Intron 20
rs36045143	11224966	G	0.9253	2.95	6.10E-03	0.500	0.600	Intron 22
rs2241099	11225064	G	0.9253	2.95	6.10E-03	0.500	0.600	Intron 22
rs62026376	11228712	T	0.9253	2.95	6.10E-03	0.500	0.600	Intron 22
rs62026377	11229128	T	0.9253	2.95	6.10E-03	0.500	0.600	Intron 22
rs12919732	11235123	G	0.8494	2.649	1.28E-02	0.500	0.600	Intron 22
rs12919828	11226779	G	0.9253	2.95	6.10E-03	0.485	0.592	Intron 22
rs7203459	11230703	C	0.8583	2.663	1.23E-02	0.412	0.529	Intron 22
rs12708713	11072459	T	0.5901	1.6	1.20E-01	0.394	0.638	Intron 8
rs12708714	11072525	C	0.5901	1.6	1.20E-01	0.394	0.638	Intron 8

Samples are sorted in order of r^2 relative to rs740319 (most significant SNP that is associated with *DEXI* expression levels).

*Statistical analysis performed using expression and genotyping data.

† r^2 values were calculated using genotyping data for 33 HapMap samples and the designated SNP as reference. ‡Intronic regions were based on Ensembl (CLEC16A - 001 ENST00000409790) (67).

§Most Significant SNP associated with type 1 diabetes.

β , linear regression coefficient; STAT, coefficient t-statistic; r^2 , correlation.

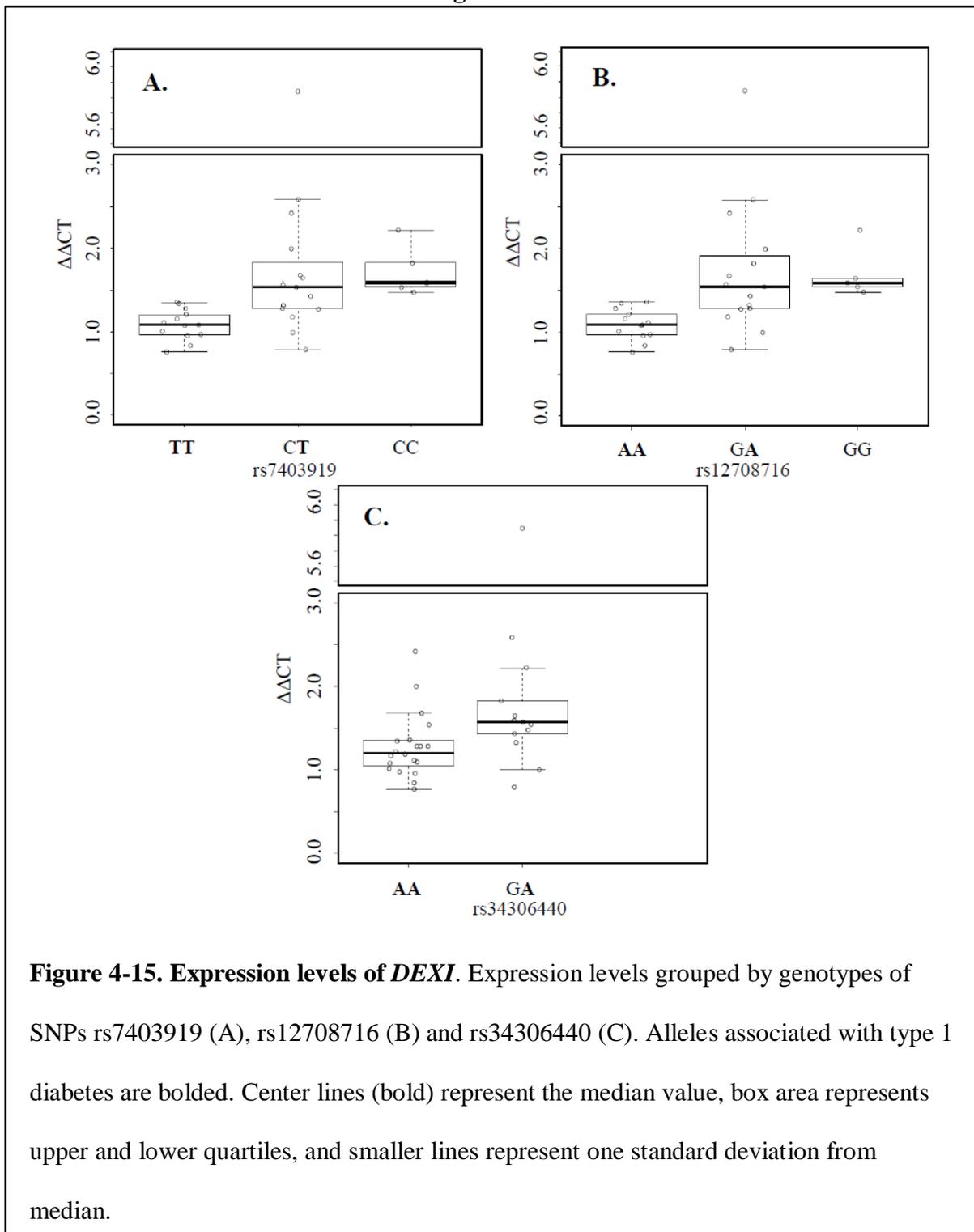
Table 4-6Top eQTL SNP *P*-values for each gene tested

Gene	Most Sig. SNP	BP (Hg19)	<i>P</i>-value
<i>CIITA III</i>	rs7199828	11006262	2.14 x 10 ⁻³
<i>CIITA IV</i>	rs4381620	11477757	1.26 x 10 ⁻²
<i>CLEC16A Iso I</i>	rs431918	11365416	5.36 x 10 ⁻³
<i>CLEC16A Iso II</i>	rs243329	11352313	3.33 x 10 ⁻²
<i>CLEC16A Iso III</i>	rs11074964	11455169	7.64 x 10 ⁻⁴
<i>DEXI</i> *	rs7403919	11085968	1.25 x 10 ⁻⁴
<i>SOCS1</i>	rs77309215	11261183	3.20 x 10 ⁻³
<i>CIITA V</i>	rs34033173	10982933	1.41 x 10 ⁻²
<i>CIITA VI</i>	rs4129933	11528893	2.68 x 10 ⁻²

*Only SNP *P*-value that reached statistical significance was found in the eQTL study for *DEXI* located in intron 10 of *CLEC16A*. (Bonferroni corrected $P \leq 1.37 \times 10^{-4}$)

We specifically examined the expression levels of *DEXI* in relation to three SNPs: rs34306440 (the SNP most strongly associated with type 1 diabetes in the region), rs7403919 (the SNP most strongly associated with variation in *DEXI* expression in the region) and rs12708716 (most often cited in type 1 diabetes literature) (Figure 4-15). For all three SNPs the risk allele always corresponded to the major allele. The homozygotes for the risk alleles had lower expression of *DEXI*, whereas the heterozygotes and homozygotes for the alternative allele displayed higher levels of expression.

Figure 4-15



Relationship of SNPs Associated with Type 1 Diabetes and/or DEXI Expression

In order to more broadly characterize the relationship between disease risk and *DEXI* expression we plotted the odds ratio (OR) for type 1 diabetes versus the linear regression coefficient (β) representing *DEXI* expression level for the minor alleles of all 809 SNPs for which these data were available (Figure 4-16). Disease risk was negatively correlated with *DEXI* transcript levels, Pearson correlation ($R = -0.66$). All SNPs for which statistically significant associations with type 1 diabetes were observed clustered in the lower right quadrant of the graph corresponding to the low disease risk and increased *DEXI* expression.

Figure 4-16

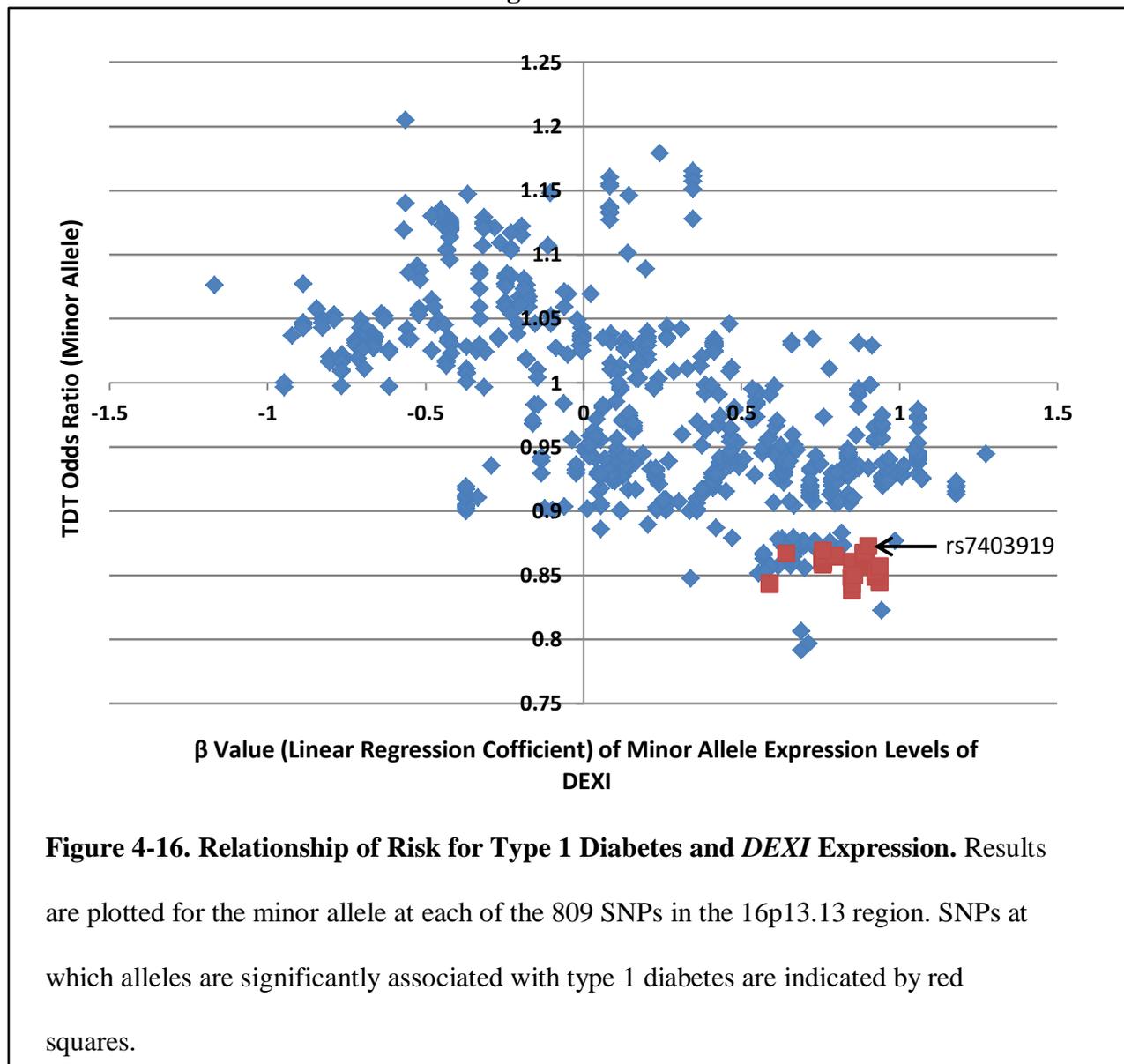


Figure 4-16. Relationship of Risk for Type 1 Diabetes and *DEXI* Expression. Results are plotted for the minor allele at each of the 809 SNPs in the 16p13.13 region. SNPs at which alleles are significantly associated with type 1 diabetes are indicated by red squares.

Discussion

Chromosomal region 16p13.13 is one of a large number of regions where there is significant, replicated evidence of allelic association with type 1 diabetes (2-5), as well as with other autoimmune disorders. As these different disorders have disparate target organs and pathologies, such findings of association imply that the loci in question have basic autoimmunity-predisposing effects.

Repeated findings of association for multiple autoimmune disorders in a single chromosomal region like 16p13.13 increases both confidence in the initial findings and the importance of the locus in understanding the underlying mechanism whereby autoimmunity develops. However, functional studies that might elucidate the mechanism depend upon the ability to specify the relevant gene in the region, if not the specific causative genetic variants. In the current study, we addressed this need for the 16p13.13 region by resequencing the region in a large collection of type 1 diabetes cases and unaffected controls to identify all common variants, genotyping these variants in a collection of multiplex type 1 diabetes families, and then separately testing for association of alleles at these SNPs with disease state and transcript levels for each of the genes in the region.

There were 46 novel variants from our re-sequencing that were included among the 939 SNPs that we genotyped in 3,070 multiplex families with type 1 diabetes. Forty-eight of these SNPs displayed a statistically significant association with type 1 diabetes. These included several SNPs that provided the most significant findings in this region in other autoimmune diseases such as rs11865121 in MS (7) and rs12924729 in PBC (10).

In all cases, it was the major allele that conferred risk for type 1 diabetes. Alleles at these 48 SNPs were not all highly correlated (pairwise r^2 range from 0.4 to 0.9), nor were the SNPs physically clustered. All of these 48 SNPs were located in introns that spanned much of the *CLEC16A* gene (introns 8-22).

The broad physical distribution of disease associated SNPs and their modest correlation raise the possibility that they either act through multiple mechanisms or the SNPs could affect multiple genes. Given their intronic locations and prior reports of cis-oriented transcriptional effects in the region, we tested for association between our entire panel of SNPs and transcripts levels for each of the documented alternatively spliced forms of the four genes in the region, *CIITA*, *DEXI*, *CLEC16A* and *SOCS1*. Only for *DEXI* were statistically significant results obtained. Similar to the disease association results, SNPs associated with *DEXI* transcript levels appear to be distributed across much of the *CLEC16A* gene. A comparison of *DEXI* expression levels in cell lines grouped by genotype at one of three disease-associated SNPs suggested that risk for disease was associated with reduced expression of *DEXI*. To explore this hypothesis more globally, we examined the relationship between the odds ratio for the minor allele at each SNP in the region and the corresponding linear regression coefficient for *DEXI* expression for the same allele. *DEXI* expression was negatively correlated with disease risk ($R = -0.66$).

Our results suggest that genetic variation over a broad region spanning much of the *CLEC16A* gene influences the expression of a neighboring gene, *DEXI* and that reduced *DEXI* expression is correlated with increased risk for type 1 diabetes. This model is consistent with a prior report that sequences in intron 19 of *CLEC16A* can interact with

the promoter region of *DEXI* (45). Our results suggest that the region of interaction may be large or that distal sequences may act indirectly to affect the stability or structure of the DNA loops formed.

Our results and those from prior studies focus attention on *DEXI* as the gene most likely to affect risk for type 1 diabetes in the 16p13.13 region. Little is known about the function of *DEXI* and its predicted 95 amino acid protein product. The protein is well-conserved, with orthologues readily detectable in multiple species. There is 95% identity between the human and mouse orthologues and 84.5% between human and zebrafish.

There are no identifiable domains in *DEXI* that might suggest a possible function for the protein. However, Miyaki *et al* showed that siRNA mediated knockdown of *DEXI* reduced the incidence of apoptosis in cells treated with the chemotherapy agent camptothecin (68). A role in a basic cellular function such as apoptosis would be consistent with the involvement of *DEXI* in multiple autoimmune diseases with different target tissues.

Acknowledgements for Research Work

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Chapter 5

Future Directions

Introduction

Clearly from this study we have unanswered questions about chromosomal region 16p13.13. Based on our data future research should be focused on understanding *DEXI*'s function and how changes in its expression confer risk for type 1 diabetes. Even though in our experiments we encountered novel isoforms of *CIITA* that could influence the region, none of our data supported these isoforms involvement. This finding may be due to lack of statistical power, wrong cell type tested or cytokine stimulation is needed, however due the lack of evidence for involvement the novel isoforms will not be examined further. Since chromosomal region 16p13.13 is one region out of many associated with type 1 diabetes, a much broader discussion of future studies with a more global approach will conclude the dissertation.

Investigating *DEXI*

Understanding the function of the previously uncharacterized protein, *DEXI*, is the most essential part of understanding how this region confers risk for type 1 diabetes and other autoimmune diseases. As mentioned previously, *DEXI* is a 14 KB gene that is transcribed in the opposite direction to *CIITA* and *CLEC16A*. *DEXI* is composed of two exons (only 1 coding) and codes for a protein 95 amino acids long (1).

DEXI has been implicated in two possible immune response related pathways. In yeast two-hybrid screens, *DEXI* was found to interact with the Golgi membrane protein 1 (*GOLM1*) and tubulin-specific chaperone D protein (*TBCD*) (2). *GOLM1*, also known as *GP73*, has been found to be up-regulated in a viral infection (3) and *TBCD* is a protein

involved in helping beta-tubulin fold correctly (4). In another study siRNA mediated knockdown of *DEXI*, reduced the incidence of apoptosis in cells treated with the chemotherapy agent camptothecin (5). This indicates that *DEXI* is possibly involved in either an anti-viral response or apoptosis or a combination of both.

Interestingly, there are two intronless retro-*DEXI* genes located at 15q11.2 and 15q13.1 in a chromosomal region known for duplications and imprinting which have been implicated in causing Prader-Willi/Angelman syndrome (6,7). Davison *et al* showed that the 15q11.2 version is minimally expressed in cells, especially lymphoblastoid cells (8) and version 15q13.1 straddles across two genes. Therefore the duplication of *DEXI* raises evolutionary questions and also complicates future experiments that need to be carefully controlled for the presence of these pseudogenes.

DEXI has no identifiable domains that could suggest function. The major focus for future research should be investigating expression levels of *DEXI* in other tissues and specifically investigating individuals with the risk alleles. Based on our data it appears expression levels of *DEXI* are the key mode of conferring risk for disease. However further investigation into the protein *DEXI* is needed in order to completely understand how it functions in a cell and causes apoptosis.

Using the previously utilized primer pair the expression levels of *DEXI* can be investigated in other tissues and cell types. It is important when performing this assay that activated T and B cells be investigated as well as resting cells because the levels of expression can easily change in inactivated/activated immune cells. *DEXI* was originally identified as being upregulated in the lungs of emphysema patients (9), and this

upregulation was suggested to be likely due to the exposure to cigarette smoke (8), hinting at an immune response to toxic chemicals (apoptosis??). This also implies that investigating DEXI expression specifically in type 1 diabetic patients is essential for defining the specific immunological response. However, the change in mRNA level does not always correspond to measurable difference in protein levels, so investigating the protein levels is important.

Measuring DEXI's protein levels and determining what proteins it interacts with are essential. In order to begin such studies, high affinity antibodies that stain DEXI and other possible interacting proteins need to be designed or purchased. Currently, commercial antibodies for DEXI are available from Sigma Aldrich and other sources. As previously mentioned, in a yeast two-hybrid screen DEXI was found to interact with GOLM1 and TBCD (2). GOLM1 might be a good candidate for further study because of its involvement in virus response. Commercial antibodies are available for this protein from Sino Biological Inc. The TBCD protein seems like an unlikely candidate for involvement in an autoimmune disease although an unknown biochemical relationship could exist.

Using the high affinity antibodies or epitope tag, protein complex immunoprecipitation (co-IP) experiments can be performed to confirm DEXI's expression levels and its interactions with GOLM1. Once a successful co-IP has been performed, the protein complex can be subjected to mass spectrometry. Mass spectrometry will allow for the validating of known interacting proteins and identification of any unknown interactions. It will also allow for identification of any post translational

modifications that occur. Identification of unknown interacting proteins will also help decipher the exact pathway that *DEXI* interacts in that up regulates cell apoptosis.

Determining the location and movement of the *DEXI* protein is the final phase to better understand how it triggers cell apoptosis. The protein will be tagged with a fluorescent tag like GFP and expressed in a cell. Using immunofluorescent microscopy the protein's exact location can be visualized. It can be speculated based on the interaction with *GOLM1* that *DEXI* could interact with/around the Golgi apparatus.

Deciphering the expression levels of *DEXI* in various tissues and individuals with type 1 diabetes is key to confirming how the region confers risk. Further investigations into the protein are needed to validate the change in expression seen in mRNA. Finally, validating/determining the proteins that *DEXI* interacts with and its location in the cell is important to decipher how it possibly causes apoptosis in a cell.

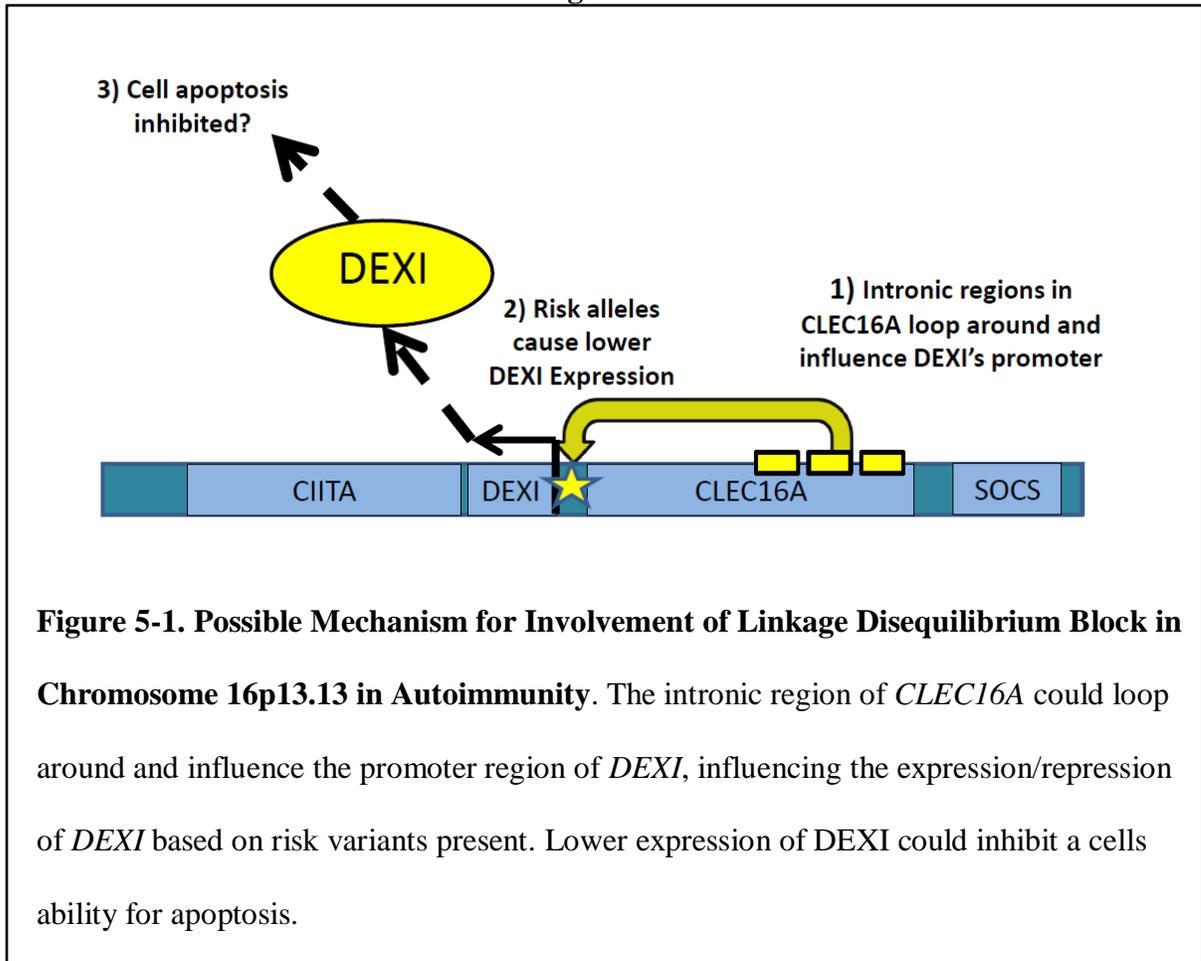
Possible Mechanisms Conferring Risk

Based on our findings the *CLECI6A* intronic region influences the expression of neighboring gene *DEXI*. Alleles associated with risk for type 1 diabetes correspond to lower expression of *DEXI*. This model is consistent with a previous finding where intron 19 of *CLECI6A* was found to interact with the promoter region of *DEXI* (8). However, our data suggests that this interaction may span multiple introns or the distal sequences in neighboring introns, which surround intron 19, influences the stability or structure of the loop. Now exactly how lower expression of *DEXI* confers risk is more theoretical and currently based on limited findings. As mentioned previously it was recently found that

DEXI interacts with GOLM1 (2), a golgi membrane protein upregulated in a virus infection. Also it was recently found when DEXI is knocked out by siRNA it inhibits the cell's ability for apoptosis (5). Based on all these findings a possible model can be hypothesized where the intronic regions of *CLEC16A* loop around and influence *DEXI*'s expression which inhibits a cells ability for apoptosis (Figure 5-1).

Exactly how this increases a individuals risk for type 1 diabetes will be explored further, but is all speculative. Assuming type 1 diabetes is triggered by a virus, lower *DEXI* expression could confer risk by inhibiting cell death during a viral infection in the pancreatic beta cells. By inhibiting apoptosis of cells a longer infection could occur, resulting in a more aggressive immune response later. A more aggressive immune response could result in a greater chance for autoimmunity to develop in the pancreas. This model is supported by the fact that DEXI interacts with GOLM1, a protein upregulated by a virus. A second model that is not viral based can also be hypothesised based on the inhibition of apoptosis. During the development of B and T cells they undergo a process of negative selection where cells that tightly bind to self antigens are removed. If any of these self reactive cells are inhibited from apoptosis, possibly caused by lower DEXI expression, they could allow for the escape of autoreactive T and B cells into the body and favor the development of autoimmunity. Clearly, these two models are very speculative and further investigations into the exact function of DEXI are needed to identify the exact mechanism of action.

Figure 5-1



Future Directions of Type 1 Diabetes Research

Clearly more time and resources are needed for deciphering the genetics behind type 1 diabetes. With the advent of GWAS the list of possible candidate regions has grown drastically and on average GWAS reported loci contain over 8.5 protein coding genes per region (10). Each of these regions require further fine mapping to identify the causative risk variant/variants. However, as seen in Chapter 4, fine mapping the region is very time consuming and may not truly identify the causative risk variant because of strong LD. Complicating issues further, as seen with chromosomal region 16p13.13, the risk variant identified by GWAS may confer risk for the disease by influencing a neighboring gene.

Future genetic studies of type 1 diabetes and other autoimmune diseases should utilize large expression microarrays in combination with GWAS panels to perform comprehensive eQTL analysis. This combination of investigation will ensure resources are not wasted pursuing genes that are associated with risk, yet have no direct influence on disease as seen with *CLEC16A*. This will narrow down the functional regions that confer risk for disease. Also, utilizing GWASs and expression data from other autoimmune disorders will help prioritize follow-up genes to study. The exact phenotypic change could ultimately be different as seen with *IL2RA* in type 1 diabetes and multiple sclerosis.

After thorough investigations of several regions identified in GWASs by fine mapping, genotyping and functional studies, SNPs were identified that clearly increase or decrease an individual's risk for disease. These risk-associated SNPs will be entered in a

database for type 1 diabetes and other autoimmune related diseases. This will add to the screening of individuals for risk with disease in a tiered risk system (11). It can be hypothesized that individuals that have the high risk MHC class II haplotype DR3/DR4, can have further increased risk if they have the HLA-A*02 allele (12) and an even greater risk if they have the shortest VNTR (class I) of the insulin gene (13).

Functional SNPs from GWAS constitute the next tier for example if the individual has risk variant/variants from *CLECI6A* that lowers *DEXI* expression this further increases their risk. However, this additive predicative model is indeed speculative at the time and per current findings the predictive power for type 1 diabetes risk after accounting for HLA is small (14,15). This limitation may be overcome by utilizing larger datasets that look at the complex interactions of SNPs (15). After all regions identified by GWAS have been fine mapped and risk variants identified, the predictive power may show a modest improvement. Currently, the established tool for predicting type 1 diabetes is identifying individuals with the high risk haplotype and monitoring them for development of autoantibodies (16,17). As previously mentioned in Chapter 1, an individual's risk for developing type 1 diabetes increases as the number of autoantibodies increases rather than the titre of autoantibodies (18-20). Utilizing the tiered screening system in combination with testing for antibodies may help improve the predictive model and future screening.

This tiered system would allow for more precise and personally adapted treatment/prevention for an individual's risk for developing type 1 diabetes and other autoimmune diseases. Utilizing this screening method might also help to ultimately

identify the environmental trigger/triggers of type 1 diabetes and sub types of the disease. Currently, type 1 diabetics are diagnosed based on the fact they no longer produce insulin, but they could be sub-grouped based on age of onset and severity. In the future, each individual may be assessed for combinations of factors which ultimately predict their risk for developing type 1 diabetes and other autoimmune diseases and allow for medical intervention/prevention.

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