PGC-1α is a male-specific disease modifier of human and experimental amyotrophic lateral sclerosis

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Amyotrophic lateral sclerosis (ALS) is a devastating, adult-onset neurodegenerative disorder of the upper and lower motor systems. It leads to paresis, muscle wasting and inevitably to death, typically within 3–5 years. However, disease onset and survival vary considerably ranging in extreme cases from a few months to several decades. The genetic and environmental factors underlying this variability are of great interest as potential therapeutic targets. In ALS, men are affected more often and have an earlier age of onset than women. This gender difference is recapitulated in transgenic rodent models, but no underlying mechanism has been elucidated. Here we report that SNPs in the brain-specific promoter region of the transcriptional co-activator PGC-1α, a master regulator of metabolism, modulate age of onset and survival in two large and independent ALS populations and this occurs in a strictly male-specific manner. In complementary animal studies, we show that deficiency of full-length (FL) Pgc-1α leads to a significantly earlier age of onset and a borderline shortened survival in male, but not in female ALS-transgenic mice. In the animal model, FL Pgc-1α-loss is associated with reduced mRNA levels of the trophic factor Vegf-A in males, but not in females. In summary, we identify PGC-1α as a novel and clinically relevant disease modifier of human and experimental ALS and report a sex-dependent effect of PGC-1α in this neurodegenerative disorder.

INTRODUCTION

Amyotrophic lateral sclerosis (ALS) is an adult-onset, fatal neurodegenerative disorder that affects 2 to 3 per 100 000 people each year with a peak age of onset of 58–63 years (1). Men are more frequently affected than women, resulting in a male to female ratio of 1.4 in Europe (2). Epidemiological studies also show that male patients tend to have an earlier age of onset, a difference recapitulated in selected transgenic rodent models (3). The cause for this gender bias remains enigmatic. Pathologically ALS is characterized by the degeneration of upper and lower motor neurons, which results in paresis, muscle wasting and inevitably in death, typically within 3–5 years, but this can vary in extreme cases from a few months to several decades. Etiologically, ALS is heterogeneous with 5–10% patients reporting a clear Mendelian inheritance hence termed “familial” ALS, while the majority of ALS cases are isolated in nature and are considered ‘sporadic’ (4). Understanding the genetic and environmental factors that modulate age of onset and disease duration promises to yield important clues for identifying novel therapeutic targets.

PGC-1α, encoded for by the PPARGC1A gene, is a transcriptional co-activator that orchestrates the cellular response to metabolic demands (5). Originally described as regulator of mitochondrial respiration in brown adipose tissue, PGC-1α is now known to participate in nearly all cell types in a wide range of ancillary metabolic processes, such as angiogenesis,
antioxidant defense and autophagy (6–9). A recent study revealed that PPARGC1A is differentially regulated in the brain versus non-CNS tissues and that variant SNPs in a novel CNS-specific promoter region are associated with a delayed age of symptom onset in Huntington disease (10). In spinal cord and CNS-specific promoter region are associated with a delayed age of onset and—where available—age of death. We thus genotyped DNA from 590 patients (237 females, 353 males) with a clinical diagnosis of sporadic ALS according to the El Escorial criteria (15) and correlated the results with age of onset and—where available—age of death. We find that homozygosity compared with major allele homozygosity for the critical SNP rs11737023 is associated with a 3.3-year shorter disease duration (1.5 versus 3.1 years). Once again, however, no effect was observed in the female population (Table 2).

**RESULTS**

**PGC-1α as a genetic disease modifier in two independent human ALS populations**

To investigate the role of PGC-1α in human ALS, we focused on three SNPs that we used to characterize a role of the brain-specific PPARGC1A promoter region in human Huntington disease (10). We thus genotyped DNA from 590 patients (237 females, 353 males) with a clinical diagnosis of sporadic ALS according to the El Escorial criteria (15) and correlated the results with age of onset and—where available—age of death. We find that homozygosity for the minor allele of SNP rs11737023 is associated with an 8-year earlier median age of death in comparison with homozygosity for the minor allele of SNP rs11737023 is associated with an 8-year earlier median age of death (64.2 versus 67.5 years) and a 50% shorter disease duration (1.5 versus 3.1 years). Once again, however, no effect was observed in the female population (Table 2).

**Effect of Pgc-1α deficiency in transgenic mutant SOD1-mediated ALS**

To gain insight into the mechanisms underlying the PGC-1α effect in ALS, we turned to a well-characterized transgenic model of mice over-expressing the human ALS-associated SOD1(G93A) transgenic mice, an animal model of ALS, mRNA and protein levels of PGC-1α are reduced (11). Recently, studies in mouse models of familial ALS demonstrated that transgenic up-regulation of PGC-1α relieves symptoms and/or extends survival, raising the prospect that this pathway could be targeted therapeutically (12–14). Of note, PGC-1α also regulates a number of pathways protective in ALS, including antioxidant defense (8), and expression of the trophic factor VEGF-A (7). The effects of PGC-1α in human Huntington disease and transgenic models of familial ALS led us to hypothesize that PGC-1α modifies onset and survival in human sporadic ALS in a clinically relevant manner.

### Table 1. PPARGC1A rs11737023 and age of onset and age of death in the German ALS cohort

<table>
<thead>
<tr>
<th></th>
<th>G/G</th>
<th>G/A</th>
<th>A/A</th>
<th>P-valuea</th>
<th>P-valueb</th>
<th>P-valuerc</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Age of onset</td>
<td>56.0 (47.0–66.0)</td>
<td>59.5 (48.0–66.0)</td>
<td>47.5 (39.0–56.0)</td>
<td>0.0064</td>
<td>0.2104</td>
<td>0.0141</td>
</tr>
<tr>
<td>Age of death</td>
<td>64.0 (54.0–69.0)</td>
<td>64.5 (56.0–70.0)</td>
<td>41.0 (34.0–48.0)</td>
<td>0.0973</td>
<td>0.9701</td>
<td>0.0342</td>
</tr>
<tr>
<td>Females</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age of onset</td>
<td>59.0 (52.0–67.0)</td>
<td>58.5 (47.0–67.0)</td>
<td>59.5 (50.0–69.0)</td>
<td>0.9530</td>
<td>0.8778</td>
<td>0.8375</td>
</tr>
</tbody>
</table>

Data represent median (lower and upper quartile) in years; statistical significance was calculated using the Kruskal–Wallis test; *additive model, bdominant model, crecessive model; dnumbers in parentheses indicate number of cases where age of death was available.

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We then monitored these mice for motor symptoms, body weight and survival (22). We found no significant effect on survival in the gender-mixed SOD1(G93A) cohorts (data not shown). However, gender stratification revealed a borderline significant survival effect of Pgc-1α deficiency in the male cohort, whereas the PGC-1α genotype did not influence the disease phenotype in female mice (Fig. 1A and B). Similarly, Pgc-1α deficiency accelerated disease onset, as defined by the peak of the weight curve of each individual animal (23) in males, while females were unaffected (Fig. 1C and D). Onset of neurological symptoms did not prove to be useful in our system as the Pgc-1α −/− mice showed reduced motor activity independent of the SOD1(G93A) transgene status (data not shown). The recapitulation of the Pgc-1α-linked gender effect in our compound transgenic/knock-out mouse model provided the opportunity for mechanism-based studies.

We determined abundance levels of Ppargc1a transcripts initiated at the CNS-specific promoter and the reference gene (RG) promoter in spinal cords of all groups of male and female animals (Supplementary Material, Fig. S2). As expected from our previous studies in mouse brain (10), CNS-specific transcripts were several-fold higher than RG transcripts in the respective groups of male and female mice. No significant sex-specific differences of CNS- and RG-specific transcripts were noted between the respective groups. FL-Pgc-1α deficiency in the SOD1(G93A) mice was associated with the lowest levels of CNS- and RG-specific transcripts in both genders. Interestingly, FL-Pgc-1α deficiency in SOD1(G93A) mice reduced CNS-specific transcripts only in male animals. We also measured transcripts initiated from the alternative exon1 that is specific for the Pgc-1α2 and -α4 isoforms (24). However, the level of these transcripts was more than two orders of magnitudes lower in the spinal cord of male or female control animals than the level of CNS-specific transcripts and such transcripts were below the detection limit of our assay in most animals of the experimental groups (data not shown).

**Table 2.** Ppargc1a rs11737023 and age of onset, age of death and disease duration in the Swedish ALS cohort

<table>
<thead>
<tr>
<th></th>
<th>rs11737023</th>
<th></th>
<th></th>
<th></th>
<th>P-value&lt;sup&gt;a&lt;/sup&gt;</th>
<th>P-value&lt;sup&gt;b&lt;/sup&gt;</th>
<th>P-value&lt;sup&gt;c&lt;/sup&gt;</th>
</tr>
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<tr>
<td></td>
<td>G/G</td>
<td>G/A</td>
<td>A/A</td>
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<tr>
<td>Males</td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sup&gt;d&lt;/sup&gt;</td>
<td>168 (170)</td>
<td>86 (88)</td>
<td>10 (10)</td>
<td></td>
<td>0.7287</td>
<td>0.4427</td>
<td>1.0000</td>
</tr>
<tr>
<td>Age of onset</td>
<td>63.0 (53.3–70.5)</td>
<td>61.4 (53.2–68.3)</td>
<td>62.4 (59.4–64.0)</td>
<td></td>
<td>0.9883</td>
<td>0.8847</td>
<td>1.0000</td>
</tr>
<tr>
<td>Age of death</td>
<td>67.5 (57.8–74.1)</td>
<td>65.1 (57.1–71.2)</td>
<td>64.2 (62.0–65.5)</td>
<td></td>
<td>0.0056</td>
<td>0.0112</td>
<td>0.0099</td>
</tr>
<tr>
<td>Disease duration</td>
<td>3.1 (1.9–4.6)</td>
<td>2.4 (1.4–3.8)</td>
<td>1.5 (1.1–2.3)</td>
<td></td>
<td>0.0157</td>
<td>0.0100</td>
<td>0.0530</td>
</tr>
<tr>
<td>Females</td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sup&gt;d&lt;/sup&gt;</td>
<td>115 (115)</td>
<td>67 (67)</td>
<td>14 (14)</td>
<td></td>
<td>0.8920</td>
<td>0.6634</td>
<td>1.0000</td>
</tr>
<tr>
<td>Age of onset</td>
<td>66.4 (56.4–71.9)</td>
<td>66.0 (59.5–76.1)</td>
<td>65.3 (58.5–79.0)</td>
<td></td>
<td>0.9883</td>
<td>0.8847</td>
<td>1.0000</td>
</tr>
<tr>
<td>Age of death</td>
<td>68.9 (60.7–75.7)</td>
<td>68.6 (61.9–77.9)</td>
<td>67.6 (62.2–80.0)</td>
<td></td>
<td>0.0681</td>
<td>0.1240</td>
<td>0.2587</td>
</tr>
<tr>
<td>Disease duration</td>
<td>2.6 (1.7–3.7)</td>
<td>2.2 (1.6–3.4)</td>
<td>3.1 (2.1–4.6)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Data represent median (lower and upper quartile) in years; statistical significance was calculated using the Kruskal–Wallis test; <sup>a</sup> additive model, <sup>b</sup> dominant model, <sup>c</sup> recessive model; <sup>d</sup> numbers in parentheses indicate number of cases where age of death was available.

**DISCUSSION**

Here, we present the results of two independent lines of investigation that address the role of PGC-1α in ALS. First, we demonstrate an important disease-modifying role for the PGC-1α encoding gene in patients with ALS. Remarkably, in both European patient populations tested, the effect is strictly confined to men. Second, we show that FL-Pgc-1α deficiency has a similar male-specific, albeit weaker, disease-accelerating effect in the SOD1(G93A) transgenic mouse model of familial ALS. In neither the human nor the animal studies is the mechanism underlying this gender-specific effect immediately evident. However, reduced availability of the neurotrophic factor VEGF-A might be a contributing factor.
Importantly, our two genetic association studies provide the first evidence that PGC-1α, which has already been implicated in Huntington disease and Parkinson disease, also modifies human ALS. We found associations of the PGC-1α-genotype with age of onset in the German population, disease duration in the Swedish population and age of death in both populations. Somewhat unexpected is the finding that in both populations the PGC-1α effect is male specific. However, PGC-1α is known to enhance the transcriptional activities of major sex hormone receptors such as the androgen receptor (31) and the estrogen receptor (32) as well as ERRα (7). Thus a transcriptional effect is plausible since rs11737023 is located in intron 1 near the novel CNS-specific transcription start site. Bioinformatic analyses using a matrix dissimilarity rate of 0 (33) suggest that the three SNPs alter putative transcription factor-binding sites. The C/T substitution at rs2048025 creates a putative binding site (TAAAT) for the pituitary-specific transcription factor POU1F1A (T00691) involved in diverse cellular processes (34). The major A allele at rs17592631 is located in a consensus site (ACAACC/T) for ENGRAILED HOMEOBOX 1 (EN1, T02016) that has been shown to protect dopaminergic neurons from MPTP toxicity in mice (35). This site is altered by the minor T allele. Finally, the substitution of G by A at the discriminatory rs11737023 creates an E-box (CANNTG) that is potentially targeted by multiple basic-loop-helix transcription factors. Specifically, the variant allele sequence CATCTG has been shown to be targeted by NF-X3 (T01514) (36). While NF-X3 has been implicated in B-cell differentiation, putative NF-X3 sites have also been mapped to other genes including the dopamine D2 receptor gene (37).

rs11737023 (or a causative SNP in linkage disequilibrium with it) may alter the CNS-specific PGC-1α expression levels and influence the co-activation of these hormone receptors in a sex-specific manner. However, how such SNP(s) play a role in ALS pathogenesis remains to be investigated. Co-activation of ERRα at the VEGF-A promoter by the CNS-specific PGC-1α isoforms may be a potential mechanism. This signaling axis may contribute to the gender effect as we found Errα mRNA levels to be lower in male spinal cords compared with females of each phenotype. Furthermore, FL-Pgc-1 deficiency on the SOD1(G93)A background resulted in a significant reduction of CNS-specific Ppargc1a transcripts only in male animals. In this context, it is noteworthy that studies of X-linked spinal and bulbar muscular atrophy (SBMA), an adult-onset motor neuron disease, caused by the abnormal expansion of a polyglutamine tract in the androgen receptor, showed that repression of VEGF-A led to motor neuron degeneration in vitro and in vivo in males (38).

The role of PGC-1α in the gender differences of ALS, however, likely is complex and not limited to its effects on VEGF-A and ERRα. For instance, Leone et al. (18) described an age-dependent sex-specific obesity in their Pgc-1α hypomorphic mice at 24 weeks which could be protective against ALS (39).

Remarkably, the modifier effect of PGC-1α on ALS onset and survival was much more pronounced in humans than in mice.
This disconnect between human and mouse studies is similar to what has been reported for other modifiers of ALS, namely ephrin 4 (40), and further challenges the sensitivity of SOD1(G93A) transgenic mice as screening tools for ALS therapy research. Along the same lines, the gender effect on survival and disease onset in the SOD1 mouse model is variable and depends, among other factors, on the genetic background (3).

In contrast, the mouse studies do offer some mechanistic insight, as they suggest that a sex-dependent reduced availability of Vegf-A in the spinal cord is part of the pathogenic cascade. However, the functionality of such an isoform that is initiated at the CNS promoter needs to be determined.

Figure 2. FL-Pgc-1α ablation sex-dependently reduces Vegf-A mRNA levels in the spinal cord. (A) mRNA levels of Vegf-A in the spinal cord of wild-type (+/+ ) and SOD1(G93A) mice expressing FL-Pgc-1α or not (PGC-1α−/−). *P < 0.05 versus Wt, P < 0.05 as indicated. Note that Vegf-A mRNA levels are decreased in SOD1(G93A) mice and that this decrease is even further reduced in compound male SOD1(G93A)/PGC-1α−/− mice, but not in female SOD1(G93A)/PGC-1α−/−. (B) mRNA levels of Igf-1 in the spinal cord of wild-type (+/+ ) and SOD1(G93A) mice expressing FL-Pgc-1α or not (PGC-1α−/−). *P < 0.05 versus Wt; P < 0.05 as indicated. N = 9 mice per group. *wt versus SOD(G93A); #PGC-1α−/+ versus PGC-1α−/−. (C) mRNA levels of Bdnf in the spinal cord of wild-type (+/+ ) and SOD1(G93A) mice expressing FL-Pgc-1α or not (PGC-1α−/−). *P < 0.05 versus Wt, P < 0.05 as indicated. (D) mRNA levels of Ngf in the spinal cord of wild-type (+/+ ) and SOD1(G93A) mice expressing FL-Pgc-1α or not (PGC-1α−/−). *P < 0.05 versus Wt; P < 0.05 as indicated. For all panels: N = 9 mice per group. Statistics were done with one-way ANOVA followed by Newman–Keuls multiple comparison test where appropriate *P < 0.05, **P < 0.01 and ***P < 0.005. Columns (error bars) represent means (SEM).

Even though FL-PGC-1α, PGC-1α4 or NT-PCG-1α is not produced in the hypomorphic mouse model, NT-PCG-1α is present in these mice. Furthermore, the latter form, initiated at the CNS-specific promoter, is likely to be formed in the FL-Pgc-1α-deficient mouse model. The ability of NT-PCG-1α to interact and co-activate ERRα appeared to be somewhat lower in comparison to the ability of native NT-PGC-1α (42). However, the functionality of such an isoform that is initiated at the CNS promoter needs to be determined.

Notably, rs11737023 is part of a haplotype block with a significant disease modulatory effect in Huntington disease, like SBMA, a polyglutamine disease (10). This observation supports the concept that the pathomechanisms in ALS and Huntington disease are related and, therefore, are of importance for neurodegeneration in general. Nonetheless, it should be emphasized that there are also intriguing contrasts between the PGC-1α effects in the two diseases. Most importantly, the PGC-1α SNP effect tends to be protective in Huntington disease, whereas in ALS it is clearly deleterious. We conclude that while the PGC-1α signaling hub is important in the pathogenesis of both Huntington disease and ALS, its effects are likely mediated by distinct mechanisms that await further studies.
MATERIALS AND METHODS

Clinical resource

All patients were assessed by experienced clinicians and provided written informed consent. ALS diagnosis was made according to the El Escorial ALS diagnostic criteria (15). The patients were clinically diagnosed and followed at the ALS centers at the Ulm University Hospital and the Charité Hospital (German cohort) and throughout Scandinavia (Swedish cohort). The patients received optimal care according to state of knowledge at the time. For the German population, age of onset and age of death were available only by year, not by exact date. In the Swedish population, exact dates for age of onset (within 2 weeks) were available. To avoid confounders by imprecision, we calculated the disease duration only in the Swedish population.

DNA was isolated from whole blood. Extracted DNA was stored at −20 °C until analysis. For genotyping of rs11737023, rs2048025 and rs17592631, we used the TaqMan genotyping assays C_473389_10, C_1222369_10 and C-3280847_10.

Animal breeding and genotyping

Pgc-1α−/−; SOD1(G93A) mice were generated using a two-step breeding procedure. In a first step, B6.Cg-Tg(SOD(G93A)) males (stock# 004435, the Jackson laboratory) were bred to B6-Pgc-1α−/− females. In a second step, Pgc-1α+/−, SOD1(G93A) males were mated with Pgc-1α+/− female mice (18). Experiments were conducted in double mutant Pgc-1α−/−; SOD1(G93A) and Pgc-1α−/− mice; SOD1(G93A), and wild-type littermates served as controls. Offspring was separated from their mothers at the age of 21 days, followed by labeling and genotyping.

Animals and genotyping

For genotyping of SOD1(G93A) mice, a multiplex-PCR reaction was applied using the following primers. miL2 forward (CTAGGCCACAGAATTGAAAGATCT) and miL2 reverse (GTAGGTGGAATTCATAGCATCATC); hSOD forward (CATCAGCTTAATCCATCTGA) and hSOD reverse (CGC GACTAACCATTAAATG). Genotyping of Pgc-1α−/− mice was performed according to the protocol published by Leone et al. (18).

Acclimatization and housing conditions

At the age of 38 days, mice were moved to the experimental unit and randomly distributed to experimental and control groups. Gender was distributed equally across the groups, with n = 17–23 mice per group. Mice were kept single caged. There was automatic control of light cycle, temperature and humidity. Light hours were 6:00 a.m. – 6:00 p.m. Daily monitoring indicated that temperature and humidity remained within the target ranges of 20 °C ± 3 °C and 50 ± 10%. All experiments were conducted according to the protocol published by the Regional Steering Committee Tübingen, Reg. 1013.

Motor activity

To monitor activity levels of each animal individually, mice were caged separately with free access to a running wheel from 42 days on. Motor activity is recorded automatically during the nocturnal phase from 6:00 p.m. – 6:00 a.m. Motor activity is directly correlated with the rotations per minute generated by each animal on the running wheel. Each full turn of the wheel generates two electromagnetic signals, which are fed directly into an electronic device and saved on a computer. For this purpose, the software ‘Mausvital’ supplied by Laser und Medizin GmbH, Berlin, was used.

Body weight

Mice were weighed twice weekly starting at the age of 42 days using a digital scale and their weights recorded.

Survival

Pgc-1α−/−; SOD(G93A) and SOD(G93A) mice were sacrificed at the time when they reached the final stage of the disease. As mandated by the Animal Ethics Committee of the Regional Steering Committee Tübingen, the final disease stage is defined as the inability to rise immediately after being placed on the side.

RT-qPCR

Total RNA was extracted using RNeasy Mini Kit (Qiagen) in accordance with the manufacturer’s instructions. Real-time RT quantitative PCR was performed with one microgram of total RNA as described (43). PCR analysis was performed on a Bio-Rad iCycler System using iQSYBR Green Supermix. A specific standard curve was performed in parallel for each gene to assess the specificity of the products, for quantification of the respective transcripts in duplicate. PCR conditions were 3 min at 94 °C, followed by 40 cycles of 45 s at 94 °C and 10 s at 60 °C. The relative levels of each RNA were normalized to two housekeeping genes (polymerase II and TBP). CNS- and RG-specific Ppargc1a transcripts were quantified using primers targeting CNS-specific exons B1 and B4 (10) and exons 1 and 2, respectively, as described (44). Oligonucleotide sequences are reported in Supplementary Material, Table S1.

Statistics

For the clinical data, allele frequencies were estimated by gene counting. Genotypes associated with the three SNPs typed fulfilled Hardy–Weinberg expectations, as ascertained using a χ² goodness-of-fit test. Effects of genotypes on age of onset and age of death, and disease duration were ascertained by the Kruskal–Wallis test rather than ANOVA, inasmuch as the distributions of the respective ages or log-transformed ages significantly deviated from a normal distribution.

For the experimental data, all statistical analysis was done using Prism, version 4.0 (GraphPad Software). For comparison of groups, ANOVA was used. Differences between means
were determined by post hoc comparisons using the Tukey honest significance test and were considered statistically significant if \( P < 0.05 \). Survival analysis was performed using the Gehan–Breslow–Wilcoxon test.

SUPPLEMENTARY MATERIAL
Supplementary Material is available at HMG online.

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Conflict of Interest statement. None declared.

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REFERENCES


