Polymorphisms of the CD24 Gene Are Associated with Risk of Multiple Sclerosis: A Meta-Analysis

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Abstract: CD24 is a cell-surface protein mainly expressed in cells of the immune and central nervous system (CNS), cells that play a critical role in the development of multiple sclerosis (MS). In the current study, we investigated four polymorphisms of the CD24 gene regarding their associations with MS. To this end, univariate and multivariate meta-analysis were applied along with modifications to include data from family-trios so as to increase the robustness of the meta-analysis. We found that the polymorphism 226 C>T (Ala57Val) of the CD24 gene is associated with MS according to the recessive mode of inheritance (odds ratio = 1.75; 95% CI: 1.09, 2.81). Moreover, the 1527–1528 TG>del polymorphism is inversely associated with MS according to the dominant mode of inheritance (odds ratio = 0.57; 95% CI 0.39, 0.83). Conversely, the 1056 A>G and 1626 A>G polymorphisms were not found to be associated with MS. We conclude that the CD24 226 C>T polymorphism increases the risk of MS, while the 1527–1528 TG>del polymorphism seems to have a protective role against MS, suggesting that these two polymorphisms can be used as predictive biomarkers for MS development.

Keywords: CD24; meta-analysis; multiple sclerosis; predictive biomarkers; genetic association; genetic polymorphisms; genetic risk; protective variant
1. Introduction

Multiple sclerosis (MS) is a chronic and complex demyelinating disease of the central nervous system (CNS) with an occurrence of about 0.1% in Caucasian young adults [1]. The average age of onset of MS is between 20 and 40, and it is twice as common in women [2]. It is widely believed that the development of MS is attributed mainly to genetic susceptibility combined with environmental factors [3,4]. The most common genetic variants that are known to date belong to HLA class II, are located in chromosome 6p21 and are in linkage disequilibrium, while a variant of HLA-A (class I) is known to confer protection from MS [5]. According to a number of genome wide association studies (GWAS), at least 29 additional genomic regions are suggested to be associated with MS susceptibility [5] (and references therein).

Of particular note, CD24, although not detected in GWAS, is a gene that has been investigated thoroughly in regard to its association with autoimmune diseases, including MS, with promising results. The CD24 gene is located in the chromosomal region 6q21. Interestingly, the particular region (6q) has previously been suggested to be in linkage with MS [6,7]. The CD24 protein is a GPI-anchored cell surface glycoprotein abundantly expressed in a variety of hematopoietic cells such as T and B cells, macrophages, neutrophiles, eosinophils and dendritic cells [8–10]. CD24 is also expressed in cells of the CNS such as neural and ganglion cells, astrocytes and microglia [8–11], cells involved in the pathogenesis of MS. When expressed in T-cells of the nervous system, CD24 expression is required for T-cell homeostatic proliferation [10]. It has also been shown that CD24 is responsible for the local expansion of T cells after migration to the CNS and the development of experimental autoimmune encephalomyelitis (EAE) in mouse models [12,13].

Four polymorphisms of the CD24 gene have been found to be implicated in the etiology of MS and various degenerative diseases [10]; these polymorphisms are: (a) a C-to-T substitution at nucleotide 226 resulting in a Ala57Val substitution; (b) a TG dinucleotide deletion at positions 1527–1528; (c) an A-to-G substitution at nucleotide 1056; and (d) an A-to-G substitution at nucleotide 1626. The later three polymorphisms are located in exon 2 in the 3’ UTR, a region that confers mRNA stability [14,15]. rs numbers have been assigned to these polymorphisms (rs52812045, rs3838646, rs1058818 and rs1058881 respectively); however, all correspond to the intronless CD24 pseudogene, which is located in the chromosomal region Yq11. A number of case-control studies have been performed to investigate the putative association of CD24 gene polymorphisms with MS development and progression, although the results are controversial. In the present study, we performed a complete meta-analysis of the currently available bibliographic data in order to decipher these associations and add statistical support to them.

2. Results

2.1. Characteristics of Studies

A total of 19 articles were retrieved from our literature search from which seven articles with eight studies were found to fulfill the eligibility criteria for the meta-analysis of the CD24 226 C>T polymorphism comprising 2085 patients and 2295 healthy controls (Table 1). One study enrolled both case/control samples and family trios [11]. The remaining studies were population-based. Only two
studies, out of a total of 19 retrieved articles, were found to include data pertinent to the meta-analysis of the polymorphisms 1527–1528 TG>del, 1056 A>G and 1626 A>G. The total numbers of patients and controls were 377 and 648, respectively. The characteristics of each study are summarized in Table 2A,B. The alleles and the genotypes of cases and controls were recorded and calculated separately for each study (Supplementary Tables S1–S4). In all studies, MS diagnosis was based on either McDonald [16] or Poser criteria [17].

Table 1. Polymorphisms of the CD24 gene explored in the present study for their association with multiple sclerosis.

<table>
<thead>
<tr>
<th>Polymorphisms</th>
<th>Number of Studies</th>
<th>Cases</th>
<th>Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>226 C&gt;T (Ala57Val)</td>
<td>8</td>
<td>2085</td>
<td>2295</td>
</tr>
<tr>
<td>1527–1528 TG&gt;del</td>
<td>2</td>
<td>377</td>
<td>648</td>
</tr>
<tr>
<td>1056 A&gt;G</td>
<td>2</td>
<td>377</td>
<td>648</td>
</tr>
<tr>
<td>1626 A&gt;G</td>
<td>2</td>
<td>377</td>
<td>648</td>
</tr>
</tbody>
</table>

Table 2. (A) Characteristics of studies included in the meta-analysis for the association of the 226 C>T polymorphism of the CD24 gene with MS; (B) Characteristics of studies included in the meta-analysis for the association of the 1527–1528 TG>del, 1056 A>G and 1626 A>G polymorphisms of the CD24 gene with MS.

<table>
<thead>
<tr>
<th>Study (First Author/Ref.)</th>
<th>Year</th>
<th>Country</th>
<th>Race</th>
<th>Cases</th>
<th>Diagnostic Criteria</th>
<th>Controls</th>
<th>Diagnostic Criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>(A)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Zhou Q. [11]</td>
<td>2003</td>
<td>USA</td>
<td>Caucasian</td>
<td>242</td>
<td>McDonald criteria</td>
<td>207</td>
<td>Blood samples from the American Red Cross (Columbus, OH)</td>
</tr>
<tr>
<td>Cui Y.Z. [18]</td>
<td>2006</td>
<td>China</td>
<td>Asian</td>
<td>110</td>
<td>Not reported</td>
<td>83</td>
<td>Not reported</td>
</tr>
<tr>
<td>Otaegui D. [20]</td>
<td>2006</td>
<td>Spain</td>
<td>Caucasian</td>
<td>141</td>
<td>McDonald criteria</td>
<td>285</td>
<td>Blood samples from anonymous healthy donors from the Gipuzkoa blood bank. (60.4% women, mean age 46.2 ± 11.6)</td>
</tr>
<tr>
<td>Ronaghi M. [21]</td>
<td>2009</td>
<td>Iran</td>
<td>Caucasian</td>
<td>217</td>
<td>McDonald criteria</td>
<td>200</td>
<td>Healthy individuals</td>
</tr>
<tr>
<td>Gonzalez S.J. [22]</td>
<td>2011</td>
<td>Argentina</td>
<td>Caucasian</td>
<td>102</td>
<td>Poser criteria</td>
<td>205</td>
<td>Age and gender-matched controls</td>
</tr>
<tr>
<td>Kollaee A. [23]</td>
<td>2011</td>
<td>Iran</td>
<td>Caucasian</td>
<td>120</td>
<td>McDonald criteria</td>
<td>120</td>
<td>37.2 ± 7.8 years, range: 22–65 with no history of autoimmune or inflammatory disorders</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Study (First Author/Ref.)</th>
<th>Year</th>
<th>Country</th>
<th>Race</th>
<th>Cases</th>
<th>Diagnostic Criteria</th>
<th>Controls</th>
<th>Diagnostic Criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>(B)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gonzalez S.J. [22]</td>
<td>2011</td>
<td>Argentina</td>
<td>Caucasian</td>
<td>102</td>
<td>Poser criteria</td>
<td>205</td>
<td>Age and gender-matched controls</td>
</tr>
</tbody>
</table>
2.2. 226 C>T (Ala57Val) Polymorphism of the CD24 Gene

The results of the eight populations analyzed in the present meta-analysis [11,18–23] suggested an association of the 226 C>T polymorphism with MS. The T vs. C contrast (incorporating data from family trios) produced a significant association with OR 1.26 and 95% CI: 1.02–1.56. Similarly, both recessive and dominant modes resulted in significant association (OR 1.75, 95% CI: 1.09–2.81 for TT vs. TC + CC and 1.36, 95% CI: 1.14–1.63 for TT + TC vs. CC) (Figure 1A–C). When the above contrasts were performed only with populations obeying Hardy Weinberg Equilibrium (HWE) the association remained significant (Table 3). Because two studies included data only for combined genotypes, only six studies were employed in the TT + TC vs. CC contrast. The allele and recessive contrasts presented higher heterogeneity compared to the dominant mode (Table 3). Time-trend and Proteus phenomenon were not detected in the cumulative meta-analysis for all contrasts. Sensitivity analysis (i.e., removing a study and performing the meta-analysis again) showed that five out of the eight studies were necessary for achieving statistical significance, a finding that was expected considering the fact that the lower limit of the 95% confidence interval of the pooled estimate was close to unity. Nevertheless, the magnitude of the pooled OR did not change significantly in the sensitivity analysis (data not shown).

![Figure 1. Cont.](image-url)
Figure 1. Forest plot of the meta-analysis for the association of the 226 C>T (Ala57Val) polymorphism of the CD24 gene with multiple sclerosis. For each study the estimate of the variance, OR and its respective 95% Confidence Interval (CI) are plotted with a box and a horizontal line, respectively. The dashed vertical lines indicate the overall estimate, whereas the solid ones indicate the null effect (OR = 1). The ORs correspond to (A) the allele contrast T vs. C; (B) the TT vs. TC + CC contrast and (C) the TT + TC vs. CC genotype contrast.
Table 3. Univariate meta-analysis for the 226 C>T (Ala57Val) polymorphism of the CD24 gene with multiple sclerosis.

<table>
<thead>
<tr>
<th>Contrast</th>
<th>Mode of Inheritance</th>
<th>Number of Studies</th>
<th>OR (Random Effects)</th>
<th>95% Confidence Interval (CI)</th>
<th>$I^2$ (%)</th>
<th>Cochran’s Q</th>
<th>BSV a</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>T vs. C</td>
<td>Co-dominant</td>
<td>8</td>
<td>1.26</td>
<td>1.02–1.56</td>
<td>78.0</td>
<td>31.87</td>
<td>0.07</td>
<td>2.16</td>
</tr>
<tr>
<td>T vs. C in HWE</td>
<td>Co-dominant</td>
<td>4</td>
<td>1.39</td>
<td>1.17–1.66</td>
<td>0.0</td>
<td>2.33</td>
<td>0.00</td>
<td>3.70</td>
</tr>
<tr>
<td>TT vs. TC + CC</td>
<td>Recessive</td>
<td>8</td>
<td>1.75</td>
<td>1.09–2.81</td>
<td>76.9</td>
<td>30.25</td>
<td>0.33</td>
<td>2.34</td>
</tr>
<tr>
<td>TT vs. TC + CC in HWE</td>
<td>Recessive</td>
<td>4</td>
<td>2.05</td>
<td>1.27–3.31</td>
<td>32.1</td>
<td>4.42</td>
<td>0.08</td>
<td>2.93</td>
</tr>
<tr>
<td>TT + TC vs. CC</td>
<td>Dominant</td>
<td>6</td>
<td>1.36</td>
<td>1.14–1.63</td>
<td>0.0</td>
<td>1.50</td>
<td>0.00</td>
<td>3.34</td>
</tr>
<tr>
<td>TT + TC vs. CC in HWE</td>
<td>Dominant</td>
<td>4</td>
<td>1.32</td>
<td>1.05–1.67</td>
<td>0.0</td>
<td>1.21</td>
<td>0.00</td>
<td>2.33</td>
</tr>
</tbody>
</table>

a BSV: Between Studies Variance.

To further elucidate the mode of inheritance, multivariate meta-analysis was performed on the combined data available from six studies. The contrast of risk homozygotes vs. wild-type allele homozygotes (TT vs. CC) yielded a robust and significant association with MS, having OR 2.44 and 95% CI: 1.77–3.38 (Table 4). Lambda ($\lambda$) was estimated to be equal to 0.18, indicating the recessive mode [24] as the prevalent mode of inheritance. The overall Wald test, employed to examine whether all ORs were equal to one (null hypothesis), suggested a definite association ($p$-value < 10$^{-4}$).

Table 4. Multivariate meta-analysis for the 226 C>T (Ala57Val) polymorphism of the CD24 gene with MS.

<table>
<thead>
<tr>
<th>Contrast</th>
<th>Number of Studies</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC vs. CC</td>
<td>6</td>
<td>1.18</td>
<td>0.97–1.42</td>
</tr>
<tr>
<td>TT vs. CC</td>
<td>6</td>
<td>2.44</td>
<td>1.77–3.38</td>
</tr>
</tbody>
</table>

2.3. 1527–1528 TG>Del Polymorphism of CD24

The potential association of the 1527–1528 TG>del polymorphism with MS was investigated using data from two independent studies [15,22]. A protective function of the del polymorphism (the TG dinucleotide deletion) against MS development was identified, since the allele contrast had OR smaller than unity and equal to 0.60 (95% CI: 0.41–0.85). The contrasts del/del vs. TG/TG + TG/del (recessive mode) yielded OR = 1.09 with 95% CI 0.06–18.64. Interestingly, the del/del + TG/del vs. TG/TG (dominant) gave a significant reverse association with OR = 0.57 with 95% CI 0.39–0.83 (Table 5).

Similarly, the TG/del vs. TG/TG contrast obtained under multivariate meta-analysis resulted in a strong association suggesting a protective effect of the polymorphism against MS (OR = 0.57 with 95% CI 0.38–0.87, Table 6). Dominance or even overdominance could be suggested since $\lambda = 1.98$ [24]. The overall Wald test further supported this association, given that the overall $p$-value was 0.038. Taken together, univariate and multivariate meta-analyses suggest that deletion of the TG at position 1527–1528 exerts a protective role against MS according to the dominant mode of inheritance.

<table>
<thead>
<tr>
<th>Contrast</th>
<th>Mode of Inheritance</th>
<th>Number of Studies</th>
<th>OR</th>
<th>95% CI</th>
<th>I² (%)</th>
<th>Cochran’s Q</th>
<th>BSV a</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>del vs. TG</td>
<td>Co-dominant</td>
<td>2</td>
<td>0.60</td>
<td>0.41–0.80</td>
<td>0.0</td>
<td>0.55</td>
<td>0.00</td>
<td>2.8</td>
</tr>
<tr>
<td>del/del vs. TG/TG + TG/del</td>
<td>Recessive</td>
<td>2</td>
<td>1.09</td>
<td>0.06–18.64</td>
<td>55.2</td>
<td>2.23</td>
<td>0.00</td>
<td>0.06</td>
</tr>
<tr>
<td>del/del + TG/del vs. TG/TG</td>
<td>Dominant</td>
<td>2</td>
<td>0.57</td>
<td>0.39–0.83</td>
<td>0.0</td>
<td>0.2</td>
<td>0.00</td>
<td>2.89</td>
</tr>
</tbody>
</table>

a BSV: Between Studies Variance.

Table 6. Multivariate meta-analysis for the 1527–1528 TG>del polymorphism of the CD24 gene with MS.

<table>
<thead>
<tr>
<th>Contrast</th>
<th>Number of Studies</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>TG/del vs. TG/TG</td>
<td>2</td>
<td>0.57</td>
<td>0.38–0.87</td>
</tr>
<tr>
<td>del/del vs. TG/TG</td>
<td>2</td>
<td>0.75</td>
<td>0.05–10.37</td>
</tr>
</tbody>
</table>

2.4. 1056 A>G and 1626 A>G Polymorphisms of CD24

Finally, meta-analyses were carried out for the 1056 A>G and 1626 A>G polymorphisms using data from two studies [15,22]. No significant association of the 1056 A>G polymorphism with MS was observed in all contrasts (allele and genotypes, Table 7). The heterogeneity was large (Table 7) while publication bias was also present (data not shown). The Barrowman et al. (2003) [25] method was applied to estimate the additional participants required for statistical significance. We found that 2059, 1901 and 2289 more participants would be required for the G vs. A, GG vs. GA + AA and GG + GA vs. AA contrasts, respectively, numbers that might not be very difficult to reach.


<table>
<thead>
<tr>
<th>Polymorphism</th>
<th>Contrast</th>
<th>Number of Studies</th>
<th>OR</th>
<th>95% CI</th>
<th>I² (%)</th>
<th>Cochran’s Q</th>
<th>BSV a</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>1056 A&gt;G</td>
<td>G vs. A</td>
<td>2</td>
<td>1.70</td>
<td>0.68–4.23</td>
<td>96.0</td>
<td>24.96</td>
<td>0.42</td>
<td>1.13</td>
</tr>
<tr>
<td></td>
<td>GG vs. GA + AA</td>
<td>2</td>
<td>2.23</td>
<td>0.58–8.61</td>
<td>95.5</td>
<td>22.26</td>
<td>0.91</td>
<td>1.16</td>
</tr>
<tr>
<td></td>
<td>GG + GA vs. AA</td>
<td>2</td>
<td>1.59</td>
<td>0.69–3.62</td>
<td>86.3</td>
<td>7.32</td>
<td>0.31</td>
<td>1.09</td>
</tr>
<tr>
<td>1626 A&gt;G</td>
<td>G vs. A</td>
<td>2</td>
<td>0.79</td>
<td>0.61–1.02</td>
<td>0.0</td>
<td>0.04</td>
<td>0.0</td>
<td>1.82</td>
</tr>
<tr>
<td></td>
<td>GG vs. GA + AA</td>
<td>2</td>
<td>0.61</td>
<td>0.24–1.58</td>
<td>0.0</td>
<td>0.12</td>
<td>0.0</td>
<td>1.02</td>
</tr>
<tr>
<td></td>
<td>GG + GA vs. AA</td>
<td>2</td>
<td>0.78</td>
<td>0.58–1.04</td>
<td>0.0</td>
<td>0.08</td>
<td>0.0</td>
<td>1.71</td>
</tr>
</tbody>
</table>

a BSV: Between Studies Variance.

Likewise, no statistically significant association was attained under any contrast for the 1626 A>G polymorphism with MS (Table 7). The heterogeneity was very low and publication bias was absent in all contrasts (data not shown). According to the Barrowman et al. (2003) method [25], statistically significant outcomes can be achieved with 164, 2760 and 322 more participants for the G vs. A, GG vs. GA + AA and GG + GA vs. AA contrasts, respectively, suggesting, as before, that statistical significance can be achieved easily.
3. Discussion

CD24 is a GPI-anchored cell membrane protein, with a molecular mass of 20 to 70 kD, and varying glycosylation. CD24 is a multifaceted protein implicated in inflammation, immunity—both adaptive and autoimmunity—and cancer [10]. Many experimental studies have focused on investigating the associations of CD24 polymorphisms with autoimmune diseases such as MS, systemic lupus erythematosus (SLE), rheumatoid arthritis or giant cell arthritis [10] (and references therein). Although CD24 was not detected in any GWASs, earlier classical linkage analyses [6] together with case control studies carried out in 2003 [11] suggested that CD24 is a very promising biomarker for MS development. The fact that CD24 was not identified in GWASs does not necessarily underestimate our study since GWASs often capture only a part of the phenotypic variance, due to intrinsic methodological limitations. The stringent criteria used for statistical significance in GWAS result, in many circumstances, in decreased power to identify a moderate effect. This happens because in the GWAS context, we usually work in an agnostic manner and the primary concern is to reduce the risk of spurious findings and false positive results arising from multiple testing. On the contrary, in the current context, we followed a hypothesis-driven approach. That is, the CD24 gene had been chosen and studied in many independent studies due to some preliminary genetic evidence (i.e., as mentioned, the linkage studies concerning the 6q region), as well as due to the presumed biological plausibility that might implicate CD24 antigen in the disease formation. Moreover, the present study includes populations from Iran and Argentina that were not included in previous GWASs. In support of the hypothesis that CD24 plays a pivotal role in the development of autoimmune diseases, Li et al. (2006) [26] found that T cells undergo uncontrolled extensive proliferation in CD24-deficient mice. Thus, the homeostatic proliferation, which should be slow-paced, loses its self-limiting capacity, and this results in the rapid death of the recipient CD24−/− mice.

The meta-analysis performed in this work, based on all the available data from the biomedical literature, clearly demonstrates a genetic association between the 226 C>T polymorphism of CD24 with MS. Our conclusion is supported by two lines of evidence. First, with univariate meta-analysis, significant association was identified with all modes of inheritance (co-dominant, recessive and dominant). Second, from multivariate meta-analysis, which can indicate the mode of inheritance, the significant association was strengthened and the recessive mode appeared to be the most prominent. In any case, the association of the CD24 226 C>T polymorphism with MS proved to be quite robust according to the overall estimate of our analysis. The findings of our study are in accordance with previous case-control studies showing that the 226 C>T polymorphism of CD24 is associated with another autoimmune disease, the SLE [27,28].

The idea that polymorphisms located in regulatory regions, can account for MS susceptibility has recently gained interest [29]. To this end, the 1527–1528 TG>del, 1056 A>G and 1626 A>G polymorphisms located in the 3′ UTR of the CD24 gene were investigated. Our analysis showed that the 1527–1528 TG>del polymorphism has a protective role against the occurrence of MS. Significant associations were found in the allele and the del/del + TG/del vs. TG/TG genotype contrasts which both had zero heterogeneity. Multivariate meta-analysis further confirmed the above association and reinforced the dominant mode of inheritance. The same TG>del polymorphism has been shown in a case-control study to confer protection against SLE, as well [15]. Our findings are
further corroborated by previous studies showing that this region [14] and especially the TG dinucleotide deletion confers instability to the CD24 transcript [15], thus granting protection against MS and SLE onset and progression.

Conversely, based on meta-analyses we performed for the 1056 A>G and 1626 A>G CD24 gene polymorphisms, no association was found under any contrast. Noticeably, all SNPs are in close chromosomal proximity to each other and one would expect Linkage Disequilibrium (LD) between them. The two associated polymorphisms with MS have a distance of about 1400 bp. Nevertheless, no definite LD has been observed between 226 C>T and 1527–1528 TG>del in the literature, neither for MS and SLE nor for other diseases such as Chron’s disease [15,30]. It is postulated that the CD24 gene may have a recombination hotspot between these two polymorphisms [15]. Moreover, the fact that the other two SNPs, though located very close to the associated ones, are not associated with MS may suggest that the 226 C>T and the 1527–1528 TG>del polymorphisms play a causal role in MS, either promoting or preventive, respectively. A haplotype analysis, that would shed more light to this hypothesis, could not be performed in the present study due to lack of data in the included studies. Hence, it is clear that more studies (or collaborative meta-analyses of the current studies) investigating CD24 haplotypes and their associations with MS are greatly needed to clarify the causative polymorphisms.

Despite the robustness of most of our results, the present study has some limitations. First, the number of studies included is relatively small, while the populations’ ethnic diversity is limited to Asians and Caucasians of European, USA, Argentinean and Iranian ancestry. Hence, additional studies with more participants from diverse ethnic backgrounds would be of great value, especially for the meta-analyses concerning the three polymorphisms located in the 3′ UTR. Second, significant heterogeneity was detected in three out of four analyzed polymorphisms. Regarding the 226 C>T polymorphism, heterogeneity was detected in the allele and the recessive mode contrasts. However, when the analyses were restricted to studies with populations in HWE, the heterogeneity was decreased. As far as the analysis of the 1527–1528 TG>del polymorphism is concerned, heterogeneity was present only in the recessive contrast, which yields non-significant results. Importantly, in the other contrasts, and particularly in the dominant mode contrast (the prevailing one) the heterogeneity was almost zero, reinforcing the robustness of the association. It is of particular interest that high heterogeneity appeared in all contrasts for the 1056 A>G polymorphism while zero heterogeneity was present in the contrasts of 1626 A>G polymorphism. Heterogeneity could be due mainly to small sample size, but also to the different criteria used to diagnose MS. Third, meta-analysis is subjected to methodological weaknesses of the original studies.

Overall, our study has several important advantages. First, a thorough and meticulous search was performed, including both a computer-aided and manual search, to identify all possible eligible studies included in published literature. Second, we did not impose any quality restriction and we did not exclude any study based on the design, the language or any other criteria, since most recent guidelines advocate against this. Third, we used modern statistical techniques in order to include all available studies (i.e., family-based and population-based ones) and to detect the mode of inheritance. The multivariate method in particular is capable not only of identifying the mode of inheritance but also preserving the nominal type I error rate and protecting from multiple comparisons. Although the method identified the most plausible mode of inheritance, we chose to report all the available contrasts only for completeness. Finally, we took any available precaution in order to minimize different sources
of bias, which is the main source of concern in this type of studies. Along these lines, we investigated
the sources of heterogeneity, we searched for influential studies, and we performed all the available
tests for detecting publication bias and time-trend bias.

In summary, we have conducted meta-analyses to investigate associations between CD24 polymorphisms
and MS using a method that combines data from case-control studies with family-based data [31].
We found that CD24 226 C>T polymorphism constitutes a risk of MS development while the
dinucleotide TG deletion at 1527–1528 confers protection against the disease, and they can be used as
prognostic biomarkers for MS onset. Any associations of 1056 A>G and 1626 A>G polymorphisms
with MS could not be identified due to the small number of studies. We also estimated the number of
the additional participants needed in order to reach significant results, using statistical methods. Given
that these numbers can be attained relatively easily, biomedical researchers should be encouraged to
investigate the association of the three 3′ UTR polymorphisms with MS and possibly with other
autoimmune diseases. Furthermore, additional studies investigating linkage disequilibrium between
these CD24 polymorphisms, gene–gene interactions, or even gene-environment interactions would be
helpful in better understanding the role of the CD24 gene in MS onset and development.

4. Experimental Section

4.1. Literature Search

A comprehensive literature search was performed until September 2014 in PubMed
(http://www.ncbi.nlm.nih.gov/pubmed) with the following keywords: “CD24 AND (gene OR variant
OR polymorphism OR mutant OR mutation OR allele) AND (‘Multiple sclerosis’ OR MS OR
‘disseminated sclerosis’ OR ‘encephalomyelitis disseminate’). Retrieved abstracts were scrutinized
and only the relevant ones were retained. The references from the retrieved articles were also
investigated and the relevant ones were included in our study. We included all identified studies that
provided data from which an estimate of the relative risk (the odds ratio) and its variance could be
calculated. We did not impose any restrictions on the type of studies included with regard to the
design, the language in which the study was written or any other quality measure.

4.2. Data Extraction

Data extraction from each manuscript was performed by two investigators (GGB, KGP) according
to the eligibility criteria. In case problems of poor agreement occurred, they were resolved after
discussion with the principle investigator (PGB) and the extracted data were recorded in a spreadsheet.
From each article, the PubMed ID, first author’s name, year of publication, the total number of the
subjects (cases/controls) as well as the population’s ethnicity and geographical location were recorded
in the spreadsheet.

4.3. Statistical Analyses

Odds ratio (OR) was used to test the association between the mutant alleles and/or genotypes and
MS, along with their 95% CIs (confidence intervals). In the case of zero cells, a continuity correction
was applied by adding the value 0.5 to all cells of the contingency table. Data were analyzed using the
The multivariate random-effects method of meta-analysis, which can infer and quantify the genetic mode of inheritance directly, was also applied by estimating the ratio $\lambda$ of the two log-odds ratios (of heterozygotes vs. homozygotes and of risk allele homozygotes vs. homozygotes for the wild type allele [24,34]).

To estimate possible publication biases, the rank correlation method of Begg and Mazumdar [35] was used. Additionally, the fixed effects regression method of Egger was applied [36]. Influential meta-analysis was further performed, by removing an individual study each time, and re-calculating the effects estimates (ORs) and heterogeneity. Cumulative meta-analysis was performed in order to estimate a possible time trend in the results over years, a bias called the “Proteus phenomenon” [37]. Two methods were used to detect the Proteus phenomenon: (a) the standard cumulative meta-analysis [38–40] approach; where we visually inspected the plot and (b) a more recently proposed regression-based method [37]. Finally, the Barrowman method [25] was used to estimate the additional participants required to achieve statistically significant results for the associations under study.

In all analyses, we used STATA 13 [41] and results with $p$-value <0.05 were considered statistically significant.

**Supplementary Materials**

Supplementary materials can be found at http://www.mdpi.com/1422-0067/16/06/12368/s1.

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**Author Contributions**

Georgia G. Braliou drafted the manuscript. Georgia G. Braliou and Katerina G. Pantavou performed the literature search and collected the data. Georgia G. Braliou, Katerina G. Pantavou and Panagiota I. Kontou performed the analysis and the interpretation of the results. Pantelis G. Bagos and Georgia G. Braliou designed the analysis. Katerina G. Pantavou, Panagiota I. Kontou and
Pantelis G. Bagos revised the manuscript critically. Pantelis G. Bagos conceived the project and supervised the work.

Conflicts of Interest

The authors declare no conflict of interest.

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