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Ptpn22 and Cd2 Variations Are Associated with Altered Protein Expression and Susceptibility to Type 1 Diabetes in Nonobese Diabetic Mice

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By congenic strain mapping using autoimmune NOD.C57BL/6J congenic mice, we demonstrated previously that the type 1 diabetes (T1D) protection associated with the insulin-dependent diabetes (Idd)10 locus on chromosome 3, originally identified by linkage analysis, was in fact due to three closely linked Idd loci: Idd10, Idd18.1, and Idd18.3. In this study, we define two additional Idd loci—Idd18.2 and Idd18.4—within the boundaries of this cluster of disease-associated genes. Idd18.2 is 1.31 Mb and contains 18 genes, including Ptpn22, which encodes a phosphatase that negatively regulates T and B cell signaling. The human ortholog of Ptpn22, PTPN22, is associated with numerous autoimmune diseases, including T1D. We, therefore, assessed Ptpn22 as a candidate for Idd18.2; resequencing of the NOD Ptpn22 allele revealed 183 single nucleotide polymorphisms with the C57BL/6J (B6) allele—6 exonic and 177 intronic. Functional studies showed higher expression of full-length Ptpn22 RNA and protein, and decreased TCR signaling in congenic strains with B6-derived Idd18.2 susceptibility alleles. The 953-kb Idd18.4 locus contains eight genes, including the candidate Cd2. The Cd2 pathway is associated with the human autoimmune disease, multiple sclerosis, and mice with NOD-derived susceptibility alleles at Idd18.4 have lower Cd2 expression on B cells. Furthermore, we observed that susceptibility alleles at Idd18.2 can mask the protection provided by Idd10/Cd101 or Idd18.1/Vav3 and Idd18.3. In summary, we describe two new T1D loci, Idd18.2 and Idd18.4, candidate genes within each region, and demonstrate the complex nature of genetic interactions underlying the development of TID in the NOD mouse model. The Journal of Immunology, 2015, 195: 4841–4852.

The NOD mouse spontaneously develops autoimmune diabete and other endocrine autoimmune disorders (1), and has greatly facilitated studies of type 1 diabetes (T1D) (2). To identify genes associated with T1D, our laboratory uses a congenic strain mapping strategy. Through the construction of a series of congenic strains, by the introgression of segments of DNA from the T1D-resistant mouse strains B6 or C57BL/10J (B10) onto the genetic background of the susceptible NOD

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mouse strain, we have previously located 14 insulin-dependent diabetes (Idd) loci (3). Five B6 protective loci—in which B6-derived alleles, compared with NOD-derived alleles, confer T1D protection—have been identified on chromosome 3: Idd3, Idd17, Idd10, Idd18.3, and Idd18.1 (4–7). In addition to T1D protection, B6- or B10-derived alleles, compared with NOD-derived alleles, can also confer T1D susceptibility. Idd7 and Idd8 loci, identified with linkage analysis, have B10-derived alleles that confer susceptibility to T1D (8), and congenic strain mapping has established Idd14 as a B6-susceptibility allele (9) and Idd5.4 as a B10-susceptibility allele (10).

In this study, we report the identification of an additional B6-susceptibility allele between Idd10 and Idd18.3, designated Idd18.2. The 1.31-Mb Idd18.2 locus contains 18 protein-encoding genes, including two strong candidates based on their known immune functions, Ptpn22 and Nras. The human ortholog of Ptpn22, PTPN22, is associated with T1D and 15 other autoimmune diseases, including rheumatoid arthritis, Graves disease, Addison disease, and systemic lupus erythematosus (11). In addition, a functional coding variant of rat Ptpn22 has been shown to be associated with T1D in the BioBreeding rat (12). Ptpn22 encodes a hematopoietic cell lineage-specific protein tyrosine phosphatase (LYP and PEP in human and mouse, respectively) that negatively regulates T (13) and B cell signaling (14, 15). We identified 183 single nucleotide polymorphisms (SNPs), 6 exonic and 177 intronic, between the B6- and NOD-derived alleles of Ptpn22 suggesting a likely functional difference. Further investigation revealed that spleen cells and thymocytes from mice with B6-derived susceptibility alleles at Idd18.2 express higher levels of Ptpn22 mRNA and PEP protein than the equivalent cell populations from NOD mice.

The congenic strain mapping strategy used to localize Idd18.2 also revealed an additional Idd locus, Idd18.4, which is 953 kb long and is immediately telomeric to Idd10. Idd18.4 contains eight genes, including the candidate Cd2. Cd2 is a cell adhesion molecule expressed on immune cells. The primary ligand of Cd2 is CD58 in humans and CD48 in rodents (16), and the interactions between these molecules is important in the formation of the immunologic synapse (17). The CD2/CD58/CD48 pathway is associated with the human autoimmune diseases multiple sclerosis and rheumatoid arthritis (18, 19) and with a model of murine lupus (20). Our studies reveal that congenic strains with NOD-derived susceptibility alleles at Idd18.4 have lower Cd2 expression on B cells.

Materials and Methods

Oligonucleotides and genotyping

Primer3 (21) was used to design primers for PCR, RT-PCR, and primer and probe sets for real-time quantitative RT-PCR (qPCR). These were synthesized by Sigma-Genosys; the probes were dual labeled with TAMRA and FAM fluorescent dyes. Sequences of D3Nds and D3Mit microsatellite markers are available at http://www.gene.cimr.cam.ac.uk/nod/public_data/mouse/NDS/NDSMicrosTop.html and http://wwwensembl.org/Mus_musculus/Info/Index, respectively. Other Idd10 and Idd18 markers have been published previously (7, 22). All remaining primers and probes used in this study are available in Supplemental Tables I, IIB, and IID. Methods for DNA extraction, microsatellite, and RFLP genotyping have been described previously (7).

Animals and diabetes frequency studies

All mice were housed under specific pathogen-free conditions, and the appropriate institutional review committee approved experimental procedures. NOD/MrkTacBr (henceforth designated as NOD) mice were purchased from Taconic Farms. The derivation of the following congenic strains has been described previously: line 3539, NOD.B6 Idd10 (N16) (22); line 1538, NOD.B6 Idd Idd10 Idd18.323 (N12) (4); line 1100, NOD.B6 Idd3 Idd10Idd18.2 (N12) (7); and line 1101, NOD.B6 Idd18.4 (N8) (5), now designated as line 7754 (N9) (7). R8 (N9) was developed contemporaneously with the strains described in Podolini et al. (5).

To develop line 2410 (NOD.B6 Idd10, Idd18.3, Idd18.1; N14), mice from line 1100 were crossed to line 1538, and the resulting progeny were intercrossed. F2 progeny with a recombination event immediately centromeric to Idd18.3, resulting in a chromosome that contained B6-derived alleles at Idd10 (from line 1100) and B6-derived alleles at Idd18.3 and Idd18.1 (from line 1538), but NOD-derived alleles between Idd10 and Idd18.3 were backcrossed to NOD. Progeny heterozygous for the desired recombinant chromosome were backcrossed to NOD again to remove the B6-derived alleles at Idd3 by recombination. The resultant progeny were bred to homozygosity. To develop line 3539 (NOD.B6 Idd18.3, Idd18.1; N16), line 2410 was crossed to NOD and progeny were intercrossed; F2 progeny with a single B6-derived allele at Idd18 were selected, backcrossed to NOD, and bred to homozygosity. To develop lines 7848 (NOD. B6 Idd18.4, Idd18.2; N11) and 8010 (NOD.B6 Idd18.4; N11) B6 mice were crossed to NOD mice and progeny were backcrossed again to NOD for several generations while selecting for recombinants as close as possible to Ptpn22. The recombinant leading to line 7848 had a B6 allele spanning Cd2 and Ptpn22, and was backcrossed to NOD, intercrossed, and bred to homozygosity. During this intercrossing, an additional recombinant was found that had retained the B6 allele at Cd2 but had lost the allele at Ptpn22. This recombinant was backcrossed to NOD and bred to homozygosity to develop line 8010. Cumulative diabetes frequency studies were conducted and analyzed as described previously (7).

Verification of Ptpn22 and Cd2 gene structure, resequencing of Ptpn22 in the NOD mouse strain, and identification of Ptpn22 and Cd2 polymorphisms

To verify the Ptpn22 genetic structure, the mRNA sequence M90388 was aligned to the B6 bacterial artificial chromosome (BAC) clone spanning Ptpn22, AC124698, using est2genome (23). The genetic structure of Cd2 was verified in the same manner with mRNA sequence Y00023 and B6 BAC clone AC131184. Cd2 SNPs and additional polymorphisms were identified by manually comparing the genomic sequence spanning 2.5 kb upstream of the initiation codon to 2.5 kb downstream of the polyadenylation signal (total distance, 16,945 bp) using AC131184 and the NOD BAC clone, AL672260.25.

To resequence Ptpn22 in the NOD mouse strain, the BAC clone end sequences from the NOD library were aligned against the B6 mouse genome sequence (24). From this, three NOD BAC clones spanning Ptpn22, forming a 465-kb minimal sequencing tile path, were sequenced at the Wellcome Trust Sanger Institute (WTSI) and deposited at the European Molecular Biology Laboratory (http://www.ebi.ac.uk; clone DN-252529, accession number CU210935; DN-31A8, CU210953; and DN-69P21, CU210868). To identify Ptpn22 and Cd2 SNPs computationally between NOD and B6, the NOD BAC clone sequences were fragmented into 1-kb sequences and aligned to the B6 mouse chromosome 3 sequence (NCBIM37) using the sequence search and alignment by hashing algorithm program (25), detected SNPs were filtered using RepeatMasker (26) to exclude SNPs present in regions of repeats or low complexity. The alignments spanning the coding sequence and splice sites of Ptpn22 were checked manually to confirm SNPs and to identify additional polymorphisms.

Sequence from whole genomic next-generation sequencing (NGS) for the related NOD/Sl/J strain (25,3-fold coverage) has become available through the Mouse Genomes Project at the WTSI (http://www.sanger.ac.uk/resources/mouseigenomes/). SNPs with a Phred score ≥ 50, identified by comparing the NCBIM37 reference sequence against the NGS NOD/Sl/J, were downloaded for the region spanning the Idd18.4 and Idd18.2 loci. SNP density plots for the BAC sequencing and NGS-determined SNPs were generated by counting the number of SNPs in 10-kb windows using 2 kb at a time, plotting the count at the midpoint of each window. For each gene in and between the Idd18.4 and Idd18.2 intervals, the Gene Scan (maximum genomic interval [NCBIM37] required to span all transcript models) for each gene was calculated from annotations present in RefSeq (NCBIM37) (27), CCDS (Release 7) (28), UCSC (mm9, http://genome.ucsc.edu/) (29), and Ensembl and Vega (both Release 67) (30). All annotations described above were entered into the T1DBase (31) displayed graphically using Gbrowse (32) and can be viewed at http://www.t1dbase.org.

Identification and RNA expression of alternatively spliced Ptpn22 transcripts

For expression studies, total RNA was extracted using TRIzol (Invitrogen) following the manufacturer’s instructions. Whole organs were immediately homogenized in TRIzol using a Polytron homogenizer, and single-cell suspensions were obtained for thymocytes before addition to TRIzol.
One microgram of total RNA was then used to make cDNA using SuperScript II reverse transcriptase (Invitrogen) following the manufacturer’s instructions. To identify alternatively spliced transcripts of Ptpn22, M90388 was searched against the mouse expressed sequence tag (EST) database at the National Center for Biotechnology Information using the basic local alignment search tool (33). Thirteen ESTs were identified and aligned to AC124698 using est2genome (23); these predicted six novel alternatively spliced transcripts, four of which were confirmed by the ability of primers spanning the unique exon-exon boundaries to amplify spleen or kidney cDNA from NOD and line 1101 congenic mice (Supplemental Table II B). RT-PCR on the same cDNA using a range of Ptpn22 exonic primers that spanned few or many exons identified products with unexpected sizes that were gel extracted using the QIAquick Gel Extraction Kit (Qiagen) following the manufacturer’s instructions, and sequenced to identify nine additional alternatively spliced transcripts with additional or spliced out exons (Supplemental Table I IC). Primer and probe sets were designed to the unique regions of full-length and a selection of alternative transcripts of Ptpn22 (Supplemental Table IID) and qPCR was used to assess the expression levels of these transcripts and β2-microglobulin in an ABI Prism 7300 Real-Time PCR system (Applied Biosystems) in thymocytes from 3- to 8-week-old male mice and whole spleen from 9-week-old female mice, both from lines 2410 and 1101. All reactions were performed using TaqMan Universal Master Mix. The expression levels are given as ΔCt, which is calculated by subtracting the cycle threshold value (the cycle number at which message is first detected) for β2-microglobulin from the cycle threshold value for each assessed transcript. Lower ΔCt values indicate higher RNA levels. As the cycle thresholds were detected in the exponential phase of amplification, a 1-ΔCt difference is equivalent to a 2-fold change, and a 4-ΔCt difference equals a 16-fold change in RNA levels. Differences in expression were compared using Student unpaired, two-tailed t test (GraphPad Prism software).

**PEP expression**

Single-cell suspensions were prepared from thyhi obtained from 6- to 8-week-old mice. Erythrocytes were lysed using RBC lysis buffer (Sigma), and the remaining thymocytes were washed in 1× RPMI 1640 (Mediatech), pelleted, and lysed in 1× TNE (10 mM Tris [Fisher], 0.2 M NaCl [Sigma], 1 mM EDTA, pH 7.4 [Sigma]) with 0.1% NP40, 10 μg/ml soybean trypsin inhibitor, and 10 μg/ml aprotinin and leupeptin (all from Sigma). Equal amounts of total lysate from each mouse were loaded onto 10% Tris glycine polyacrylamide gel (Invitrogen), blotted onto nitrocellulose membrane, probed with rabbit polyclonal anti-PeP Ab (1:3000; provided by Andrew C. Chan, Genentech) or mouse anti-α-TUBULIN Ab (1:2000; Santa Cruz Biotechnology), and respective secondary Abs linked to HRP (GE Healthcare), and detected with ECL (GE Healthcare) and autoradiography films (HyBlot CL; Denville Scientific). The films were scanned, backgrounds were adjusted using Adobe Photoshop CS3, and densitometry readings were obtained using ImageJ software (34). Relative ratios of PEP to α-TUBULIN were calculated for each of the four independent blotting experiments by normalizing each ratio to the lowest ratio obtained in each experiment. The relative ratios for congenic mice with NOD- or B6-derived alleles at Ptpn22 were pooled, and the Mann-Whitney U test was used to calculate statistical significance (GraphPad Prism software).

**Measuring p44-MAPK phosphorylation**

Splenocytes were dissociated into single-cell suspensions and filtered through a nylon strainer (70 μm). RBCs were lysed by addition of water, followed by equal volumes of 2x PBS and RPMI 1640. Spolenic T cells were isolated by negative depletion by incubation with rat anti-mouse B220 and rat anti-cDNA11b (M1/70) Abs, followed by incubation with sheep anti-Rat IgG Dynabeads (Invitrogen). T cells were resuspended in RPMI with 5% FBS and warmed to 37°C for 5 min. For stimulation, 20 μg/ml anti-money CD3 (2C11) was added, followed by the addition of 20 μg/ml mouse anti-Armenian and Syrian Hamster IgG Abs (G94-56; BD Pharmingen). Cells were incubated for 2 min at 37°C and lysed immediately in 1× Cell Lysis Buffer (Cell Signaling Technology). Levels of phospho-p44 MAPK were measured by ELISA using the PathScan Phospho-p44 MAPK (Thr202/Tyr204) Sandwich ELISA Ab Pair (Cell Signaling Technology) following the manufacturer’s instructions. Samples were performed in triplicate and averaged. Statistical significance of the difference between conegenic mouse strains was determined by Student unpaired, one-tailed t test (GraphPad Prism software).

**CD2 Ab staining and flow cytometry analysis**

Single-cell suspensions were prepared from the spleen and bone marrow obtained from 8- to 12-week-old mice. Cells were stained using B220-PerCP and CD2-FITC (both from BioLegend) and analyzed on a FACSCalibur (Becton Dickinson) using FlowJo software (Tree Star). The mean fluorescence intensity (MFI) of CD2 on various cell subsets was determined, and the Mann–Whitney U test was used to calculate statistical significance between groups (GraphPad Prism software).

**Results**

**Identification of a B6 susceptibility allele, Idd18.2, located between Idd10 and Idd18.3**

The previously published congenic strain mapping of the Idd10 and Idd18 loci detailed in Podolin et al. (5) involved the development of several congenic strains including one not reported in that study, line R8. This strain was homozygous for a single B6 introgressed segment located between Idd10 and Idd18.3 (Fig. 1A) and, unexpectedly, was more susceptible to T1D than NOD mice (p = 2.0 × 10⁻³; Fig. 1B). We, therefore, hypothesized that a B6 susceptibility allele, designated Idd18.2, exists between Idd10 and Idd18.3 in the introgressed segment present in line R8. To confirm the existence of Idd18.2, we developed a new congenic mouse strain, line 2410, which has NOD alleles at Idd18.2 and is homozygous for two B6 introgressed segments: one spanning Idd10 and the second spanning Idd18.3 and Idd18.1 (Fig. 1A). Line 2410 mice have a lower T1D frequency (p = 3.0 × 10⁻²; Fig. 1C) compared with the control strain, line 1101, which is homozygous for a single B6 introgressed segment spanning Idd10, Idd18.2, Idd18.3, and Idd18.1 (Fig. 1A). The T1D frequency comparison of lines 1101 and 2410 was repeated in a later study and produced the same results (Fig. 1D; 1101 versus 2410, p = 5.4 × 10⁻⁶). As lines 1101 and 2410 differ only at Idd18.2, these results confirm that Idd18.2 is a B6 susceptibility locus, which can reduce the protection associated with the combined B6-derived alleles of Idd10, Idd18.3, and Idd18.1.

The Idd18.2 B6 susceptibility alleles partially mask the protection associated with the B6-derived alleles of Idd10, or Idd10 and Idd18.1.

The congenic strain mapping of Idd10 and Idd18 (now known to be composed of two loci, Idd18.3 and Idd18.1) (7) has always been performed by truncating the Idd10 or Idd18 loci present in line 1101, NOD.B6 Idd10 Idd18.2 Idd18, or line 1538, NOD.B6 Idd3 Idd10 Idd18.2 Idd18. Truncation of either the centromeric Idd10 locus or the telomeric Idd18 locus reduced the T1D frequency to a NOD-like or nearly NOD-like frequency for those derived from line 1101 (5), and Idd3-like frequency for those derived from line 1538 (4). Our interpretation at the time was that the truncated congenics contained only a single Idd locus, either Idd10 or Idd18, in those derived from line 1101, or two Idd loci, either Idd3 and Idd10 or Idd3 and Idd18, in those derived from line 1538, and that both Idd10 and Idd18 were required in combination to observe substantial T1D protection, and either locus alone did not confer protection. However, with the existence of the B6 susceptibility allele Idd18.2, located between Idd10 and Idd18 now evident in the current study, we now know that what we thought were isolated Idd10 and Idd18 congenic segments, with or without Idd3, actually also contained the B6 susceptibility alleles of the Idd18.2 locus. To observe the protection of isolated Idd10 and Idd18 loci without the presence of the B6 susceptibility alleles at Idd18.2, we separated the Idd10 and Idd18 DNA segments present in line 2410 and performed a frequency study on the resulting NOD.B6 Idd10 (line 3538) and NOD.B6 Idd18 (line 3539) congenic strains (Fig. 1A). Both congenic strains, NOD.B6 Idd10 and NOD.B6 Idd18, were highly protected from T1D as compared with NOD (p = 2.2 × 10⁻⁷, 2.9 × 10⁻⁵, respectively; Fig. 1D). Remarkably, the Idd18 locus present in line 3539 provided as much...
T1D protection as the combination of the isolated Idd18 and Idd10 segments (line 2410). This indicates that in the previous studies, where we had observed negligible T1D protection in the congenic strains with B6-derived alleles at Idd10 and Idd18.2 or Idd18.2 and Idd18 that the B6-derived Idd18.2 susceptibility alleles had been masking the protective effects of the Idd10 and Idd18 protective loci.

**Novel congenic strains, lines 7848 and 8010, help refine Idd18.2 to a 1.31 Mb locus and confirm the candidacy of Ptpn22**

Of the two congenic strains (lines R8 and 2410) that delineate the Idd18.2 locus, line R8 has the smaller locus and, thus, defines Idd18.2 as a 4.8-Mb locus between, but not including, the microsatellite markers AC122219_3 and R8_micro_2 (Fig. 1A). This locus contains 71 genes, the most centromeric and telomeric being Nrt1h5 and Aehy11, respectively. At least seven of these are involved in autoimmune diseases or immune cell function: Ptpn22, Adora3, Rbm15, Lrig2, Cd53, Nras, and a cluster of six chitinase-like genes. Ptpn22 is the most striking candidate, as the human ortholog, PTPN22, is associated with several autoimmune diseases (35).

To confirm the positional candidacy of Ptpn22, we developed two new congenic strains, lines 7848 and 8010, which are homozygous for B6 introgressed segments in Idd18.2 that share the same centromeric recombination point, but that differ at the telomeric recombination point, resulting in lines 7848 and 8010 having B6- and NOD-derived alleles at Ptpn22, respectively (Fig. 1A). Line 7848 congenic mice, which have B6 alleles at Ptpn22, have a higher frequency of T1D than line 8010 does, which has NOD alleles at Ptpn22 (p = 9.0 × 10⁻³; Fig. 1E). These results indicate that line 7848 contains the Idd18.2 B6 susceptibility locus and, therefore, confirms the candidacy of Ptpn22.

The locus delineated by lines 7848 and 8010 (Fig. 1A) overlaps with the Idd18.2 locus delineated by line R8 (Fig. 1A). As both loci contain Idd18.2, the Idd18.2 locus is, therefore, located between the centromeric recombination point in line R8 (between AC122219_3 and R8_p_SNp_1) and the telomeric recombination point in line 7848 (between Magt3 and Susc_96.62; Fig. 1A). Therefore, Idd18.2 is a 1.31-Mb locus between, but not including, the microsatellite markers AC122219_3 and Susc_96.62 (Fig. 1A), and contains only 18 protein-encoding genes, including the candidate Ptpn22 (Fig. 2A).

**Novel congenic strains, lines 7848 and 8010, also identify a second Idd locus, Idd18.4**

The diabetes protection provided by the small B6 congenic segment in line 8010 (Fig. 1A) as compared with NOD control mice was unexpected (Fig. 1E), and it leads to the localization of an additional B6 protective Idd locus, designated Idd18.4, located between Idd10 and Idd18.2 (Fig. 1A). Idd18.4 is defined by the centromeric (Ptgfrn_Int1_SNP2 and AL672281_7) and telomeric (D3Mit77 and Ch3:101,864) recombination points in line 8010 to a 953-kb locus between, but not including, markers Ptgfrn_Int1_SNP2 and Ch3:101,864. The centromeric recombination point of Idd18.4 and the telomeric recombination point of Idd10 (22) are located between the same polymorphisms, Ptgfrn_Int1_SNP2 and AL672281_7. The B6 and NOD BAC clone sequence between these polymorphisms is identical in NOD and B6. Therefore, the NOD/B6 polymorphisms present in the Idd10 and Idd18.4 loci are distinct, and the protection observed for line 8010 is due to Idd18.4 alone and not Idd10. Idd18.4 contains eight genes (Fig. 2A), including the candidate Cd2. The interactions between CD2 and the murine and the human ligands (CD48 and CD58, respectively) are important for immune function. These genes are associated with several human autoimmune diseases, including multiple sclerosis and rheumatoid arthritis, and with a murine model of lupus (18–20).

**Resequencing of Ptpn22 reveals a high degree of variation between NOD and B6, but excludes an analogous R620W human polymorphism**

In humans, the PTPN22 variant associated with susceptibility to autoimmune disease is a nonsynonymous SNP, R620W, in exon 14, which encodes a proline-rich region that interacts with C-terminal Src kinase. We therefore tested the possibility that an analogous polymorphism was present in Ptpn22. To identify any sequence polymorphisms in Ptpn22 between NOD and B6, three NOD BAC clones spanning Ptpn22 (Fig. 2A) were selected and sequenced at the WTSI. Mouse Ptpn22 spans 52 kb and consists of 21 exons. All the donor and acceptor splice sites of mouse and human PTPN22 genes are in agreement with the canonical GT-AG splice site except for the splice site between mouse exons 13 and 14 that contains a noncanonical GC-AG splice site (36). Six SNPs between NOD and B6 were identified in the coding sequence of Ptpn22 (Supplemental Table IIA), five of which were synonymous.
FIGURE 2. Idd18.2 and Idd18.4 annotation and sequence polymorphisms in NCBIM37. (A) The congenic boundaries of line 8010 define the Idd18.4 locus, and the centromeric boundary of line R8 and the telomeric boundary of line 7848 define the Idd18.2 locus. The T1DBase Gene Span track displays the maximum genomic interval for each gene: candidate genes are displayed in green, blue indicates other protein-encoding genes, and yellow indicates small cytoplasmic RNA genes. The NOD TilePath track represents the sequenced NOD BAC clones, and the NOD_BAC_SNP_graph represents the SNP density per 10 kb, detected by comparing the NOD BAC clone sequence to the B6 reference sequence. The NOD_NGS_SNP_graph displays the SNP density per 10 kb of SNPs detected between the NCBIM37 B6 reference sequence and NOD/ShiLtJ NGS data. (B and C) The coding sequences of the transcripts from the Idd18.2 and Idd18.4 candidate genes Ptpn22 and Cd2 are shown, respectively, in the T1DBase Curated Transcripts track. The SNPs surrounding these genes are shown underneath. These SNPs have been detected by comparing the B6 reference sequence to either the NOD BAC clone sequence (NOD Variation track) or the NOD/ShiLtJ NGS data (NGS NOD SNPs track). Black, red, blue, and green lines (Figure legend continues)
and one nonsynonymous SNP in exon 12, none of which were analogous with B620W. The nonsynonymous SNP (rs33557973) V319I is located in the interdomain region of PEP between the phosphatase domain and PEST-rich region, which is involved in interactions with various ligands (37). A multiple-species alignment of LYP/PEP indicates that this residue is present in an unconserved region and is conserved as a hydrophobic aliphatic residue in most species (Supplemental Fig. 1). As valine and isoleucine are both hydrophobic aliphatic residues and are similar, we believe it is unlikely that V319I will alter the structure or phosphatase activity of PEP. An additional 177 SNPs were identified in the noncoding regions of Ptpn22 (Fig. 2B). Although polymorphisms were not identified in the core promoter region or 3′ untranslated region (UTR) of Ptpn22, many SNPs are located in polyypyrimidine tracts and branch site sequences and, therefore, could affect splicing (38, 39); they are also located in putative downstream sequence elements that could affect polyadenylation (40).

Ptpn22 alternatively spliced transcripts are differentially expressed between NOD- and B6-derived alleles

To determine whether the polymorphisms present between NOD and B6 could affect the splicing and expression of Ptpn22, we first searched for alternatively spliced Ptpn22 transcripts in EST databases and by RT-PCR. The expression of 13 different alternatively spliced transcripts (Supplemental Table III, IIC) was confirmed (data not shown); a contributing factor to this large number may be the rare GC-AG splice site, as noncanonical splice sites are associated with higher levels of alternatively spliced transcripts (41). The expression of the Ptpn22 transcripts from NOD- and B6-derived alleles at Idd18.2 was compared using qPCR. In addition to full-length Ptpn22, three transcripts were found to be differentially expressed: Ptpn22_J, Ptpn22_J', and Ptpn22_K (Fig. 3A). Ptpn22_J contains all exons apart from exon 12 and 13, resulting in a change of reading frame in exon 14 and a premature termination codon in exon 15. Ptpn22_J', like Ptpn22_J, excludes exons 12 and 13 but contains a novel exon 14 that includes the first 13 nucleotides in intron 14; this inclusion returns the reading frame to that of full-length Ptpn22 in exon 15. Ptpn22_K contains all exons apart from exon 15; this results in a change of reading frame and a premature termination codon in exon 17 (Fig. 2B). Full-length Ptpn22 is expressed 2-fold and 1.4-fold higher in line 1101 compared with line 2410 and 8010 congenic mice that have NOD-derived alleles at Ptpn22. We found the same differential expression pattern of PEP as observed for full-length Ptpn22 transcripts: B6-derived Idd18.2 alleles result in 2-fold higher PEP expression as compared with the NOD-derived alleles (p = 2.0 × 10^-4; Fig. 3C). Since LYP/PEP is known to regulate TCR signaling negatively (42, 43), we examined whether the difference in PEP expression would affect TCR signaling by examining the levels of induced phosphorylation of MAPK in splenic T cells following activation. We found that B6-derived Idd18.2 alleles present in line 7754 congenic mice had ∼1.6-fold lower levels (p = 0.026) of p44 MAPK phosphorylation after stimulation compared with the NOD-derived alleles in 2410 congenic mice (Fig. 3D).

NOD-derived susceptibility alleles at Idd18.4 result in lower CD2 expression on B cells

As Cd2 is the candidate gene for Idd18.4, we investigated whether potentially functional polymorphisms were present between the NOD and B6 alleles. The genes encoding CD2 in human and mouse are similar; both span ~12 kb and consist of five exons, and all the donor and acceptor splice sites are in agreement with the canonical GT-AG splice site. Genomic sequence from B6 and NOD BAC clones spanning Cd2 was publicly available because of the mapping and sequencing of the Idd10 locus (22, 44) and these were aligned to identify polymorphisms (Fig. 2C). Although polymorphisms were not detected in the coding sequence, 5′ or 3′ UTRs nor splice acceptor and donor sites, excluding an obvious structural difference between NOD and B6, four SNPs and six insertion–deletion polymorphisms were identified in the introns of Cd2, and four microsatellite polymorphisms were detected within 2.5 kb upstream of the 5′ UTR (Supplemental Table III), all of which could affect the expression or splicing of Cd2.

To determine whether Cd2 was expressed differently in congenic mice with B6- or NOD-derived alleles at Idd18.4, we investigated the cell surface expression of CD2 on immune cells from the spleen and bone marrow in line 2410 congenic mice, which have NOD-derived alleles at Idd18.4, and in line 7754, 7848, and 8010 congenic mice that have B6-derived alleles at Idd18.4. We found that splenic B cells from congenic mice with B6-derived Idd18.4 alleles had a 1.4-fold higher CD2 surface expression compared with mice with NOD-derived alleles at Idd18.4 (p = 2.9 × 10^-5; Fig. 4A–C). A similar expression difference was observed in B220^hi (mature) and B220^lo (immature) bone marrow derived cells, with congenic strains with B6-derived alleles at Idd18.4 having 1.6-fold (p = 5.3 × 10^-5) and 1.9-fold (p = 9.3 × 10^-5) higher cell surface expression of CD2, respectively, compared with mice with NOD-derived alleles at Idd18.4 (Fig. 4D–F). However, this expression difference was not observed for splenic T cells (Fig. 4B, 4C), and was also not observed when we looked specifically at CD4^+ and CD8^+ splenic T cell subsets (data not shown), suggesting that this expression difference is specific to B cells.

Discussion

Identification of two novel Idd loci, Idd18.2 and Idd18.4, on chromosome 3

Using congenic strain mapping, we have identified two novel Idd loci, Idd18.2 and Idd18.4, both of which are located between

represent G, T, C, and A NOD alleles, respectively. The NGS data also contain ambiguous bases. R, Y, M, K, W, and S are represented as brown, orange, pink, cyan, gold and gray lines, respectively. Yellow lines are SNPs where the base information is unknown. Note that where multiple SNPs are located close together in these two tracks, the lines in the NOD variation or NGS NOD SNPs track may represent more than one SNP. There is a higher SNP density over Ptpn22: to represent this density better, the NOD_BAC_SNPs_graph and NOD NGS_SNPs_graph display the density of SNPs per 10 kb.
Idd10 and Idd18.3 on chromosome 3. Idd18.4 is located immediately telomeric to Idd10 and is a 953-kb locus, containing eight genes, in which the B6-derived alleles confer T1D protection. Conversely, the B6-derived alleles of the 1.31 Mb Idd18.2 locus, which contains 18 protein-encoding genes, confer T1D susceptibility. Although many of the genes in these two loci have polymorphisms between B6 and NOD, and are therefore positional candidates for altering susceptibility to T1D, we focused on Ptpn22 and Cd2 because these genes or the signaling pathways they are involved in have been associated with several human autoimmune diseases (18, 19, 35). Although we did not identify polymorphisms in either gene that would be expected to affect protein function, we did find several polymorphisms likely to affect gene expression, and we went on to identify ∼2-fold higher RNA and protein expression of Ptpn22 in mice with susceptible B6-derived alleles at Idd18.2 and ∼1.5-fold higher CD2 expression in mice with protective B6-derived alleles at Idd18.4. Furthermore, we observed that mice with susceptible alleles at...
Idd18.2 have decreased signaling downstream of the TCR upon immune stimulation, a phenotype consistent with an increased level of a negative regulator of signaling, such as the PEP phosphatase encoded by *Ptpn22*. Differential expression by the B6 and NOD *Ptpn22* alleles of alternatively spliced mRNAs was also observed, but the presence of protein from these transcripts and their potential influences on disease susceptibility were not investigated. It is important to note that despite the expression differences observed for *Ptpn22* and *Cd2*, they remain only candidate genes for their regions. Other polymorphic genes within the regions could be responsible for the change in autoimmune disease susceptibility.

**Challenges of fine mapping Idd loci with congenic strain mapping**

As exemplified in this study, the use of congenic strain mapping in locating *Idd* and other disease associated loci in the mouse has been highly successful, and in many cases the original loci identified appear to be constituted of several smaller clustered loci. Two main challenges arise in the fine mapping of these clustered loci—namely, the development of congenic strains with much smaller introgressed segments containing, ideally, only the putative candidate gene to confirm the candidacy by exclusion of all others, and the complex genetic interactions that can occur between loci and can mask or reveal protection associated with a particular allele.

Congenic strain mapping has proved less successful in the fine-mapping of loci because the production of congenic mice is dependent on recombination, which does not occur evenly throughout the genome but has observable regions of hot spots, typically 1–2 kb long, surrounded by regions lacking recombination that can extend 10–100 kb or more (45). For instance, after identifying the candidate gene *Ptpn22* using line 2410, we wanted to develop a congenic strain with as small an introgressed B6 region as possible containing *Ptpn22*, but excluding all neighboring candidate genes, or at least those known to function in immune cells. We were able to find a mouse with a suitable recombination point telomeric to *Ptpn22*. However, after genotyping nearly 1000 mice,
we did not find our desired additional recombination event centromeric to \textit{Ptpn22} that would exclude \textit{Cd2}. Therefore, we continued with the most informative recombination events detected, which resulted in lines 7848 and 8010, the refinement of \textit{Idd18.2}, and serendipitously identified \textit{Idd18.4}. A similar inability to obtain a desired recombination event was observed during the fine-mapping of the \textit{Idd3} locus, where it was not possible to find a recombination event between the \textit{Ii2} and \textit{II21} genes (46). Congenic strains with single introgressed genes at \textit{Ptpn22} or \textit{Cd2} would be useful tools to confirm the candidacy of these functional candidates; however, it seems improbable that these could be developed. Different technologies, such as gene targeting, will need to be used to confirm the candidate genes. However, if the gene-targeting constructs are generated in cells not derived from NOD mice, the experimental approach is still limited by recombination events because of carryover of neighboring non-NOD genetic material.

Complex genetic interactions have been observed to occur between clustered loci. In this article, we report that B6-susceptible alleles at \textit{Idd18.2} masked the protection associated with B6 protective alleles at \textit{Idd10} or \textit{Idd18.3/18.1}. This masking became apparent when comparing the low levels of T1D protection observed in NOD.B6 \textit{Idd10}, 18.2 (T1D frequency similar to NOD) and NOD.B6 \textit{Idd18.2}, 18.3, 18.1 (T1D frequency slightly higher than NOD) congenic strains published in a previous study (5) (see strains R3 and R6, respectively) with the high levels of T1D protection observed in this study for line 3538, NOD.B6 \textit{Idd10}, (T1D frequency similar to line 1101) and line 3539, NOD.B6 \textit{Idd18.3, 18.1} (T1D frequency similar to line 2410; Fig. 1D), where the levels of T1D protection of \textit{Idd10} and \textit{Idd18.3/18.1} were assessed without the presence of B6 susceptibility alleles at \textit{Idd18.2}. Interestingly, in the previous study, the interaction between \textit{Idd10} and \textit{Idd18.3/18.1} was believed to be additive because both the \textit{Idd10} and \textit{Idd18.3/18.1} alleles were required in combination to observe any protection from T1D as either locus alone provided negligible protection (5). However, because of the identification of the \textit{Idd18.2} locus in the current study, we now know that this is incorrect and that the genetic interaction between \textit{Idd10} and \textit{Idd18.3/18.1} as observed when comparing lines 2410, 3538, and 3539 appears to be nonadditive, because the level of T1D protection derived from \textit{Idd10/18.3/18.1} (line 2410) is the same as that of \textit{Idd18.3/18.1} (line 3539) and not greater, as would be expected from an additive interaction. Moreover, this result highlights the importance of the congenic context in which \textit{Idd} loci are mapped because of the effects of masking. A comparison of \textit{Idd10/18.3/18.1} (line 2410) with \textit{Idd18.3/18.1} (line 3539) alone would suggest that the \textit{Idd10} locus does not confer protection against T1D. However, we can see from comparing NOD and NOD.B6 \textit{Idd10} (line 3538) that it does confer protection from T1D. In this genetic context, \textit{Idd18.3/18.1} masks the protection associated with \textit{Idd10}. We have previously observed the importance of congenic context in the mapping of other \textit{Idd} loci: the protection associated with the B6-derived alleles of the \textit{Idd18.1} locus is observed only when B6-derived alleles are present at \textit{Idd3} (7), suggesting that NOD-derived alleles at \textit{Idd3} mask the protection associated with B6-derived alleles at \textit{Idd18.1}. Interestingly, as line 3539 (\textit{Idd18.3/18.1}) has NOD-derived alleles at \textit{Idd3}, this could imply that the protection associated with line 3539 may be due solely to the \textit{Idd18.3} locus, or it could be that NOD-derived alleles at \textit{Idd3} mask the protection associated with \textit{Idd18.1} only in the context of other \textit{Idd} loci that are not present in line 3539. Individual \textit{Idd18.3} and \textit{Idd18.1} congenic strains would need to be developed to address this issue. Similar complex genetic interactions have also been reported for the cluster of \textit{Idd} loci on chromosome 1; in this case, the susceptible alleles of \textit{Idd5.4} are apparent only in the context of susceptibility alleles at \textit{Idd5.1/Clara}. Most of the genetic interactions between \textit{Idd} loci have been identified by chance through the various congenic mapping techniques used to fine-map loci and are, therefore, more likely to be detected for clustered loci. However, genetic interactions can occur between nonclustered loci (47). A detailed knowledge of how \textit{Idd} loci interact would be beneficial in understanding the complete interplay between different genes and susceptibility to T1D. However, it would be prohibitively expensive and time-consuming to perform combinatorial analyses using congenic strains to determine how all the known (>30) \textit{Idd} loci interact with each other.

\textit{Ptpn22} is a strong candidate for \textit{Idd18.2}

\textit{Ptpn22} is a strong candidate for causing the susceptibility associated with the B6-derived alleles of \textit{Idd18.2}, because the human homolog \textit{PTPN22} contains a nonsynonymous R620W polymorphism that is associated with several autoimmune diseases, including T1D. The protein product of \textit{PTPN22/Ptpn22}, LYP/PEP, downregulates immune signaling by dephosphorylating positive regulatory tyrosine residues on several of the key molecules involved in initiation of immune signal transduction, including ZAP-70, TCR-ζ chain, LCK, and FYNT (42, 48). In addition, LYP/PEP associates with the potent negative regulator of \textit{T} cell signaling, C-terminal Src kinase, which also helps to downregulate TCR signaling by phosphorylating the negative regulatory Tyr505 residue on LCK (35); evidence in mice, but not humans, suggests that this interaction is synergistic (42, 49, 50). Recent studies suggest that PEP functions to regulate TCR signaling based on the strength of binding between MHC-cognate ligand and TCR. PEP can down-regulate TCR signaling in the context of weak or self-antigens in naive, effector and memory T cells (51). This negative regulatory function of LYP/PEP is clearly observed in the phenotype of \textit{Ptpn22} knockout mice in which activated T cells have a growth advantage, restimulated effector T cells have increased proliferation and cell signaling, and older mice have increased numbers of CD4\textsuperscript+ and CD8\textsuperscript+ effector and memory T cells (43). The effect of reduced or eliminated \textit{Ptpn22} expression in mice on autoimmune susceptibility varies according to the target tissue and the effector mechanisms used and may depend on the genetic background of the mouse strain. Several studies have demonstrated increased percentages of FOXP3\textsuperscript+ CD4\textsuperscript+ T cells in the periphery and reduced organ-specific autoimmune disease susceptibility, including T1D in the NOD model (52–54). These results are consistent with our current observations of the NOD \textit{Ptpn22} allele associated with decreased PEP expression and decreased type 1 diabetes in the NOD.B6 \textit{Idd10}, \textit{Idd18.3}, \textit{Idd18.1} congenic strain. However, given the high level of sequence polymorphism and evolutionary distance between the B6 and NOD \textit{Ptpn22} alleles (Fig. 2B), it is unlikely that the only functional change between them is a change of baseline expression levels in T cells. Regulation of the expression of \textit{Ptpn22} in immune cell types other than those examined in this study, especially following activation, could be responsible for the disease association. We also note the further complexity that a disease allele associated with susceptibility to one or more autoimmune disease can actually be protective for a different autoimmune disease, which is the case for the human R620W polymorphism in human LYP, where the rare R620W variant is associated with protection from Crohn disease, but with susceptibility for most autoimmune diseases where association has been discovered (11). Similarly, autoimmunity in mouse models has been increased by knocking out \textit{Ptpn22} when disease is driven via Abs (50, 55).
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The only other strong candidate gene based on its immune function in the Idd18.2 locus is Nras. The coding sequence for Nras was sequenced previously (4), and polymorphisms between NOD and B6 were not identified. The NGS data show that there is little variation between NOD/ShiLiJU and B6 around Nras (Fig. 2A), and the only polymorphism detected in Nras is an ambiguous SNP call [C/Y]. The single polymorphism in Nras is highly unlikely to be functional because it is located in the poly-pyrimidine track of intron 4, and both NOD- and B6-derived alleles encode for pyrimidines.

The function and association of the CD2/CD48/CD58 pathway with several autoimmune diseases highlights Cd2 as a strong functional candidate for Idd18.4

CD2 is a cell-surface molecule expressed on T cells, NK cells, B cells, dendritic cells, and monocytes (56–58). In humans, the primary ligand of CD2 is CD58. However, in mice and rats, a CD58 ortholog has not been identified, and CD48 is believed to be the primary ligand because it is observed to bind to CD2 with much higher affinity in rodents than in humans (16). CD2 and CD58/CD48 interactions have an important role in the formation of the immunologic synapse. Clustering of CD2-CD58/CD48 molecules has been implicated in the repositioning of cell surface molecules to the immunologic synapse and is believed to position T cell and APC membranes at a distance that is suitable for TCR-peptide-MHC complex association (17, 59, 60). Blocking the interaction of CD2 and CD58 by mAbs inhibits T cell proliferation, T and NK cell cytolysis, and production of cytokines by T cells (61), confirming the critical role this ligand pair has in T cell activation (22, 44). In this scenario, we would expect CD101 to function on a branch of the immune pathway that is upstream of PEP. Susceptible B6-derived PEP may downregulate immune signaling much more strongly than CD101 and, therefore, the effect of variations in CD101 are negligible compared with the susceptible PEP-induced inhibition of immune signaling. Additional experiments are required to investigate these hypotheses concerning interacting molecular and cellular pathways influenced by Idd genes.

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