CD4+ T cells support glial neuroprotection, slow disease progression, and modify glial morphology in an animal model of inherited ALS

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Neuroinflammation, marked by gliosis and infiltrating T cells, is a prominent pathological feature in diverse models of dominantly inherited neurodegenerative diseases. Recent evidence derived from transgenic mice ubiquitously overexpressing mutant Cu/Zn superoxide dismutase (mSOD1), a chronic neurodegenerative model of inherited amyotrophic lateral sclerosis (ALS), indicates that glia with either a lack of or reduction in mSOD1 expression enhance motoneuron protection and slow disease progression. However, the contribution of T cells that are present at sites of motoneuron injury in mSOD1 transgenic mice is not known. Here we show that when mSOD1 mice were bred with mice lacking functional T cells or CD4+ T cells, motoneuron disease was accelerated, accompanied by unexpected attenuated morphological markers of gliosis, increased mRNA levels for proinflammatory cytokines and NOX2, and decreased levels of trophic factors and glial glutamate transporters. Bone marrow transplants reconstituted mice with T cells, prolonged survival, suppressed cytotoxicity, and restored glial activation. These results demonstrate for the first time in a model of chronic neurodegeneration that morphological activation of microglia and astroglia does not predict glial function, and that the presence of CD4+ T cells provides supportive neuroprotection by modulating the trophic/cytotoxic balance of glia. These glial/T-cell interactions establish a novel target for therapeutic intervention in ALS and possibly other neurodegenerative diseases.

Amyotrophic lateral sclerosis | astrocytes | bone marrow transplant | microglia | superoxide dismutase

Dysfunction or death of specific neuronal populations most at risk for dominantly inherited neurodegenerative diseases is not mediated solely by the expression of the mutant protein within target neurons (1). Dominant mutations in the Cu/Zn superoxide dismutase (mSOD1) gene are the most frequent cause of inherited amyotrophic lateral sclerosis (ALS), an inextricably progressive and fatal neuromuscular disease, and current evidence suggests that motoneuron injury is non-cell-autonomous and involves damage caused by mSOD1 proteins within glia of the central nervous system (CNS) (1–4). Reduced mSOD1 protein levels in astroglia have been shown to delay microglial activation and to sharply slow disease progression (5). Eliminating or reducing mSOD1 expression from microglia also slows motoneuron loss and disease progression (6, 7). Although neuroinflammation is a pathological hallmark in transgenic mice ubiquitously overexpressing mSOD1 (8, 9), the role of T cells in this model of chronic neurodegeneration is not understood; however, they have been shown to modulate microglial activation and provide neuroprotection in acute models of neuronal injury (10–16). Thus, to assess the role of T cells in a chronic neurodegenerative disease such as ALS, immunodeficient mice were bred with mSOD1 transgenic mice and selective reconstitution experiments with bone marrow transplants (BMT) were used to elucidate the roles of T cells. These studies provide compelling evidence that the presence of CD4+ T cells, either directly or indirectly, morphologically and functionally alter microglial and astroglial activation, and may support neuroprotection by modulating the glial balance between trophism and cytotoxicity.

Results

CCR2−/− Donor Cells Are Not Neuroprotective. To examine possible contributions of the peripheral immune system on disease progression, mSOD1G93A/PU.1−/− mice on a B6/SJL genetic background [supporting information (SI)] received BMT from CCR2−/− mice lacking the receptor for monocyte-chemoattractant protein−1 (MCP-1/CCL2) (6). MCP-1 recruits CCR2-expressing cells, including activated T cells and monocytes, to sites of injury (17, 18) and is increased in mSOD1G93A mice (19). Although mean onset times were not different between groups (SI Text, Fig. S1), mSOD1G93A/PU.1−/− mice receiving CCR2−/− BMT had shorter life spans and disease durations than mSOD1G93A/PU.1−/− mice transplanted with wild-type (WT) bone marrow (survival, P = 0.026; duration, P = 0.032), similar to mSOD1G93A/PU.1−/− mice transplanted with mSOD1G93A bone marrow and mSOD1G93A/PU.1−/− littermates (Fig. 1 A and B). With the exception of expressing CCR2, the engrafted microglia were WT and yet demonstrated less immunohistochemical evidence of morphological activation than mice transplanted with WT bone marrow (Fig. 1C and D). Unlike mSOD1G93A/PU.1−/− mice that received mSOD1G93A or WT BMT, CD4+ T cells were not observed in mSOD1G93A/PU.1−/− mice with CCR2−/− BMT (Fig. 1 E and F).

T and/or B Cells Contribute to Neuroprotection. The significance of infiltrating lymphocytes were assayed by breeding mSOD1G93A mice with recombination-activating gene 2 knockout (RAG2−/−) mice that lack functional T and B cells (20). Although onset times were not different (Fig. S2), mSOD1G93A/RAG2−/− mice on a C57BL/6 genetic background (SI Text) had shorter life spans and disease durations than mSOD1G93A/RAG2−/− littermates (mean survival, P = 0.00001; duration, P = 0.00001) (Fig. 1G and H), suggesting T and/or B cells contribute to neuroprotection. To determine whether RAG2 has unknown CNS functions, sublethally γ-irradiated mSOD1G93A/RAG2−/− mice were reconstituted with functional T and B cells by BMT from either mSOD1G93A or WT mice. Transplanted mSOD1G93A/RAG2−/− mice survived longer with a slower disease progression than non-transplanted mSOD1G93A/RAG2−/− mice (mSOD1G93A: survival, P = 0.00004 and duration, P = 0.0016; WT: survival, P = 0.001 and duration, P = 0.0025), similar to mSOD1G93A/RAG2−/− mice (Fig. 1G and H).


The authors declare no conflict of interest.

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leukocytes and the radiation treatment, sublethally γ-irradiated mSOD1G93A/RAG2+/- mice received BMT from RAG2+/- mice that have normal functioning monocytes/macrophages, neutrophils, etc (20). Survival times of mSOD1G93A/RAG2+/- mice receiving RAG2+/- BMT were similar to non-transplanted mSOD1G93A/RAG2+/- mice, but shorter survival times and disease durations than mSOD1G93A/RAG2+/- mice transplanted with either mSOD1G93A or WT bone marrows (mSOD1G93A, survival, P = 0.0001 and duration, P = 0.003; WT: survival, P = 0.001 and duration, P = 0.005) (Fig. 1G and H, and Fig. S2).

T and/or B Cells Influence the Rate of Disease Progression. Rates of disease progression (6) were different at 11 weeks of age when mSOD1G93A/RAG2+/- mice were compared with mSOD1G93A/RAG2+/- mice (P = 0.0006) and further diverged between 14 and 18 weeks, a time at which disease progression plateaued in mSOD1G93A/RAG2+/- mice (Fig. 1I) (23). Following BMT with mSOD1G93A cells, mSOD1G93A/RAG2+/- mice had a similar 4 week latency progression profile as mSOD1G93A/RAG2+/- mice.

Fig. 1. T cells prolong survival. (A) mSOD1G93A/Pu.1+/+ mice on a B6/SJL genetic background receiving CCR2+/+ BMT have a shorter survival time (133 ± 2 days, n = 10) than mSOD1G93A/Pu.1+/+ mice after WT BMT (141 ± 3 days, n = 12), and were similar to mSOD1G93A/Pu.1+/+ littermates (133 ± 2 days, n = 12; data not shown for clarity) and mSOD1G93A/Pu.1+/+ mice with mSOD1G93A BMT (133 ± 2 days, n = 12). (B) Disease duration was attenuated in mSOD1G93A/Pu.1+/+ mice receiving CCR2+/+ BMT. Data for mSOD1G93A/Pu.1+/+ mice were eliminated for clarity but were similar to mSOD1G93A/Pu.1+/+ mice with mSOD1G93A BMT (P = 0.55). (C) CD11b immunohistochemistry of morphologically activated microglia at end-stage disease in mSOD1G93A/Pu.1+/+ mice. (D) Following BMT with CCR2+/+ donor-derived cells, the CD11b signal from microglia of mSOD1G93A/Pu.1+/+ was reduced. (E) CD3+ T cells were observed in mSOD1G93A/Pu.1+/+ mice. (F) CD3+ T cells were absent in mSOD1G93A/Pu.1+/+ mice receiving CCR2+/+ BMT. (G) Survival times were shorter in mSOD1G93A/RAG2+/- mice, on a C57BL/6 genetic background, lacking functional T and B cells (145 ± 2 days, n = 14) than in mSOD1G93A/RAG2+/- littermates (161 ± 2 days, n = 13), but were prolonged following BMT (mSOD1G93A, 164 ± 3 days, n = 10; WT, 161 ± 2 days, n = 10). RAG2+/- BMT did not increase survival (148 ± 2 days, n = 10). Survival of mSOD1G93A/RAG2+/- mice were similar to mSOD1G93A/RAG2+/- (160 ± 3 days, n = 20, P = 0.61). (H) Disease duration was shorter in mSOD1G93A/RAG2+/- mice than mSOD1G93A/RAG2+/- littermates, but was prolonged following BMT. (I) Disease progression in mSOD1G93A/RAG2+/- mice lacked the 4-week plateau of mSOD1G93A/RAG2+/- mice and was re-established after mSOD1G93A BMT. #, different from mSOD1G93A/Pu.1+/+ mice with WT BMT; †, different from mSOD1G93A/RAG2+/-; *, different from mSOD1G93A/RAG2+/- mice (Scale bars: C and D, 100 μm; E and F, 50 μm.)
CD3+, CD4+, or CD8+ T cells were observed in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice. CD3+ T cells were observed at every age examined, with increasing numbers as the disease progressed. At 75, 105, and 140 days of age, there were 6, 10, and 19 CD3+ cells per section, respectively, localized predominantly to the ventral gray matter (Fig. 2E). At these ages, only CD4+ cells were observed with cell numbers similar to CD3+ cells; no CD8+ cells were observed at end-stage disease, there were 27 CD3+ cells per section. ~60% were CD4+ with the remaining cells staining for CD8. Similar numbers and subtypes of T cells were observed in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice following BMT with either mSOD1<sup>G93A</sup> or WT donor-derived cells. Using antibodies to CD19, a B-cell marker, B cells were not present in any lumbar spinal cord section examined from 105- and 140-day-old mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> mice and mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice with BMT. At end-stage disease, there was no consistent convincing evidence for the presence of B cells.

**Presence of CD4+ T Cells Is Responsible for Prolonged Disease Duration and Survival.** Because only CD4+ T cells were observed at all phases of disease, mSOD1<sup>G93A</sup> transgenic mice were bred with CD4 knockout (CD4<sup>−/−</sup>) mice that lack surface expression of CD4, but have unaltered myeloid-, CD8+ T and B cells (24). Although disease onset was not different (Fig. S4A), survival of mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice was shorter than mSOD1<sup>G93A</sup>/CD4<sup>+</sup> littermates (P = 0.001) (Fig. 2F) and was similar to the difference in survival times between mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> and mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> mice (15.6 days vs 15.8 days). Disease duration was also different between mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> and mSOD1<sup>G93A</sup>/CD4<sup>+</sup> littersmates (P = 0.0024) (Fig. S4B) and was again analogous to mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice (17.4 vs 17.3 days). Disease progression with mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice reached a plateau between 15 and 19 weeks, whereas mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice continued to decline (Fig. 2G, P = 0.03 at 15 weeks and diverged further thereafter).

**Morphological Markers of Glial Activation Are Attenuated in mSOD1<sup>G93A</sup> Mice Lacking Functional T-Cells.** Immunohistochemical evaluations of lumbar spinal cords at end-stage disease revealed less morphological activation of microglia in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice compared with mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> littersmates, even though their survival time was shorter (Fig. 3A–C and G–J and Fig. S5A–J). Following mSOD1<sup>G93A</sup> BMT, the CD11b, CD68, CD11c, and CD40, and MHC II immunoreactivities were restored in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice and were comparable to those observed in mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> mice. Similar results were obtained with mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice reconstituted with WT BMT. Quantitative real-time polymerase chain reaction (RT-PCR) confirmed that there was less CD68 mRNA in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice than in mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> littermates (P = 0.001) and was restored following BMT (Fig. 4A). At 105 days of age, there was a reduction of CD11b (Fig. 3S–U) and CD68 (Fig. 3V–X) signal in lumbar spinal cord sections from mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice compared with mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> littermates. However, at 75 days of age, this distinction was not evident (Fig. S3S–M). To control for other leukocytes possibly influencing the status of microglial activation in these mice, transplantation of RAG2<sup>−/−</sup> bone marrow cells into mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice did not restore the morphological activation of microglia (Fig. 3D and J).

To address the question of whether all glial responses were reduced, astroglial morphology was evaluated in lumbar spinal cords. At end-stage disease, GFAP immunoreactivity was increased in transgenic mice compared with WT mice (Fig. 3M–O). This increase was confirmed using quantitative RT-PCR for GFAP (Fig. 4B). Furthermore, both qualitatively and quantitatively, there were no differences in the expression of GFAP between any transgenic mouse line or after BMT (Fig. 3P). At 105 days of age, mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice had reduced GFAP signal compared to mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> mice and BMT restored the GFAP immunoreactivity (Fig. 3Y–AA). GFAP immunoreactivity was observably less at 75 days of age in sections from mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice compared with sections from mSOD1<sup>G93A</sup>/RAG2<sup>−/+</sup> mice (Fig. S5N and O).

Immunohistochemical evaluation of microglia in lumbar spinal cords of mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice showed a similar attenuation of CD11b and CD68 signal as observed in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice (Fig. 3E, F, K, and L). Quantitative RT-PCR confirmed that the message for CD68 in lumbar spinal cords was reduced in mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice (P = 0.03) (Fig. 4A). However, unlike the astrogliosis noted at end-stage disease for mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice, there was an observable reduction in GFAP immunoreactivity in mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice compared with mSOD1<sup>G93A</sup>/CD4<sup>−/+</sup> mice (Fig. 3Q and R). Although CD4+ and CD8+ T cells were observed in mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice (data...
GDNF, and BDNF in mSOD1G93A/RAG2 were reduced message levels for IGF-1, mSOD1G93A/RAG2 known to affect motoneuron viability, also paralleled survival (25, 26). The mRNA levels of IL-4 and TGF-β, two anti-inflammatory factors, were increased in mSOD1G93A and mSOD1G93A/RAG2−/− mice compared with WT mice, but was again restored following mSOD1G93A BMT. Microglia From Mice Lacking T-Cells Are Not Dysfunctional. Following lipopolysaccharide (LPS) treatment, a treatment known to produce proinflammatory agent TNF-α, increased compared with mSOD1G93A/RAG2−/− mice (Fig. 4H and I) but were decreased in mSOD1G93A/RAG2−/− and mSOD1G93A/CD4−/− mice; BMT restored IL-4 and TGF-β levels to levels observed in mSOD1G93A and mSOD1G93A/RAβ−/− mice. The expression of Ym1 mRNA mirrored the IL-4 results across all genotypes of mSOD1G93A mice, suggesting a loss of alternatively activated macrophages that are involved in resolving inflammation and promoting wound healing (Fig. 5C) (27). Fractalkine receptor (CX3CR1), expressed on microglia, monocytes, dendritic cells, and subsets of T cells, which has been shown to decrease microglial toxicity possibly by regulating the release of cytokitic substances (28), was reduced in mSOD1G93A/RAG2−/− and mSOD1G93A/CD4−/− mice (Fig. 5D). mSOD1G93A/RAG2−/− mice with mSOD1G93A donor-derived cells restored the levels of IL-4 and GLAST mRNA to levels observed in mSOD1G93A mice (Fig. 5E and F). BMT of mSOD1G93A/RAG2−/− mice with mSOD1G93A donor-derived cells restored the levels of FLT-1 and GLAST mRNA to levels observed in mSOD1G93A/RAG2−/− mice. EAAC1 mRNA levels were decreased in mSOD1G93A, mSOD1G93A/RAG2−/−, mSOD1G93A/RAG2−/−, and mSOD1G93A/CD4−/− mice compared with WT mice, and BMT of mSOD1G93A/RAG2−/− mice did not alter EAAC1 levels in these mice (Fig. 5B).

Microglia From Mice Lacking T-Cells Are Not Dysfunctional. To ensure that the morphological reduction of microglia activation in mSOD1G93A/RAG2−/− mice was not caused by an inherent dysfunction of the microglia, in vitro cultures of microglia from RAG2−/− mice were compared with microglia from WT mice for their ability to undergo morphological and functional activation. Following lipopolysaccharide (LPS) treatment, a treatment known to increase the release of tumor necrosis factor–α (TNF-α) and interleukin-1β (IL-1β), there were no differences in the production of TNF-α or IL-1β between microglia isolated from RAG2−/− mice compared with WT mice at any dose of LPS (Fig. S6A and B). Morphologically, there were also no differences between LPS-treated RAG2−/− microglia and LPS-treated WT microglia (data not shown). Thus, activated microglia from RAG2−/− mice are morphologically and functionally similar to activated WT microglia.

The Presence of CD4+ T-Cells Enhances Neuroprotection and Suppresses Cytotoxic Factors. mRNAs for the neurotrophic factors IGF-1 and GDNF were quantitatively decreased in the lumbar spinal cords of mSOD1G93A/RAG2−/− mice compared with mSOD1G93A and mSOD1G93A/RAG2−/− mice and were similar to levels in WT mice (Fig. 4C and D). The mRNA for BDNF was decreased in both mSOD1G93A and mSOD1G93A/RAG2−/− mice but was further decreased in mSOD1G93A/RAG2−/− mice (Fig. 4E). BMT of mSOD1G93A/RAG2−/− mice with mSOD1G93A donor-derived cells restored the levels of IGF-1, GDNF, and BDNF to those of mSOD1G93A/RAG2−/− mice. Levels of these trophic factors were similar between mSOD1G93A/RAG2−/− and mSOD1G93A/CD4−/− mice. In contrast, the mRNA expression for NGF was not different between WT mice and any genotype of mSOD1G93A mice in this study (Fig. S7A).

mRNA levels for several glutamate transporters, which are known to affect motoneuron viability, also paralleled survival (25, 26). Expression of GLUT-1 and GLAST mRNAs was decreased in mSOD1G93A/RAG2−/− and mSOD1G93A/CD4−/− mice (Fig. 4F and G); GLAST mRNA levels were similar to levels in WT mice. BMT of mSOD1G93A/RAG2−/− mice with mSOD1G93A donor-derived cells restored the levels of GLUT-1 and GLAST mRNA to those of mSOD1G93A/RAG2−/− mice. EAAC1 mRNA levels were decreased in mSOD1G93A, mSOD1G93A/RAG2−/−, mSOD1G93A/RAG2−/−, and mSOD1G93A/CD4−/− mice compared with WT mice, and BMT of mSOD1G93A/RAG2−/− mice did not alter EAAC1 levels in these mice (Fig. S8B).
The NADPH oxidase isoform NOX2 mRNA was elevated 70-fold in mSOD1G93A and mSOD1G93A/RAG2−/− mice compared with WT mice, and was increased 110-fold in mSOD1G93A/RAG2−/− and mSOD1G93A/Cd4−/− mice (Fig. 4B). BMT in mSOD1G93A/RAG2−/− mice reduced the NOX2 mRNA levels to those seen in mSOD1G93A or mSOD1G93A/RAG2−/− mice. The increased expression of proinflammatory cytokines and NOX2 does not lead to increased mouse or mutant human SOD1 mRNA expression, indicating that the shortened survival times are not caused by enhanced SOD1 mRNA expression (Fig. S7J and K) (29, 30).

Discussion

Immune dysfunction is a pathological feature in human ALS and mSOD1 transgenic mice (31). Because T cells are present at sites of motoneuron injury (9) and their role in injury is not known, this study directly addressed whether T cells contribute to the disease process of mSOD1G93A-initiated chronic motoneuron degeneration. The results establish that the lack of T-cell recruitment, either through the loss of CCR2 or developmental inhibition, accelerates disease progression and the demise of these mice. These studies demonstrate for the first time that CD4+ T cells, directly or indirectly, are possibly the subpopulation of T cells that are neuroprotective in this model of inherited chronic neurodegeneration.

To determine whether recruitment of peripheral immune cells and/or microglia is essential for neuroprotection, mSOD1G93A/Pu.1−/− mice received BMT from CCR2−/− donor mice. Although onset of disease was not altered, disease progression was accelerated. In addition, these mice lacked CD3+ T cells and morphologically activated microglia, which were observed in mSOD1G93A/Pu.1−/− mice transplanted with mSOD1G93A or WT bone marrow. Acceleration of disease after CCR2−/− BMT suggests that recruitment of microglia/monocytes and/or lymphocytes is involved in the pathogenesis of motoneuron injury, possibly by modulating glial function. A similar outcome was noted in a transgenic mouse model of Alzheimer disease, in which CCR2 deficiency accelerated disease progression and impaired microglial accumulation (18).

To dissociate the effects of microglia/myeloid cell recruitment from lymphocyte recruitment as mediators of disease progression, mSOD1G93A/RAG2−/− mice were developed. Although disease onset was not altered, the lack of functional T cells accelerated disease progression in mSOD1G93A/RAG2−/− mice. These data demonstrate, in a chronic neurodegenerative disease model, that lymphocytes are possibly needed for neuroprotection and microglial morphological activation. Although two recent reports suggest that 1100-cGy γ-irradiation dose may artificially induce circulating myeloid cells to infiltrate the CNS (21, 22), following a sublethal 400-cGy dose, spinal cord sections from mSOD1G93A/Cd4−/− mice transplanted with GFP+ donor-derived bone marrow contained only GFP+ lymphocytes; no GFP+ cells with myeloid cell morphologies were present (data not shown). Furthermore, these previous studies did not report on the recruitment or infiltration of T cells into the CNS after lethal γ-irradiation treatment. In this study, the composition of T-cell subpopulations was similar between mSOD1G93A/RAG2−/− mice and γ-irradiated mSOD1G93A/RAG2−/− mice after BMT; the number and subtypes of T cells was not altered because of γ-irradiation treatment. Nevertheless, to rule out the possibility that irradiation, myeloid cells, or other leukocytes influenced disease onset, survival, or duration, mSOD1G93A/Cd4−/− mice were transplanted with RAG2−/− derived bone marrow, and no beneficial effects were noted. In addition, WT and mSOD1G93A bone marrow cells have equivalent neuroprotective abilities to prolong survival, possibly by modulating glial function. A possible explanation for these equivalent effects is that the donor-derived bone marrow precursor T cells are “educated” by the recipient’s own local immune environment and, regardless of the T-cell genotype, the host will direct the activation of these transplanted lymphocytes.

Because CD4+ T cells were observed in the spinal cord during all phases of disease, including disease onset and during the plateau phase, and CD8+ T cells were present only in the terminal stages, CD4+ T cells may represent the relevant neuroprotective subpopulation of lymphocytes that prolonged survival in transplanted mSOD1G93A/RAG2−/− mice. To test this hypothesis, mSOD1G93A/Cd4−/− mice were generated and compared with their mSOD1G93A/Cd4−/− littermates, and although disease onset was not altered, disease progression in mSOD1G93A/Cd4−/− mice was accelerated to the same extent as in mSOD1G93A/RAG2−/− mice. Thus, the CD4+ T cells that entered the spinal cord at sites of motoneuron injury appear to be neuroprotective (12, 14, 16), whereas the CD8+ T cells present at end-stage disease are possibly associated with injury.

In mSOD1G93A/RAG2−/− and BMT mSOD1G93A/RAG2−/− mice, the T cells were localized throughout the ventral gray matter. Although 5 to 10 T cells per section were observed in mSOD1G93A/RAG2−/− mice between the disease onset and the plateau phase of disease progression, which later increased to 19 T cells per section, similar numbers and subtypes of T cells were observed in mSOD1G93A/RAG2−/− mice following BMT with either mSOD1G93A or WT donor-derived cells. In contrast, although T cells are known to be present in the central nervous system of mice under normal conditions, their presence is a rare event. Thus, as has been previously reported (32), even at these earlier time points, the documented presence of T cells may have a considerable impact on the area’s local immune response and may alter the trophic versus toxic balance of glia in these areas of chronic CNS neurodegeneration. However, it is also possible that the neuroprotective benefits of T-lymphocytes may be amplified by their presence at the neuromuscular junction or contiguous with injured motoneuron axons.

CD4+ T cells have also been reported to influence survival in an acute facial motoneuron injury model, possibly related to CD4+ secretion of BDNF (12). In that model, CD4+ T-cell–mediated neuroprotection was found to depend on both resident microglia and peripherally derived antigen-presenting cells (15). The activation of microglia, which causes them to function as antigen-presenting cells and to express MHC class II proteins, is correlated with a better outcome following CNS injury (11). Thus, the beneficial or deleterious outcome of the local microglial response is determined by a well-controlled dialog between the innate and adaptive immune systems; and, under specific circumstances and with the correct stimulation, T cells are anti-inflammatory and protect motoneurons from degenerating. Furthermore, in conjunction with previous BMT data (6), the CCR2−/− BMT and RAG2−/− data suggest that disease progression is influenced by lymphocytes as well as by glia (5–7). Most significantly, these data indicate that CD4+ T cells, either directly or indirectly, are the subpopulation of T cells that may be responsible for prolonging survival in this model of neurodegeneration.

The activation states of microglia and astrocytes, with respect to protection versus toxicity, cannot be inferred solely from their morphologies. The conventional morphological markers for activation were attenuated in mSOD1G93A/RAG2−/− and mSOD1G93A/Cd4−/− mice; yet the mRNA for NOX2, which is known to enhance microglial release of reactive oxygen species (33), was elevated and contributed to more rapid disease progression and death. Thus, morphological (CD11b, CD68, GFAP) markers of glial “activation” do not accurately predict the functional (TNF-α and NOX2) markers of “activation.” The apparent morphological reduction of microglial activation occurs early in disease, indicating that the presence of T cells may increase the morphological activation state and antigen presentation abilities of microglia and may contribute to increased survival. Although not different at end stage, these results also suggest that all glial responses are not attenuated and that an increased astroglial response at earlier time points is neuroprotective. Furthermore, the data suggest that
Neuroprotection **mSOD1G93A/RAG2+/−** mice compared with **mSOD1G93A/RAG2−/−** mice. 

**mSOD1G93A/RAG2−/−** + BMT mice compared with **mSOD1G93A/RAG2+/−** mice.

Cytotoxicity 

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**Fig. 5.** The presence of T cells shifts the balance of microglial and astrogial responses from reduced protection and increased cytotoxicity to increased neuroprotection and decreased toxicity following BMT. \( \uparrow \uparrow \uparrow \uparrow \uparrow \) > 75% decrease; \( \uparrow \uparrow \uparrow \uparrow \downarrow \downarrow \) 50–75% decrease; \( \uparrow \uparrow \downarrow \uparrow \downarrow \downarrow \downarrow \) 0–50% decrease; NC, no change; \( \uparrow \) 100–500% increase; \( \uparrow \uparrow \) > 1000% increase; \( \uparrow \uparrow \uparrow \) > 1500% increase; \( \uparrow \uparrow \uparrow \uparrow \) > 2000% increase.

Disease progression may be influenced by lymphocytes indirectly or possibly even directly, interacting with glia, balancing the trophic versus cytotoxic responses of microglia and astroglia. CD4+ T cells should now be included in the non–cell-autonomous hypothesis of neuroprotection (1).

The shortened length of survival in **mSOD1G93A/RAG2−/−** and **mSOD1G93A/C4D−/−** mice is partly due to decreased levels of neurotrophic factors and the reduced abilities of glia to remove glutamate, thus enhancing motoneuron excitotoxicity. Not only are neurotrophic and anti-inflammatory factors reduced in **mSOD1G93A/RAG2−/−** and **mSOD1G93A/C4D−/−** mice, the messages for TNFα and superoxide are increased, suggesting a decrease of protective factors and an increase in toxic molecules (Fig. 5). More importantly, BMT reconstituted mice with functional T cells and restored the neuroprotective factors, and also decreased the toxic and proinflammatory responses. These results suggest that CD4+ T cells directly or indirectly provide neuroprotection by modulating the trophic/cytotoxic balance of glia. Expanding this population may offer further protection in diverse forms of dominantly inherited chronic neurodegenerative diseases and may provide a novel target for critically needed therapies.

### Materials and Methods

**mSOD1G93A, PU.1, RAG2, and CD4 Mice.** All animal protocols were approved by the Methodist Research Institute’s Institutional Animal Care and Use Committee in compliance with National Institutes of Health guidelines. Housing, breeding, and screening details are found in [SI Methods](#).

**Bone Marrow Transplantation.** Donor bone marrow was obtained from 9 to 12 veterinary-old WT, **mSOD1G93A**/−, or **CCR2−/−** mice, and transplanted into the **mSOD1G93A/Pu.1−/−** pups within 24 h of birth as previously described (6). **mSOD1G93A/RAG2−/−** mice were sublethally γ-irradiated (400 rads) and transplanted with WT, **mSOD1G93A**, or **RAG2−/−** donor-derived bone marrow. Details are provided in [SI Methods](#).

**Quantitative RT-PCR.** RNA was isolated and purified from lumbar spinal cords, and quantitative RT-PCR was performed as previously described (19). Technical details are given in [SI Methods](#).

**Immunohistochemistry and Antibodies.** Spinal cord tissue was evaluated for the expression of CD3, CD4, CD8, CD11b, CD11c, CD19, CD40, CD68, MCH class II, and GFAP. Technical details are found in [SI Methods](#).

**Primary Microglia Cultures.** Primary microglial cultures were prepared from 8- to 10-day-old mice and treated with LPS as previously described (6). Details are given in [SI Methods](#).

**Statistical Analyses.** Data were analyzed using two-tailed Student’s t test using Excel (Microsoft) software. Data are expressed as mean ± SEM; \( p < 0.05 \) was considered statistically significant. Differences in onset and survival times were computed using Kaplan–Meier survival statistics (log-rank-sum test; Number Cruncher Statistical Systems, Kaysville, UT). Disease progression and the *in vitro* studies were analyzed using a one-way analysis of variance (ANOVA) with repeated measures (SigmaStat, Richmond CA). Differences between groups were analyzed using a two-way ANOVA (SigmaStat).

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Supporting Information

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SI Materials and Methods

**SOD1G93A Mice.** All transgenic animals were bred and maintained in our animal facility (1, 2). All mice were housed in microisolator cages within a modified pathogen-free barrier facility and had access to food and water *ad libitum.* All animal protocols were approved by the Methodist Research Institute’s Institutional Animal Care and Use Committee in compliance with National Institutes of Health guidelines. Genomic tail DNA was isolated using a standard protocol.

Transgenic mice overexpressing the fALS associated G93A SOD1 mutation (G1H) (mSOD1G93A) were originally purchased from Jackson Laboratories (Bar Harbor, ME); strain designations were as follows: B6SJLTg(SOD1*G93A)1Gur/J and B6.Cg-Tg(SOD1*G93A)1Gur/J. mSOD1G93A mice on a B6/SJL genetic background had a mean survival time of 132 days, whereas mSOD1G93A mice on a C57BL/6 genetic background survived for 160 days. Transgenic mSOD1G93A animals were identified and copy number verified by quantitative PCR using SOD1 mutation (G1H) (mSOD1G93A) were originally purchased from 9- to 12-week-old WT, mSOD1G93A, or CCR2 mice and was transplanted into the mSOD1G93A/PU.1−/− mice were bred with B6Cg-Tg(SOD1*G93A)1Gur/J for at least eight generations. The presence or absence of the SOD1G93A gene was also determined by PCR (Eppendorf Mastercycler) using 250 ng of tail DNA and using Eppendorf TaqDNA polymerase according to the manufacturer’s instructions. The following primers were used: A) 5′-GGGAGGACACCTACACTTGC-CAG-3′ and B) 5′-AGTCAGGAAGTCTACTTTCCTC-3′ and Neo C) 5′-GGCCGGGAGAACCCTCGTGCAAA-3′. Homozygotic mice will have one 350 bp band. Heterozygotic mice will have bands at 350 and 263 bp bands. Wild-type mice will have one 263 bp band. The PCR protocol was: 95°C for 15 min (denatured at 94°C for 45 sec, annealed at 55°C for 1 min, and extended at 72°C for 1 min for 35 cycles, then 72°C for 7 min, and finally held at 4°C. The PCR products were resolved by 1.0% agarose/ethidium bromide gel electrophoresis and photographed under UV illumination. Transgenic mSOD1G93A mice transgene copy numbers remain stable. After the initial cross, mSOD1G93A/RAG2+− mice were bred with RAG2−/− mice that enabled a direct comparison of mSOD1G93A/RAG2−/− mice with their mSOD1G93A/RAG2−/− littermates.

**RAG2 Mice.** RAG2−/− mice were initially bred with B6.Cg-Tg(SOD1*G93A)1Gur/J for at least eight generations. The presence or absence of the RAG2 gene was determined by PCR (Eppendorf Mastercycler) using 250 ng of tail DNA and using Eppendorf TaqDNA polymerase according to the manufacturer’s instructions. The following primers were used: A) 5′-GGGAGGACACCTACACTTGC-CAG-3′ and B) 5′-AGTCAGGAAGTCTACTTTCCTC-3′ and Neo C) 5′-GGCCGGGAGAACCCTCGTGCAAA-3′. Homozygotic mice will have one 350 bp band. Heterozygotic mice will have bands at 350 and 263 bp bands. Wild-type mice will have one 263 bp band. The PCR protocol was: 95°C for 15 min (denatured at 94°C for 45 sec, annealed at 55°C for 1 min, and extended at 72°C for 1 min) for 35 cycles, then 72°C for 7 min, and finally held at 4°C. The PCR products were resolved by 1.0% agarose/ethidium bromide gel electrophoresis and photographed under UV illumination. Transgenic mSOD1G93A mice transgene copy numbers remain stable. After the initial cross, mSOD1G93A/RAG2+− mice were bred with RAG2−/− mice that enabled a direct comparison of mSOD1G93A/RAG2−/− mice with their mSOD1G93A/RAG2−/− littermates.

**CD4 Mice.** CD4−/− mice were initially bred with B6.Cg-Tg(SOD1*G93A)1Gur/J for at least eight generations. The presence or absence of the CD4 gene was also determined by PCR (Eppendorf Mastercycler) using 250 ng of tail DNA and using Eppendorf TaqDNA polymerase according to the manufacturer’s instructions. The following primers were used: CD4 A) 5′-CTTCCTTGTTAATGGGAGGAT-3′ and CD4 B) 5′-TTTTCTGGTGATGCTAC-3′ and CD4 C) 5′-GGTGGTGG-TGCTTGTTGTTGC-3′. Knockout mice will have one band 225 bp; heterozygotic mice will have bands 380 and 225 bp; and wild-type mice will have one band 380 bp. The PCR protocol was as follows: 94°C for 3 min; [denatured at 94°C for 30 sec, annealed at 57°C for 1 min, and extended at 72°C for 1 min] for 35 cycles; then 72°C for 2 min, and finally held at 4°C. The PCR products were resolved by 1.0% agarose/ethidium bromide gel electrophoresis and photographed under UV illumination. Transgenic mSOD1G93A mice transgene copy numbers remain stable. After the initial cross, mSOD1G93A/CD4+− mice were bred with CD4−/− mice to enable a direct comparison of mSOD1G93A/CD4−/− mice with their mSOD1G93A/CD4−/− littermates.

**Bone Marrow Transplantation.** The donor bone marrow was obtained from 9- to 12-week-old WT, mSOD1G93A, or CCR2−/− mice and was transplanted into the mSOD1G93A/PU.1−/− mice were bred with B6.Cg-Tg(SOD1*G93A)1Gur/J for at least eight generations. The presence or absence of the RAG2 gene was determined by PCR (Eppendorf Mastercycler) using 250 ng of tail DNA and using Eppendorf TaqDNA polymerase according to the manufacturer’s instructions. The following primers were used: A) 5′-GGGAGGACACCTACACTTGC-CAG-3′ and B) 5′-AGTCAGGAAGTCTACTTTCCTC-3′ and Neo C) 5′-GGCCGGGAGAACCCTCGTGCAAA-3′. Homozygotic mice will have one 350 bp band. Heterozygotic mice will have bands at 350 and 263 bp bands. Wild-type mice will have one 263 bp band. The PCR protocol was: 95°C for 15 min (denatured at 94°C for 45 sec, annealed at 55°C for 1 min, and extended at 72°C for 1 min) for 35 cycles, then 72°C for 7 min, and finally held at 4°C. The PCR products were resolved by 1.0% agarose/ethidium bromide gel electrophoresis and photographed under UV illumination. Transgenic mSOD1G93A mice transgene copy numbers remain stable. After the initial cross, mSOD1G93A/RAG2+− mice were bred with RAG2−/− mice that enabled a direct comparison of mSOD1G93A/RAG2−/− mice with their mSOD1G93A/RAG2−/− littermates.

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marrow was flushed out of the femurs with Dulbecco’s modified Eagle’s medium (DMEM) plus 10% fetal calf serum. The hematopoietic cells were successively passed through 18-, 21-, 23-, and 25-gauge needles. The cells were then pelleted at 250 g for 10 min, washed with 5 ml DMEM without FCS, and resuspended at 2 × 10^6 cells/ml DMEM without FCS. Using a 27-gauge needle, a 50-μl aliquot (1 × 10^7 cells per mouse) was injected i.p. into mSOD1^G93A^/PU.1^−/−^ mice, or a 200-μl aliquot (3 × 10^7 cells per mouse) was injected i.v. via the tail vein for mSOD1^G93A^/RAG2^−/−^ mice.

Quantitative RT-PCR. RNA was isolated from homogenized flash-frozen murine lumbar spinal cords using TRIzol (Gibco) and purified using RNeasy (Qiagen) according to the manufacturer’s recommendations. The concentrations were determined spectrophotometrically (NanoDrop 1000). Quantitative RT-PCR was performed on 10 ng mRNA using an iQ5 Multicolor Real-Time PCR Detection System (BioRad), all normalized with β-actin. The iScript One-step RT-PCR kit with SYBR Green (BioRad) or QuantiTect SYBR Green RT-PCR kit (Qiagen) was used to perform the quantitative RT-PCR according to the manufacturer’s instructions. The primers sets were tested over a temperature gradient for amplification efficiency and specificity, and verified over 3 orders of magnitude for linearity. The relative expression levels of each mRNA were calculated using the ΔΔCt method normalizing to β-actin or GAPDH and relative to the control samples. The presence of one product of the correct size was verified by 1.5% agarose gel electrophoresis and by melting curve analyses containing a single melt curve peak. All samples were run in duplicate and were tested in a minimum of three separate experiments.

Immunohistochemistry and Antibodies. Lethally anesthetized mice were first perfused with ice-cold PBS and then ice-cold 3% paraformaldehyde. Spinal cords were removed, postfixified overnight in 3% paraformaldehyde, and placed in 30% sucrose. Sections 30 μm thick were cut from fixed spinal cord tissue, washed three times in PBS, and blocked for endogenous peroxidase activity (0.3% H<sub>2</sub>O<sub>2</sub> in distilled water for 30 min). The sections were pretreated with 5% normal goat serum (Vector Laboratories, Burlingame, CA) for 1 h at RT to block nonspecific IgG binding. The CD3, CD4, CD68, and MCH class II were rat anti-mouse, CD11c was hamster anti-mouse Ab (Serotec Inc., Raleigh, NC; 1:500, 1:1000, 1:500, 1:1000, 1:500, 1:2000, 1:500, and 1:500 dilutions, respectively), and GFAP was rabbit anti-bovine (DAKO; 1:500, 1:1000, 1:500, 1:2000, 1:2000, 1:500, and 1:500 dilutions, respectively), and the CD3, CD4, CD8, CD11b, CD19, CD40, CD68, and MCH class II were rat anti-mouse, CD11c was hamster anti-mouse Ab (Serotec Inc., Raleigh, NC; 1:500, 1:500, 1:500, 1:1000, 1:500, 1:2000, 1:2000, 1:500, and 1:500 dilutions, respectively), and GFAP was rabbit anti-bovine (DAKO; 1:50,000). The primary Ab were diluted in PBS containing 5% normal goat serum and incubated with the sections overnight at 4°C. As a negative control, the primary Ab were omitted during the reaction. After rinsing in PBS, the sections were incubated with biotinylated goat anti-rabbit IgG (1:200 dilution in PBS containing 5% normal goat serum, Serotec), biotinylated goat anti-hamster IgG (1:200 dilution in PBS containing 5% normal goat serum, Serotec), or biotinylated goat anti-rabbit IgG (1:200 dilution in PBS containing 5% normal goat serum, Vector) for 2 h at RT. After washing in PBS, the sections were further incubated with biotin-avidin complex conjugated to HRP (Vector Elite kit, Vector Laboratories, Burlingame CA) for 1 h at RT. After washing in PBS, the peroxidase was visualized with the Immunopure Metal enhanced DAB substrate kit (Pierce, Rockford, IL) for 15 min. The reaction was stopped by washing in PBS. The sections were then mounted onto glass slides, dried over-night, dehydrated in graded series of ethanol, cleared in xylene, and coverslipped with Permount (Fisher Scientific, Fair Lawn NJ). The immunostained sections were examined using a Zeiss Imager-Z1m microscope equipped with a Zeiss AxioCam MRc5 color camera and Zeiss digital image analysis system.

Primary Microglia Cultures. Primary microglial cultures were prepared from 8- to 9-day-old mice and treated with LPS, as previously described (4). Briefly, after removal of the meninges, the cortextes were minced and digested with 0.25% trypsin and 0.01% DNase. After mechanical dissociation, the cells were resuspended in SATO’s medium supplemented with 10% FBS and seeded in 150 cm<sup>2</sup> flasks at a density of 2 × 10<sup>5</sup> cells per flask. Twenty-four hours later, the medium was changed. After the cells were incubated at 37°C with 5% CO<sub>2</sub> for 1 week, the medium was changed. The flasks were then shaken at 100 rpm for 15 h. More than 95% of the floating cells were microglia, as determined by OX42 (Chemicon, Temecula, CA) immunocytochemical staining. Microglia monocultures were plated at a density of 20,000 cells per well. Microglia were activated with LPS. Microglial activation was determined by measuring the levels of TNF-α and IL-1β in the culture media using a sandwich enzyme-linked immunosorbent assay (ELISA; R&D Systems). A 5-μl quantity of medium from a microglia culture was incubated with 50 μl Assay Diluent RD1 – 41 in the TNF-α assay plate for 2 h at RT. After washing away any unbound substances, an enzyme-linked polyclonal antibody specific for rat TNF-α was added to the wells. Following the addition of the peroxidase substrate solution, the enzyme-reactive color product was detected by a microplate reader set to 450 nm with a wavelength correction set to 540 nm. The same procedure was used for IL-1β.

Statistical Analyses. Data were analyzed using two-tailed Student’s t test using Excel (Microsoft) software. Data are expressed as mean ± SE; P < 0.05 was considered statistically significant. Differences in onset and survival times were computed using Kaplan-Meier survival statistics (log-rank-sum test; Number Cruncher Statistical Systems). Disease progression and the in vitro studies were analyzed using one-way ANOVA with repeated measures (SigmaStat). Differences between groups were analyzed using a two-way ANOVA (SigmaStat).

Fig. S1. mSOD1<sup>G93A</sup>/PU.1<sup>−/−</sup> mice transplanted with CCR2<sup>−/−</sup> donor-derived cells have onset times (88 ± 2 days, n = 10) similar to mSOD1<sup>G93A</sup>/PU.1<sup>−/−</sup> mice following WT bone marrow transplantation (85 ± 1 days, n = 12) and similar to mSOD1<sup>G93A</sup>/PU.1<sup>−/−</sup> mice with mSOD1<sup>G93A</sup> bone marrow transplants (89 ± 1 days, n = 12). The curve for mSOD1<sup>G93A</sup>/PU.1<sup>−/−</sup> mice was eliminated for clarity but was similar to mSOD1<sup>G93A</sup>/PU.1<sup>−/−</sup> mice with mSOD1<sup>G93A</sup> bone marrow transplants (P = 0.49).
Fig. S2. Onset was not different in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice lacking functional T and B cells (72 ± 2 days, n = 14) compared with mSOD1<sup>G93A</sup>/RAG2<sup>+/−</sup> mice (71 ± 1 days, n = 13) or with mice receiving bone marrow transplants (mSOD1<sup>G93A</sup>: 74 ± 2 days, n = 10; WT: 74 ± 1 days, n = 10; RAG2<sup>−/−</sup>: 74 ± 1 days, n = 10).
Fig. S3. CD3⁺ T-cells were documented at end-stage disease in mSOD1<sup>G93A/RAG2<sup>−/−</sup></sup> mice were absent in mSOD1<sup>G93A/RAG2<sup>−/−</sup></sup> mice (A). CD8⁺ T cells are observed in lumbar spinal cord sections of end-stage disease mSOD1<sup>G93A/RAG2<sup>−/−</sup></sup> mice (B), absent in sections from mSOD1<sup>G93A/RAG2<sup>−/−</sup></sup> mice (C), but were observed in mSOD1<sup>G93A/RAG2<sup>−/−</sup></sup> mice receiving BMT (D).
Fig. S4.  (A) Onset was not different in mSOD1<sup>G93A</sup>/CD4<sup>+/−</sup> mice lacking cells surface expression of CD4 (80 ± 2 days, n = 12) compared with mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice (80 ± 2 days, n = 10). (B) Disease duration is attenuated in mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice.
Fig. S5. Immunohistochemical evaluations of lumbar spinal cord sections. Activated microglia morphology (CD40 signal, a marker of dendritic cells) observed at end-stage disease in mSOD1G93A/RAG2−/− mice (A) was decreased in mSOD1G93A/RAG2−/− mice (B) and restored following mSOD1G93A bone marrow transplantation (C). Similar results were observed at end-stage with antibodies to CD11c (D–F) and MHC class II (G–I). At 75 days of age, CD11b staining patterns were not different between mSOD1G93A/RAG2−/− (J) and mSOD1G93A/RAG2−/− mice (K). This was also observed with CD68 antibodies (L and M). At 75 days of age, compared with mSOD1G93A/RAG2−/− mice (M), GFAP signal was less in mSOD1G93A/RAG2−/− mice (O). (Scale bars: A–M, ~100 μm; N and O, 100 μm.)
Fig. S6. Characterization of microglia in vitro. TNF-α (A) or IL-1β (B) released in cultures of primary microglia with and without LPS treatment. No differences were observed between RAG2-/- and WT microglia at any dose of LPS.
Fig. S7. Quantitative RT-PCR. Note the different ordinate for each graph. (A) There was no difference in message levels for NGF. (B) EAAC1/EAAT3 was reduced in all mSOD1<sup>G93A</sup> genotypes compared with WT mice. (C) Ym1 mirrored the IL-4 results across all genotypes of mSOD1<sup>G93A</sup> mice studied. (D) CX3CR1 (fractalkine receptor) was reduced in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice compared with mSOD1<sup>G93A</sup>/RAG2<sup>+/−</sup> mice, but was restored following BMT. mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice also had a reduced mRNA level for CX3CR1. (E) IL-6 was increased in mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice. (F and G) TNF-α receptors I and II were elevated compared with WT mice, but were not different between all genotypes of mSOD1<sup>G93A</sup> mice. (H) iNOS was not different between WT mice and any mSOD1<sup>G93A</sup> genotypes. (I) IL-1β was elevated compared with WT mice, but were not different between all genotypes of mSOD1<sup>G93A</sup> mice. (J) Mouse SOD1 was not different in any genotype. (K) Mouse + human SOD1 was elevated in all genotypes of mSOD1<sup>G93A</sup> mice compared with WT mice. 1, WT mice; 2, mSOD1<sup>G93A</sup> mice; 3, mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice; 4, mSOD1<sup>G93A</sup>/RAG2<sup>+/−</sup> mice + BMT; and 6, mSOD1<sup>G93A</sup>/CD4<sup>−/−</sup> mice. n = 3 for all groups of mice. n.s., not significant. *, Decreased compared with mSOD1<sup>G93A</sup> or mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice, P < 0.05; #, not different from mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice; ‡, not different from mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice; **, increased compared with mSOD1<sup>G93A</sup> or mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice, P < 0.05; ##, decreased compared with mSOD1<sup>G93A</sup>/RAG2<sup>−/−</sup> mice, P < 0.05.