Huntington’s disease (HD) is an inherited neurodegenerative disorder characterized by both neurological and systemic abnormalities. We examined the peripheral immune system and found widespread evidence of innate immune activation detectable in plasma throughout the course of HD. Interleukin 6 levels were increased in HD gene carriers with a mean of 16 years before the predicted onset of clinical symptoms. To our knowledge, this is the earliest plasma abnormality identified in HD. Monocytes from HD subjects expressed mutant huntingtin and were pathologically hyperactive in response to stimulation, suggesting that the mutant protein triggers a cell-autonomous immune activation. A similar pattern was seen in macrophages and microglia from HD mouse models, and the cerebrospinal fluid and striatum of HD patients exhibited abnormal immune activation, suggesting that immune dysfunction plays a role in brain pathology. Collectively, our data suggest parallel central nervous system and peripheral pathogenic pathways of immune activation in HD.
the immune system, or both, is activated in HD, and the alterations in each immunomodulatory cytokine at each disease stage are unknown. The cause of the immune activation peripherally is also unknown. IL-6, which triggers the acute phase response, is produced primarily by monocytes and lymphocytes, but this could be due to dysfunction of these cells caused by expression of mutant huntingtin (i.e., a cell-autonomous effect) or in response to inflammation-triggering events outside these cells, such as huntingtin-induced tissue damage or the mutant protein itself being interpreted as an antigen (i.e., non–cell-autonomous pathways). Of interest in this respect is the finding that the IkB kinase/NF-kB signaling pathway that triggers IL-6 release is up-regulated by mutant huntingtin, and this may contribute to neurotoxicity (7).

Critically, the relationship between peripheral inflammation and CNS pathology in HD is unknown. Certain inflammatory proteins, such as complement proteins and clusterin, are also up-regulated both peripherally and in the brain in HD (6, 8, 9). In vivo imaging, in vitro and postmortem studies have shown that microglia, the CNS counterpart of macrophages, are activated in premanifest (10) and manifest HD (11), that microglial activation correlates with disease severity (12), and that mutant huntingtin is expressed in microglia (13). Thus, inflammation is an established, though incompletely understood, feature of HD with likely pathogenic importance. Inflammatory changes in the CNS and peripheral tissues in HD may be due to independent effects of mutant huntingtin in both compartments, causing analogous derangements centrally and peripherally; or inflammatory activation may begin peripherally and spread to the CNS, or vice versa, through the passage of immunomodulatory molecules across the blood–brain barrier.

Insights into CNS and peripheral immune system interactions in HD may provide new biomarkers and improve knowledge of key pathogenic mechanisms, possibly leading to novel therapeutic approaches. The present work seeks to elucidate further the nature of the peripheral inflammatory activation in HD through quantification of levels of key inflammatory and immunomodulatory molecules in human plasma, and serum from three different mouse models of HD. To investigate possible links between peripheral inflammation and neuronal dysfunction, we examined correlations between individual inflammatory molecules and clinical features of HD. We used targeted transcription profiling to examine expression of key immunomodulatory proteins in the HD striatum to determine whether the inflammatory activation seen peripherally is mirrored in the CNS. We examined expression of huntingtin in its WT and mutant forms in human monocytes to investigate the possibility that the immune activation is due to a disease-related cell-autonomous dysfunction of these cells. We confirmed this with functional studies of human monocytes, and macrophages and microglia from HD mouse models, demonstrating that there is disease-related dysfunction of CNS and peripheral inflammatory cells in HD.

RESULTS

We collected 194 plasma samples from HD mutation carriers ranging from premanifest to moderate HD and from control subjects (Table S1, available at http://www.jem.org/cgi/content/full/jem.20080178/DC1) and quantified levels of key inflammatory and immunomodulatory molecules using multiplex sandwich ELISAs and single radial immunodiffusion assays. We found an altered profile of cytokine levels in HD patients (Fig. 1). The most striking increases across subject groups from controls to progressing disease were in IL-6 and IL-8 (P < 0.0001 in each case). In addition, IL-4, IL-10, and TNF-α levels increased significantly with disease progression (Fig. 1 B). Moreover, IL-6 levels were significantly increased in premanifest subjects with an estimated mean of 16 yr until motor onset (Fig. 1 A) (14). Interestingly, the cytokines that were increased earliest in the disease course (IL-6 and IL-8) are involved in the innate immune response (15). IL-10 and IL-4, antiinflammatory cytokines involved in the adaptive immune response, increased significantly in moderate stage disease. There was no difference in levels of Igs (IgG, IgA, or IgM) at any disease stage in this respect is the finding that the IkB kinase/NF-kB signaling pathway that triggers IL-6 release is up-regulated by mutant huntingtin, and this may contribute to neurotoxicity (7).

Figure 1. Altered immune profile peripherally in HD. (A) Multiplex ELISA quantification of cytokine levels in plasma from HD patients (premanifest, early and moderate HD stages) compared with control subjects. Graphs show mean concentrations with standard error bars. Significant differences between individual groups are shown [ANOVA with post-hoc Tukey HSD test]. (B) The overall trend for increasing levels of cytokines across all groups, analyzed using linear regression, was highly significant for IL-6 and IL-8 and significant for IL-4, IL-10, TNF-α, and IL-5. R-values (partial correlation coefficients) are corrected for age and sex. *, P < 0.05; **, P < 0.01; ***, P < 0.001; ****, P < 0.0001.
stage (Fig. 2), arguing against widespread activation of the adaptive humoral immune system.

We then examined correlations between these cytokine changes and clinical characteristics. Plasma IL-8 levels increased markedly with disease progression (Fig. 1) and correlated with clinical measures of HD. Levels of IL-8 correlated positively with worsening disease, as demonstrated by unified HD rating scale (UHDRS) (16) chorea scores ($R = -0.37; P < 0.01$) and total motor scores ($R = 0.27; P < 0.05$), as well as negatively with total functional capacity (TFC) scores where lower scores indicate more severe disease ($R = -0.28; P < 0.05$) (Fig. 3 A). TNF-α levels in plasma correlated with UHDRS chorea scores ($R = 0.28; P < 0.01$) and UHDRS motor scores ($R = 0.26; P < 0.05$) (Fig. 3 B); a negative correlation with TFC was seen that approached statistical significance ($R = -0.20; P = 0.07$).

Objective markers of HD progression are needed to facilitate the conduct of clinical trials of disease-modifying therapies in HD (17). We used stepwise logistic regression analysis to construct receiver operating characteristic (ROC) curves that demonstrated a strong ability of combinations of plasma cytokine levels to discriminate between disease groups (Fig. 4). We found that a combination of IL-6, IL-10, and IL-5 best discriminated between premanifest HD and controls with an area under the curve (AUC) of 0.81. A combination of IL-6, IL-8, and IL-10 best discriminated all HD expansion carriers (premanifest and manifest) from controls (AUC 0.82). IL-6, IL-8, and IL-10 together best discriminated between premanifest and manifest HD patients (AUC 0.85).

IL-6 triggers the acute phase response and is produced primarily by monocytes/macrophages and lymphocytes (15). To define the possible source of peripheral cytokines, we purified monocytes from whole blood from HD patients and control subjects by flow cytometric and magnetic sorting. Using RT–quantitative PCR (QPCR), we found monocytes from HD patients to express mutant huntingtin (Fig. 5, A and B).

We then stimulated isolated monocytes with LPS and found that monocytes from premanifest HD mutation carriers behave abnormally, displaying excess IL-6 production compared with cells from control subjects (Fig. 6 A). Mutant huntingtin thus appears to produce functional overactivity of monocytes. We stimulated isolated macrophages from the yeast artificial chromosome (YAC)128 mouse model of HD with LPS. Echoing the results seen in human HD monocytes, macrophages from the YAC128 responded with enhanced...
secretion of IL-6 in response to stimulation compared with macrophages from WT mice (Fig. 6 B). To test whether the presence of mutant huntingtin per se is sufficient to produce dysfunction, we then examined the response to LPS stimulation in macrophages from the YAC18 mouse, which differs from the YAC128 only in the length of the polyglutamine stretch. Excessive IL-6 release was not seen in YAC18 cells (Fig. 6 C). To determine whether microglia, the CNS equivalent of monocytes/macrophages, are also dysfunctional in HD, we performed LPS stimulation of microglia isolated from the widely used R6/2 transgenic mouse model of HD (18). HD microglia, too, demonstrated hyperactivity in response to stimulation (Fig. 6 D).

We investigated expression of inflammatory transcripts in postmortem human striatal tissue using RT-PCR and found markedly increased expression of IL-6, IL-8, and TNF-α in HD (Fig. 7), mirroring the key changes seen in plasma much earlier in the disease.

To investigate the relationship between central and peripheral inflammatory processes, we measured IL-6 and IL-8 in matched plasma and cerebrospinal fluid (CSF) samples from HD patients and controls using ELISA. CSF and plasma levels of IL-6 and IL-8 correlated closely (Fig. 8; R = 0.74 and R = 0.66, respectively; P < 0.0001 for both).

We used multiplex ELISA to determine whether peripheral immune activation is present in serum in HD mouse models and found increased levels of several cytokines in the R6/2 transgenic mouse and the full-length knock-in model of HD (HdhQ150/Q150) (19). In 12-wk R6/2 mice, IL-6, IL-10, IL-1β, and IL-12p70 were significantly increased (Fig. 9 A). In 22-mo knock-in HdhQ150/Q150 mice, IL-6, IL-10, and IL-12p70 were significantly elevated (Fig. 9 B). In the YAC128 mouse model of HD at 12 mo of age, we saw similar elevations in serum IL-6 and mKC, a mouse functional homologue of IL-8 (20) (Fig. 9 C). 12-mo YAC128 animals are phenotypically equivalent to early HD (21), and these animals therefore model the human patients whose plasma was studied.

**DISCUSSION**

Collectively, our data show that immune activation in HD is widespread and detectable in peripheral plasma across disease stages. Key cytokines of the innate immune system are upregulated both centrally and peripherally, and robust changes
even take place in premanifest HD mutation carriers many years before the onset of motor abnormalities. To our knowledge, the elevated IL-6 level seen in premanifest subjects with a mean of 16 yr until predicted clinical onset represents the earliest plasma abnormality identified to date in HD. The peripheral changes correlate well with clinical variables and are accompanied by alterations in striatal gene expression.

Although cytokines such as IL-4 and IL-10 are increased later in the disease, normal Ig levels throughout the disease course suggest that there is no generalized activation of the adaptive immune response. Whereas IL-6 and IL-8 production are triggered by NF-κB activation (7, 22), IL-4 and IL-10 act to down-regulate NF-κB (15). The late involvement of these cytokines may reflect an adaptive response to chronic immune activation, possibly involving altered interactions between monocytes/macrophages and Th2 cells.

The correlation we show between plasma and CSF levels of IL-6 and IL-8 links the central and peripheral immune activation in HD. We show that IL-6 and IL-8 are increased in plasma and the striatum. These cytokines are not thought to cross the healthy blood–brain barrier in the acute setting (23, 24), and studies of brain penetration of specific molecules in HD have not identified alterations of the blood–brain barrier (e.g., reference 25). Mutant huntingtin therefore probably induces parallel dysfunction in both compartments (Fig. 10). The immune dysfunction we demonstrate in monocytes from premanifest HD gene carriers may reflect similar central changes in HD microglia and therefore act as a window onto central disease pathogenesis at this very early stage in the disease process. Given the dramatic changes seen in striatal cytokine expression and the chronic nature of these changes, passage of cytokines from the CNS into blood is a possibility we cannot exclude, although cytokines are rapidly broken down (26) and would likely be subject to considerable dilution in plasma. However, the presence of primary abnormalities of both peripheral and central cytokine-producing...
ever, it is possible that HD also causes differences in the level of background immune stimulation, which could contribute to the later up-regulation of the adaptive immune response cytokines IL-4 and IL-10.

There is a need for markers of progression ("state biomarkers") in HD and other neurodegenerative diseases (29). Our results suggest that inflammatory changes detected in peripheral plasma may be biologically relevant and mirror the neurodegenerative process occurring in the CNS (Fig. 10). Indeed, combined peripheral markers of inflammation were recently suggested to be biomarkers for diagnosis and progression in Alzheimer’s disease (29). Remarkably, peripheral inflammatory changes may also reveal early pathogenic events in HD, occurring more than 15 yr before the onset of neurological manifestations. The inflammatory changes seen in patients are echoed in mouse models of HD. Importantly, they may therefore provide translational biomarkers for the use of HD mouse models in the development of therapeutic interventions. Finally, the mechanism of early innate immune activation in HD warrants further study as a potential source of targets for disease-modifying therapies.

MATERIALS AND METHODS

Ethical approval. All human experiments were performed in accordance with the declaration of Helsinki and approved by University of British Columbia (UBC) Clinical Research Ethics Board (Canadian patients) or University College London (UCL)/UCL Hospitals Joint Research Ethics Committee (UK patients), as appropriate. All subjects gave informed written consent. All animal experiments were performed in accordance with relevant legislation and approved by local and national regulatory authorities (Institutional Review Board of the University of Washington, King’s College London Animal Care and Use Committee, or UBC Committee on Animal Care and the Canadian Council on Animal Care, as appropriate).

Collection and processing of human plasma samples. Blood samples were obtained from control subjects and genetically diagnosed HD patients.
and processed as described previously (6). Subjects with inflammatory or infectious conditions were excluded. A subset of subjects was assessed on the LHDRS (16) by a neuropsychologist experienced in assessment of HD patients. Subjects’ demographic and clinical data are given in Table S1.

Collection of matched CSF and blood samples. CSF donors were recruited through the UBC HD Medical Clinic. 20 HD patients and 10 control subjects, age-matched and lacking the HD mutation, were recruited (Table S1). Mutation-positive subjects were staged early or moderate according to independence score. CSF and matched blood samples were obtained within 1 h and plasma was extracted as described previously (6).

Collection of mouse serum samples. For the present experiments, HdhQ120/Q120 knock-in and R6/2 exon 1 models that develop comparable and widespread molecular phenotypes (19) were used. R6/2 (18) and HdhQ120/Q120 mice (original nomenclature, CHL2) (30) were bred and serum samples were collected as described previously (19). All animals had unlimited access to water and breeding chow (Special Diet Services) under a 12-h light–12-h dark cycle. YAC128 mice were maintained on the FVB/N strain background (21). Numbers and ages of animals are shown in Table S4 (available at http://www.jem.org/cgi/content/full/jem.20080178/DC1).

Sequencing. RNA was prepared from pellets of 5 × 10⁶ cells using an RNeasy mini kit (Qiagen) according to the manufacturer’s instructions. Quality and quantity of RNA was assessed using the RNA nanochip method on a Bioanalyzer (Agilent Technologies). RT of 1 μg of total RNA was performed in 50 mM KCl, 10 mM Tris–HCl, pH 9.0, 0.1% Triton X-100, 6.5 mM MgCl₂, 10 mM DTT, 1 mM dNTPs, 10 ng/μl random hexamers with 0.35 μg/μl H11002 and H9004. Protocol was done at 45 °C for 5 min in 9 μl of Hi-D6 formamide. The run conditions were as follows: capillary size, 36 cm, Polymer–Pop-P-7. The run module was oven temperature, 66°C; buffer temperature, 35°C; prerun voltage, 15 kV; prerun time, 180 s; injection voltage, 3 kV; injection time, 20 s; first readout time, 200 msec; second readout time, 200 msec; run voltage, 10 kV; voltage number of steps, 10; voltage step interval, 20 s; voltage tolerance, 0.6 kV; current stability, 10 μA; ramp delay, 1 s; data delay, 120 s; run time, 2,700 s. Data analysis was performed using the plate manager application GeneMapper v5.2–3730XL.

Functional study of human monocytes. Whole blood was collected in heparin (CP Pharmaceuticals). Leukocytes were isolated by density gradient centrifugation over Histopaque 1077 solution (Sigma-Aldrich). Monocytes were obtained by magnetic sorting to increase yield and minimize handling time. Mononuclear cell suspensions were labeled with anti-CD14 microbeads and sorted through magnetic cell separation columns (Miltenyi Biotec) to at least 95% purity (Fig. S1 B). Monocytes were counted, and 5 × 10⁵ cells per well seeded into 24-well culture plates in RPMI culture medium supplemented with 5% FBS, 2 mM l-glutamine, and 1% penicillin/streptomycin (Invitrogen). Cells were incubated for 16 h before stimulation. The medium was then changed to fresh cell culture medium with or without 10 ng/ml IFN-γ (R&D Systems). For LPS stimulation, 2 μg/ml LPS was added to the medium (Sigma-Aldrich). After 24 h, supernatants were harvested from separate wells for each subject/condition. The cells remaining were lysed in 50 mM Tris, pH 8, 150 mmol NaCl, 0.5% sodium deoxycholate, and 0.5% Triton X-100 and assayed for total protein concentration using a protein assay kit according to the manufacturer’s instructions (Bio-Rad Laboratories). IL-6 concentrations in supernatants were determined using the MSD assay and adjusted for total protein concentration.

Functional study of tissue macrophages. Alveolar macrophages were isolated from 12-mo-old WT, YAC18, and YAC128 mice, all maintained on a pure FVB/N strain background. The YAC128 (line 53) mouse line expresses high levels of full-length human huntingtin with ~128 polyglutamine repeats and is a well-established model of HD. These mice develop an age-dependent phenotype similar to that seen in HD patients, including cognitive deficits, motor dysfunction, and selective neurodegeneration; 12-mo mice are equivalent to early human HD (21). YAC18 mice (line 212) express transgenic human WT huntingtin and do not exhibit any disease phenotype relative to their WT littermates. They differ from YAC128 mice only in the length of the polyglutamine tract.

Animals were killed using 10 mg avertine via i.p. injection. Blood was drawn from the inferior vena cava, and serum samples were obtained by two-stage centrifugation. Alveolar macrophages were extracted by intratracheal infusion of ice-cold PBS (Invitrogen) followed by centrifugation and resuspension of extracted cells. Cells were counted and seeded at 1.5 × 10⁵ cells/ml onto 96-well gelatin-coated plates and incubated in culture media containing 5% medium (RPMI 1640 [Invitrogen], 5% FBS [Cansera], and 1% penicillin/streptomycin [Invitrogen]). After 24 h this was changed to 1% medium (RPMI 1640, 1% FBS, and 1% penicillin/streptomycin). Functional studies were performed after an additional 24 h. The medium was changed to fresh 1% medium or 1% medium containing 10 μg/ml IFN-γ (R&D Systems) with or without 100 μg/L control standard endotoxin (Associates of Cape Cod). After 24 h, IL-6 concentrations were measured in supernatants from two independent wells from each animal for each condition, using a commercial mouse IL-6 ELISA kit according to the manufacturer’s instructions (Bioscience). Numbers of animals used in each experiment are given in Table S4.

Functional study of microglia. Mixed primary glial cultures were prepared from single brains of R6/2 mice (B6CBA-Tg(HDexon1)12Gtb/J; Jackson ImmunoResearch Laboratories) as described previously (32). In
brief, 4-d-old mice were decapitated. The brains were removed and submerged in ice-cold Hank’s saline. The meninges and blood vessels were removed before the tissue was trypsinized, carefully dissociated with a 5-ml pipette, resuspended, and filtered twice (100-μm diameter Falcon filter; Becton Dickinson) before seeding the cells in 5 ml of medium per flask (one brain/flask). Cells were cultured in poly-ornithine–coated 25-cm² flasks in DME and supplemented with 10% FBS (D10F).

Littermate heterozygote R6/2 and WT mice were used. Each brain was processed and cultured individually to prevent cross-contamination between animals. Genotype and CAG repeat length were determined by PCR from tail samples taken at the time of CNS culture preparation (Laragen). Once astrocytes reached confluence (5–7 d), D10F medium was supplemented with 2 ng/ml GM-CSF. Microglial cells were collected, pooled according to genotype, and seeded in 96-well Primaria plates (2.5 × 10⁶ cells in 250 μl D10F per well; Becton Dickinson). Cultures were >95% pure as assessed by CD11b immunostaining. For each experiment, WT and R6/2 microglial cells were processed in parallel.

24 h after plating, the cells were serum starved (MEM, 0.2 ng/ml GM-CSF) for an additional 24 h. They were then stimulated with 10 U IFN-γ ± 10 ng/ml LPS or carrier control. After 24 h of stimulation, supernatant was collected and stored at −80°C for further analysis.

IL-6 concentration was measured by Luminox bead array system (QIAGEN). 60 μl of supernatant of three representative experiments (n = 4 for each condition) was thawed and processed using the BioPlex platform (Bio-Rad Laboratories).

Striatal gene expression study. Total RNA was isolated and purified from striatal samples obtained from The New Zealand Neurological Foundation Human Brain Bank and the New York Brain Bank at Columbia University (6 controls and 17 patients with pathological grades as shown in Table S3, which is available at http://www.jem.org/cgi/content/full/jem.20080178/DC1) with the RNeasy mini kit (QIAGEN). mRNA was transcribed into cDNA with SuperScript III (Invitrogen). RT-QPCR was performed in triplicate with target-specific Roche Universal Library probes (FAM) and Roche universal master mix (Roche Diagnostics), and analyzed with the Roche LightCycler software. Primers were designed into the mouse genome using Primer3 software, and the reaction was run in a 20-μl reaction volume on the C1000 Touch Thermal Cycler (Bio-Rad). The C(t) threshold cycle value (CT) method (33) was used to calculate the fold change in gene expression using the formula of Langbehn et al. (14).

Calculations of estimated time to onset in premanifest subjects were made using the age- and CAG-dependent conditional onset probability formula of Langbehn et al. (14). Correlations with clinical variables were examined using linear regression analysis and partial correlations. Because the distribution of UHDRS test scores was not Gaussian, bootstrapping with 1,000 replications was used to enable linear regression analysis and the use of age as a covariate. This analysis inevitably involved the use of multiple statistical tests, but because the associations under investigation were of independent scientific interest, p-values were not corrected for multiple comparisons (34).

To examine the ability of combinations of plasma cytokines to distinguish between different subject groups, stepwise logistic regression was used (35). The model tested the six cytokines with statistically significant correlations across disease stage in order of diminishing R-value (IL-6, IL-8, IL-4, IL-10, TNF-α, and IL-5; see Fig. 1B); variables were removed from the model when P < 0.05 for the logistic regression. The comparisons assessed were as follows: controls versus premanifest HD; controls versus all HD expansion–positive subjects; and premanifest versus manifest HD.

Unpaired two-tailed t tests were used to identify significantly different serum levels for each cytokine in mouse serum and to compare mRNA levels (expressed as 2ΔΔct) between controls and HD patients in the two gene expression studies. Unpaired one-tailed t tests were used to test the hypothesis that monocytes, macrophages, and microglia produce more IL-6 than WT animals when stimulated with LPS.

Online supplemental material. Fig. S1 shows representative flow cytometry plots demonstrating purity of cells obtained by flow cytometry and magnetic sorting. Table S1 shows the characteristics of subjects in each human biofluid study. Table S2 shows plasma cytokine levels by disease stage measured by multiplex ELISA assay. Table S3 shows characteristics of subjects in the postmortem striatal expression study. Table S4 shows details of animals used for mouse experiments. Table S5 shows details of the subjects whose blood was used for the monocyte huntingtin expression study. Table S6 shows the primers used for the human monocyte expression study. The online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20080178/DC1.

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