Data S1

Multiple Sclerosis

Multiple sclerosis (MS, MIM 126200) is a chronic inflammatory demyelinating disorder of the central nervous system (reviewed in [1,2]). The disease has a predilection for females and may manifest as relapsing and/or progressive forms. The only region of the genome that has shown consistent evidence of linkage and association with multiple sclerosis (MS) is the HLA locus (reviewed in [3]). The association of the *HLA-DR2* haplotype with multiple sclerosis was first noted in 1972 [4] and remains one of the most reproduced findings in MHC genetics [5-15].

In all of the linkage scans performed to date, the HLA locus is the only one to have achieved genome-wide significance as an MS susceptibility locus both in a meta-analysis of linkage studies [10] and in a subsequent large high-resolution linkage screen in MS [11]. An initial SNP-based association study of the MHC as well as more focused efforts dissecting the effects of the MHC in MS have recently confirmed the preeminent role of the *DRB1*1501* (encompassed within the *DR2* specificity) haplotype in MS in populations of northern European ancestry [12-14]. Indeed, populations with a high concentration of the *DRB1*1501-DQB1*0602* haplotype, such as northern Scotland, exhibit some of the highest known prevalence rates of MS [16]. Due to strong LD within the MHC, it remains unclear whether the primary driver for the association of the HLA locus to MS is the *DQB1*0602* allele or the *DRB1*1501* allele (reviewed in [3]). However, evidence is mounting that, of these two alleles, *DRB1*1501* appears to be the allele with stronger

evidence of association both in African-Americans [17] and, possibly, in

European populations (PLD, unpublished data). The long-range LD noted within the DRB1*1501-DQB1*0602 haplotype and its effect strength (OR = 2.7for one copy of the DRB*1501 allele, [18]) hinders the interpretation of other associations in this region, even those several megabases away in the MHC class I region. Thus, it is uncertain whether MHC class I associations are truly independent of the DRB1*1501-DQB1*0602 haplotype effect [3], though some evidence suggests that the DRB1*1501-DQB1*0602 associated HLA-A3 allele may be an independent susceptibility signal in MS [19]. Investigators in the Netherlands have also reported an association with the microsatellite HLA C1_3_2*354 that is independent of DR2, although in strong LD with DR3 [20]. A more recent study of a different family-based cohort failed to demonstrate such independent HLA-A or -B effects [21]. On the other hand, another study that took both the DR15 and DR3 effects into account offers substantial evidence that the HLA C*05 allele may be independently associated to MS susceptibility [14]. Thus, the role of class I alleles remains open for now and awaits the interrogation of much larger subject samples in an effort to powerfully address the issue of DRB1-independent susceptibility loci.

Within the *DRB1* gene itself, there appears to be evidence for allelic heterogeneity, particularly in non-European populations [22]. Nonetheless, the haplotype tagged by *HLA DRB1*1501* remains a risk haplotype for MS in non-European populations, especially when one considers the typical disseminated forms of demyelinating disease captured by the MS diagnostic rubric [23-25]. Barcellos and colleagues [13] have recently explored the question of allelic heterogeneity in 1339 families of European ancestry with

MS, and this robust analysis reports a dominant effect for DRB1*15, a recessive effect for DRB1*03, a protective effect for DRB1*14, as well as evidence for interaction between DRB1*15 and DRB1*08 in increasing susceptibility to MS. A separate study that shared some subjects with the latter study suggests that the HLA DRB1*0103 may also be a susceptibility allele, once the effects of DRB1*15 and DRB1*03 are taken into account [14]. A small study of Portuguese subjects recently also found an association to HLA DRB1*03 [26], as did earlier studies of Sardinian families [27]. Mediterranean populations such as the Sardinians also display associations to DR4 (reviewed in [1], and the DR4 effect has now been demonstrated in another Italian population consisting of families with MS and other autoimmune diseases [28]. Finally, as with the DRB1*14 allele described above, several HLA class II alleles (DR1, DR7, and DR11) have been implicated in protection against MS [29], while HLA-A*0201 has been shown to reduce DRB1*15-associated risk [19]. Such protective effects are notoriously difficult to distinguish from under representation of certain alleles in the face of the effects of DRB1*15, and therefore these findings await further validation.

Evidence for association of other *DRB1* alleles comes from other human populations. In Japan, disseminated MS similar to that seen in Europeans may be associated with *DRB1*1501*, but the association of the *DRB1*1501* haplotype with the opticospinal MS variant fails to reach significance (reviewed in [24]). Instead, opticospinal MS may be associated with *DPB1*0501* and *DPB1*0301* in the Japanese population [24,30]. An

association with *DR6* in Japanese has also been reported, but without replication [31]. In the Turkish population, an association has been suggested with *DR4* ([32]reviewed in [33]). The same haplotype is also reported to be associated with susceptibility to MS in Mexican Mestizos [34]. In African-Americans, MS association has also been demonstrated with *DRB1*0301* and *DRB1*1503* in addition to the expected *DRB1*1501* [17].

Outside of MHC genes, polymorphisms in the immunologically relevant class III genes, TNF and NOTCH4, have been associated with MS, but this association was shown to be secondary to that of DRB1*1501 [35]. At least 10 studies no HLA-independent association small have shown with microsatellites and SNPs in linkage disequilibrium with the TNF gene (ibid.), though one as yet unreplicated larger study [36] suggests an association in a Spanish population. Recently, a small study of Tasmanian families has highlighted a haplotype containing a myelin oligodendrocyte glycoprotein (MOG) allele after conditioning for the effect of HLA-DRB1*15 [37]. Thus, the role of non-HLA genes also remains an area of active investigation that will benefit from much larger studies that comprehensively interrogate genetic variation within the extended MHC in MS.

As expected, our pooled analysis of studies exploring the role of the MHC with MS susceptibility highlights the pre-eminent role of the extended haplotype defined by *HLA DRB1*1501* and *DQB1*0602* (Figure 1). Whether typed as *Dw2, DR2, DR15*, or *DRB1*1501*, the presence of a *1501* allele of the *HLA-DRB1* gene is associated with an OR > 2.0 for susceptibility to MS. This allele,

or another allele in strong LD with it, is therefore an important risk factor for the onset of this disease. Given the extended LD that haplotypes bearing *HLA-DRB1*1501* display, the problem of identifying the causal variant or variants within the haplotype is extremely challenging. In the data available to us, we have evaluated the alleles *HLA-A3*, *-B7*, *-DQA1*0102*, *-DQB1*0602* and *TNFa11* which lie on the ancestral *DRB1*1501*-containing haplotype. For the most part, the pooled analysis suggests that none of these alleles is as strongly associated to MS susceptibility as is *HLA-DRB1*1501*; thus, in general, the more modest effects of these other alleles are probably due to LD with *HLA-DRB1*1501*. This result is consistent with the exclusion of *DQB1*0602*, the allele in highest LD with *HLA DRB1*1501*, as a risk allele in African-Americans with MS [17].

Two other ancestral haplotypes, *DR3* and *DR4*, appear to play a role in MS susceptibility, although the effect of these haplotypes on disease is more modest than that of the *DR2* haplotypes. Figure 1 displays those alleles found on *DR3* haplotypes that show significant association with susceptibility to MS in our pooled analysis. Here, it is less clear than in the *HLA DRB1*1501* analysis whether the *DRB1*0301* allele is primarily driving the association or whether one of the alleles of *TNF*, for example, could be in stronger LD with a risk allele. On the other hand, the *DR4* haplotypes seem to display their strongest association with their *HLA-DRB1* alleles: four different *DR4* alleles – *0402, 0403, 0404,* and *0405* – display significant association in our analysis. The *DR4* haplotype-associated *DQB1*0302* allele is also associated with MS susceptibility but appears to have a more modest effect than the *DRB1* alleles, and therefore, as with the *DR2* haplotypes, alleles within the *DRB1*

gene may be playing a causal role. However, given the relatively rare frequencies of these alleles, one must interpret our results cautiously: largescale studies will be needed to more accurately evaluate the effect of the various *DR4* haplotypes. Nonetheless, our analysis suggests that, while the population risk of *DR4* haplotypes on MS susceptibility may be relatively small, those rare individuals bearing these alleles may have a large increase in disease risk; the odds ratios for *DR4* haplotypes range from 1.7 for *DRB1*0404* to 2.8 for *DRB1*0403*.

In MS, our pooled analysis highlights the class II gene, HLA-DRB1 as the primary candidate for MS susceptibility at the MHC, with a number of different alleles contributing to disease risk. Evidence implicating the HLA-DR specificities, DR2 and DR4, includes the genetic analyses summarized here and also the results of functional studies. While the key target antigens in MS remain elusive, human and animal studies have shown that different protein components of myelin, including myelin basic protein (MBP), myelin oligodendrocyte glycoprotein (MOG), and myelin proteolipid protein (PLP), all contain peptide sequences that can be presented by DR2 or DR4. DR2 alleles have been studied extensively, with reactivity to MBP 84-102 [38,39]; PLP 95-116, 184-199 and 190-206 [40,41]; and overlapping MOG peptides [42]. The data on DR4 alleles is limited, with the MBP 111-129 epitope being recognized in subjects with DRB1*0401 [43], but PLP and MOG epitopes were also recognized in one study where subjects with at least one DR4 allele were studied [44]. Further studies are required to fully elucidate and validate the allelic heterogeneity seen at DRB1, particularly in terms of the role of rare alleles such as DRB1*0403; recent efforts are offering increasing evidence

supporting the role of the more common DRB1*03 allele in disease

susceptibility [13,14].

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