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HAINARD, Alexandre, et al.

Abstract

BACKGROUND: Human African trypanosomiasis (HAT), also known as sleeping sickness, is a parasitic tropical disease. It progresses from the first, haemolymphatic stage to a neurological second stage due to invasion of parasites into the central nervous system (CNS). As treatment depends on the stage of disease, there is a critical need for tools that efficiently discriminate the two stages of HAT. We hypothesized that markers of brain damage discovered by proteomic strategies and inflammation-related proteins could individually or in combination indicate the CNS invasion by the parasite. METHODS: Cerebrospinal fluid (CSF) originated from parasitologically confirmed Trypanosoma brucei gambiense patients. Patients were staged on the basis of CSF white blood cell (WBC) count and presence of parasites in CSF. One hundred samples were analysed: 21 from stage 1 (no trypanosomes in CSF and ≤ 5 WBC/microL) and 79 from stage 2 (trypanosomes in CSF and/or >5 WBC/microL) patients. The concentration of H-FABP, GSTP-1 and S100beta in CSF was measured by ELISA. The levels of thirteen inflammation-related proteins (IL-1ra, IL-1beta, [..]
A Combined CXCL10, CXCL8 and H-FABP Panel for the Staging of Human African Trypanosomiasis Patients

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Abstract

Background: Human African trypanosomiasis (HAT), also known as sleeping sickness, is a parasitic tropical disease. It progresses from the first, haemolymphatic stage to a neurological second stage due to invasion of parasites into the central nervous system (CNS). As treatment depends on the stage of disease, there is a critical need for tools that efficiently discriminate the two stages of HAT. We hypothesized that markers of brain damage discovered by proteomic strategies and inflammation-related proteins could individually or in combination indicate the CNS invasion by the parasite.

Methods: Cerebrospinal fluid (CSF) originated from parasitologically confirmed Trypanosoma brucei gambiense patients. Patients were staged on the basis of CSF white blood cell (WBC) count and presence of parasites in CSF. One hundred samples were analysed: 21 from stage 1 (no trypanosomes in CSF and ≤5 WBC/μL) and 79 from stage 2 (trypanosomes in CSF and/or >5 WBC/μL) patients. The concentration of H-FABP, GSTP-1 and S100β in CSF was measured by ELISA. The levels of thirteen inflammation-related proteins (IL-1ra, IL-1β, IL-6, IL-9, IL-10, G-CSF, VEGF, IFN-γ, TNF-α, CCL2, CCL4, CXCL8 and CXCL10) were determined by bead suspension arrays.

Results: CXCL10 most accurately distinguished stage 1 and stage 2 patients, with a sensitivity of 84% and specificity of 100%. Rule Induction Like (RIL) analysis defined a panel characterized by CXCL10, CXCL8 and H-FABP that improved the detection of stage 2 patients to 97% sensitivity and 100% specificity.

Conclusion: This study highlights the value of CXCL10 as a single biomarker for staging T. b. gambiense-infected HAT patients. Further combination of CXCL10 with H-FABP and CXCL8 results in a panel that efficiently rules in stage 2 HAT patients. As these molecules could potentially be markers of other CNS infections and disorders, these results should be validated in a larger multi-centric cohort including other inflammatory diseases such as cerebral malaria and active tuberculosis.

Introduction

Human African trypanosomiasis (HAT), also called sleeping sickness, is a parasitic disease that occurs in sub-Saharan Africa. More than sixty million people are at risk of being infected. The World Health Organization (WHO) has reported impressive progress since 1995 in the control of HAT, leading to a substantial reduction of new cases detected yearly to 10’800 in 2007. The total number of cases is now estimated to be between 50’000 and 70’000 per year [1].

The parasite that causes HAT belongs to the Trypanosoma brucei family with two subspecies, Trypanosoma brucei gambiense and Trypanosoma brucei rhodesiense, responsible for the human disease. Trypanosomes are transmitted to humans by the bite of a tsetse fly and are initially confined to the blood, lymph nodes and peripheral tissues. This corresponds to the first stage (early stage; or haemolymphatic stage) of the disease. After an unknown period that varies from weeks to months, the parasites invade the central nervous system (CNS). This is called the second stage (late stage; or neurologic; or meningo-encephalitic stage) of HAT.

Clinical symptoms of HAT are not specific for the disease, and definite diagnosis is always based on parasitological examination of body fluids. The card agglutination test for trypanosomiasis (CATT), an assay that is based on trypanosome-specific antibody detection, is widely used for mass screening. However, it suffers from limited sensitivity and restricted to the T. b. gambiense form of...
Author Summary

The actual serological and parasitological tests used for the diagnosis of human African trypanosomiasis (HAT), also known as sleeping sickness, are not sensitive and specific enough. The card agglutination test for trypanosomiasis (CATT) assay, widely used for the diagnosis, is restricted to the gambiense form of the disease, and parasitological detection in the blood and cerebrospinal fluid (CSF) is often very difficult. Another very important problem is the difficulty of staging the disease, a crucial step in the decision of the treatment to be given. While eflornithine is difficult to administer, melarsoprol is highly toxic with incidences of reactive encephalopathy as high as 20%. Staging, which could be diagnosed as early (stage 1) or late (stage 2), relies on the examination of CSF for the presence of parasite and/or white blood cell (WBC) counting. However, the parasite is rarely found in CSF and WBC count is not standardised (cutoff set between 5 and 20 WBC per μL). In the present study, we hypothesized that an early detection of stage 2 patients with one or several proteins in association with clinical evaluation and WBC count would improve staging accuracy and allow more appropriate therapeutic interventions.

Proteomic analysis of human body fluids has become an important approach for biomarkers discovery [20]. In this context, we recently explored the concept of post-mortem CSF as a model of massive and global brain insult [21], which allowed the identification of potential brain damage biomarkers by proteomics strategies. Indeed, heart-fatty acid binding protein (H-FABP), identified from post-mortem CSF, has been validated as a marker of stroke [22] and Creutzfeldt-Jakob disease [23], respectively. Similarly, GSTP-1 was also found over-expressed in post-mortem CSF [24] compared to ante-mortem, and was recently validated as an early diagnostic marker of stroke and traumatic brain injury (Turck et al. Personal communication). Additionally, S100β protein has already been demonstrated to be a marker of blood-brain barrier (BBB) and neuronal damage [25] as well as a useful serum biomarker of CNS injury and a potential tool for predicting clinical outcome after brain damage [26].

In this context, we hypothesized that markers of brain damage discovered by proteomic strategies as well as inflammation-related proteins could individually or in combination indicate the CNS invasion by the trypanosome parasite. We measured the CSF concentrations of H-FABP, GSTP-1, S100β and thirteen inflammation-related proteins (IL-1α, IL-1β, IL-6, IL-9, IL-10, G-CSF, VEGF, IFN-γ, TNF-α, CCL2, CCL4, CXCL12 and CXCL10) and evaluated their potential for staging the disease.

Material and Methods

Samples

Samples originated from a prospective observational study on shortening of post treatment follow-up in gambiense human African trypanosomiasis (THARSAT), conducted between 2005 and 2008 at Dipumba hospital in Mbuji-Mayi (Kasai Oriental province, Democratic Republic of the Congo). Details of the THARSAT study design and results are reported elsewhere (D. Mumba Ngoyi, in preparation). The study protocol was approved by the Ministry of Health, Kinshasa, DRC and by the Ethical Committee of the University of Antwerp, Belgium. Briefly, 360 T. b. gambiense patients in total were enrolled into the THARSAT study. Inclusion criteria were 1° confirmed presence of trypanosomes in lymph nodes, blood or CSF; 2°≥12 years old and; 3° living within a perimeter of 100 km around Mbuji-Mayi. Exclusion criteria were 1° pregnancy; 2° no guarantee for follow-up; 3° moribund; 4° haemorrhagic CSF before treatment and; 5° presence of another serious illness (active tuberculosis - treated or not, bacterial or cryptococcal meningitis). HIV and malaria were not considered as exclusion criteria. Each patient underwent a clinical examination. Staging of disease was based on CSF examination. WBC count was performed in disposable cell counting chambers (Uriglass, Menarini) and was performed in duplicate when the first count was <20 cells/μL. Trypanosomes were searched for in CSF by direct examination prior or during the cell counting procedure, followed by the modified single centrifugation method [27]. Second stage patients were defined as having >5 WBC/μL and/or trypanosomes in the CSF. First stage patients were defined as having 0–5 WBC/μL and no trypanosomes in the CSF. Patients having >5 and ≤20 WBC/μL and no trypanosomes in CSF were defined and treated as stage 2 patients, but highlighted as being in the potential intermediate stage. Patients or their responsible were informed about the study objectives and modalities and were asked to provide written consent. Treatment was provided according to the guidelines of the national control program for HAT (PNLTHA).

CSF samples were centrifuged immediately after collection. The supernatant remaining after the diagnostic procedure was
S100β, H-FABP and GSTP-1 measurements

The concentration of S100β was measured using a commercially available sandwich ELISA assay kit (Abnova, Taiwan) following the manufacturer’s instructions. Briefly, calibrators, Quality control (QC) and CSF samples diluted 1:4 were incubated 2 hours on microwell strips pre-coated with polyclonal anti-cow S100β antibodies. After 3 washes, horseradish peroxidase (HRP) labelled anti-human S100β antibodies were added, incubated for 90 minutes and washed again before addition of the substrate solution (tetramethylbenzidine). Color development was stopped with sulphuric acid and absorbance was read on a Vmax Kinetic microplate reader, (Molecular Devices Corporation, Sunnyvale, CA, U.S.A.) at a wavelength of 450 nm.

H-FABP concentration was also determined using a commercially available ELISA kit (Hycult Biotechnology, Uden, Netherlands) according to the manufacturer’s instructions. CSF samples (non-diluted) and standards were incubated (1 hour) together with peroxidase conjugated secondary antibodies in microwell strips coated with antibodies recognizing human H-FABP. After 3 washes, tetramethylbenzidine was added and color development was stopped by adding citric acid.

The concentration of GSTP-1 was determined using a homemade ELISA as described by Allard et al. [28]. Briefly, biotinylated anti-GSTP-1 antibodies (2 µg/mL) (Biosite, California, USA) were coated onto a 96-well Reacti-Bind NeutrAvidin coated Black Plates (Pierce, Rockford, IL) for 1 hour at 37°C. After 3 washes, CSF samples (diluted 1:4), quality controls and standards (recombinant GSTP-1 at concentrations ranging from 0 to 100 ng/mL) were incubated for 1 hour at 37°C, and followed by a washing step. Alkaline phosphatase conjugated antibodies against human GSTP-1 (Biosite, California, USA) at 2 µg/mL were added and incubated for 1 hour at 37°C. After 3 washes, Attophos AP fluorescent substrate (Promega, Madison, WI) was added and plates were read immediately on a SpectraMax GEMINI-XS ( Molecular Devices Corporation, Sunnyvale, CA, U.S.A.) plate reader, using the kinetic mode. Vmax values were automatically calculated by the instruments based on relative fluorescence units (RFU) ($\lambda_{\text{excitation}} = 444$ nm and $\lambda_{\text{emission}} = 553$ nm).

Concentrations of S100β, H-FABP and GSTP-1 in the CSF samples were back-calculated using a linear calibration curve based on measured standards values.

Bead suspension array

The levels of thirteen cytokines and chemokines (IL-1ra, IL-1β, IL-6, IL-9, IL-10, G-CSF, VEGF, IFN-γ, TNF-α, CCL2, CCL4, CXCL5 and CXCL10) were determined using the Bioplex bead suspension arrays according to the manufacturer’s instructions (Bio-Rad, Hercules, CA). Briefly, thirteen sets of color-coded polystyrene beads were conjugated separately with one of the thirteen different antibodies against the molecule of interest. All the sets were then mixed together by the supplier and delivered ready-to-use. An equal amount of beads was added to each well of a 96-well filter plate. After a series of washes, standards and samples (diluted 1:4) were added and incubated for 30 minutes at room temperature. After washing, a mix of the corresponding thirteen biotinylated detection antibodies was added and incubated 30 minutes at room temperature. After washing, streptavidin-phycocerythrin (streptavidin-PE) was added for 10 minutes. After a last series of washes, beads were re-suspended in the provided assay buffer and each well was aspirated using the Bio-Plex system. Each bead was identified and the corresponding target simultaneously quantified based respectively on bead color and fluorescence. The concentration of each target was automatically calculated by the Bio-Plex Manager software using corresponding standard curve (5-PL regression) obtained from recombinant protein standards.

Data and statistical analysis

Descriptive statistics were performed using the SPSS (version 16.0, SPSS Inc., Chicago, IL, USA) and GraphPad Prism (version 4.03, GraphPad software Inc., San Diego, CA, USA) software. Because none of the markers presented a normal distribution in concentrations (Kolmogorov-Smirnov test), differences between groups were tested with non-parametric Mann-Whitney U test (comparison between two groups) and Kruskal-Wallis test followed by Dunn’s post-hoc test (comparison between three groups). Statistical significance for these tests was set at 0.05 (2-tailed tests).

To calculate the sensitivity and specificity of each individual predictor with respect to staging, the specific receiver operator characteristic (ROC) curve of each analyte was determined and the cutoff value was selected as the threshold predicting stage 2 patients with 100% of specificity (Figure S1).

Panel development

Panel selection was mainly performed as described by Reynolds et al. [30]. Briefly, the optimized cutoff values were obtained by modified iterative permutation-response calculations (rule-induction-like, RIL) using only the molecules that presented a $p$ value<$0.0001$ (Mann-Whitney U test), an AUC above 75% and a significant Spearman correlation with WBC above 0.4 (Table 2). Each cutoff value was changed iteratively by quantile of 2% increment and sensitivity was determined after each iteration until a maximum sensitivity was achieved for 100% specificity. The permutation-response calculations were conducted using a PERL program (ActivePerl version 5.10.0.1004, ActiveState Software Inc.) and data were coded in CSV format.

Results

Biomarker concentration as a function of disease stage

The main characteristics of the 100 patients evaluated in this study are presented in Table 1. The analytes were classified into
### Table 1. Characteristics of the studied population.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Stage 1</th>
<th>Stage 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population</td>
<td>n</td>
<td>21</td>
</tr>
<tr>
<td>Gender</td>
<td>Male</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>13</td>
</tr>
<tr>
<td>Age</td>
<td>Median (range)</td>
<td>32.0 (14–60)</td>
</tr>
<tr>
<td>WBC/μl</td>
<td>Median (range)</td>
<td>2 (0–5)</td>
</tr>
<tr>
<td>Parasite in CSF</td>
<td>N</td>
<td>0</td>
</tr>
<tr>
<td>Neurological signs*</td>
<td>Absence</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>Moderate</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>Severe</td>
<td>0</td>
</tr>
<tr>
<td>&gt;5 and ≤20 WBC/μL</td>
<td>N</td>
<td>0</td>
</tr>
</tbody>
</table>

*Neurological signs were not reported for two patients.

**Correlation is significant at the 0.01 level (2-tailed).

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### Table 2. Detailed results for all the molecules tested in respect with the stage of the disease.

<table>
<thead>
<tr>
<th>Markers</th>
<th>Absence of parasite and ≤5 parasite/μL</th>
<th>Presence of parasite and/or &gt;5 parasite/μL</th>
<th>Mann-Whitney U test</th>
<th>Correlation with WBC</th>
<th>ROC curve</th>
<th>Cutoff (pg/mL)</th>
<th>Sensitivity, % (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GR3</td>
<td>CXCL10 347.3 (243.3–2048.8)</td>
<td>14130.0 (243.3–128900.0)</td>
<td>&lt;0.0001</td>
<td>0.625**</td>
<td>95</td>
<td>&gt;2080.0</td>
<td>84 (74–91)</td>
</tr>
<tr>
<td></td>
<td>CXCL8 56.9 (13.3–96.5)</td>
<td>179.3 (1.6–1791.0)</td>
<td>&lt;0.0001</td>
<td>0.557**</td>
<td>94</td>
<td>&gt;97.1</td>
<td>82 (72–90)</td>
</tr>
<tr>
<td></td>
<td>IL-10 6.7 (0.9–19.6)</td>
<td>74.5 (2.1–573.1)</td>
<td>&lt;0.0001</td>
<td>0.702**</td>
<td>89</td>
<td>&gt;20.0</td>
<td>80 (69–88)</td>
</tr>
<tr>
<td></td>
<td>TNF-α 3.3 (0.5–8.4)</td>
<td>22.5 (1.0–295.4)</td>
<td>&lt;0.0001</td>
<td>0.636**</td>
<td>93</td>
<td>&gt;8.5</td>
<td>78 (68–87)</td>
</tr>
<tr>
<td></td>
<td>H-FABP 226.4 (19.8–564.0)</td>
<td>748.3 (0.0–16680.0)</td>
<td>&lt;0.0001</td>
<td>0.417**</td>
<td>86</td>
<td>&gt;571.8</td>
<td>62 (50–73)</td>
</tr>
<tr>
<td></td>
<td>IL-6 5.0 (0.2–57.7)</td>
<td>63.8 (0.8–3286.0)</td>
<td>&lt;0.0001</td>
<td>0.732**</td>
<td>94</td>
<td>&gt;58.0</td>
<td>52 (40–63)</td>
</tr>
<tr>
<td></td>
<td>IL-1β 0.1 (0.1–0.7)</td>
<td>0.6 (0.1–42.2)</td>
<td>&lt;0.0001</td>
<td>0.445**</td>
<td>80</td>
<td>&gt;0.7</td>
<td>48 (37–60)</td>
</tr>
<tr>
<td></td>
<td>GSTP-1 1272.9 (149.7–5026.9)</td>
<td>3018.0 (61.2–75810.0)</td>
<td>&lt;0.0001</td>
<td>0.437**</td>
<td>79</td>
<td>&gt;5078.0</td>
<td>24 (15–35)</td>
</tr>
<tr>
<td>GR2</td>
<td>IFN-γ 68.7 (8.6–209.2)</td>
<td>100.4 (1.7–995.5)</td>
<td>0.0049</td>
<td>0.094</td>
<td>70</td>
<td>&gt;210.9</td>
<td>10 (4–19)</td>
</tr>
<tr>
<td></td>
<td>IL-9 23.4 (3.6–44.5)</td>
<td>30.7 (3.6–209.6)</td>
<td>0.0051</td>
<td>0.041</td>
<td>70</td>
<td>&gt;45.0</td>
<td>23 (14–34)</td>
</tr>
<tr>
<td></td>
<td>S100β 43.2 (4.9–113.0)</td>
<td>78.4 (0.0–353.0)</td>
<td>0.0053</td>
<td>0.269**</td>
<td>70</td>
<td>&gt;114.3</td>
<td>29 (19–40)</td>
</tr>
<tr>
<td></td>
<td>CCL2 428.1 (58.6–632.9)</td>
<td>590.2 (15.8–5391.0)</td>
<td>0.0055</td>
<td>0.156</td>
<td>70</td>
<td>&gt;664.7</td>
<td>44 (33–56)</td>
</tr>
<tr>
<td>GR1</td>
<td>G-CSF 43.4 (2.4–209.8)</td>
<td>63.2 (2.0–785.9)</td>
<td>0.0866 (ns)</td>
<td>–0.029</td>
<td>62</td>
<td>&gt;281.7</td>
<td>4 (1–11)</td>
</tr>
<tr>
<td></td>
<td>IL-1α 817.3 (128.6–3087.6)</td>
<td>782.0 (34.0–11760.0)</td>
<td>0.5229 (ns)</td>
<td>–0.065</td>
<td>55</td>
<td>&gt;3092.0</td>
<td>13 (6–22)</td>
</tr>
<tr>
<td></td>
<td>CCL4 94.2 (1.5–301.0)</td>
<td>91.9 (5.4–753.9)</td>
<td>0.5423 (ns)</td>
<td>–0.143</td>
<td>54</td>
<td>&gt;316.6</td>
<td>5 (1–12)</td>
</tr>
<tr>
<td></td>
<td>VEGF 48.3 (20.0–215.7)</td>
<td>49.4 (3.5–1009.0)</td>
<td>0.9393 (ns)</td>
<td>–0.105</td>
<td>54</td>
<td>&gt;222.4</td>
<td>9 (4–17)</td>
</tr>
</tbody>
</table>

*Sensitivity was set for a specificity of 100% (95% CI, 84–100).

**Correlation is significant at the 0.01 level (2-tailed).

DOI:10.1371/journal.pntd.0000459.t002

Biomarkers for Staging HAT

Three groups, based on the results presented in Table 2. Criteria for the classification were the significance (Mann-Whitney U test), the AUC and the correlation with WBC. In the first group (GR1) comprising IL-1α, G-CSF, CCL4, and VEGF, no significant difference in CSF concentrations between the two stages of HAT was observed. The second group (GR2) encompassed IFN-γ, IL-9, CCL2 and S100β for which concentrations in the CSF were significantly different between stage 1 and stage 2 patients (0.001< p <0.01, Mann-Whitney U test). The third group (GR3) included GSTP-1, H-FABP, TNF-α, IL-1β, IL-6, IL-10, CXCL8 and CXCL10, for which the difference between stages was highly significant (p<0.0001, Mann-Whitney U test) (Figure S2).

To assess the sensitivity and specificity of these analytes for S2 HAT, ROC curves were built. GR1 and GR2 had a low to medium area under ROC curve (AUC) ranging from 54 to 70% and also displayed a low sensitivity in detecting S2 patients (4–13% for GR1 and 10–44% for GR2, see Table 2) at a predefined specificity of 100%. GR3 showed higher AUC (79–95%), and sensitivities for identification of S2 patient up to 84% (Table 2). CXCL10 appeared then as the most accurate predictor for staging, as, with a cutoff set at 2080 pg/mL, this molecule identified 66 out of 79 late stage patients and ruled-out all the early-stage patients.

Correlation between WBC and biomarker concentrations

As the white blood cell count was one of the two reference staging parameters, we investigated the correlation between the concentrations of the sixteen biomarkers and the number of WBC in CSF (Table 2). There was no significant correlation in the concentrations of the first and second group of analytes (GR1 and GR2) with WBC, except for S100β, which had a significant but low Spearman rho coefficient (0.269, p<0.01). Otherwise, strong correlations were observed between WBC and the concentrations of GR3 biomarkers (GSTP-1, IL-1β, IL-6, H-FABP, TNF-α, IL-10, CCL8 and CXCL10), with Spearman rho ranging from 0.417 to 0.732 (Table 2 and Figure 1). The levels of GR3 molecules in 8 potential intermediate stage patients (parasite not detected in CSF and having >5 and ≤20 WBC/μL) demonstrated the intermediate behaviour of this category with some patients appearing as S1 and others as S2 patients (Figure 1). Based on the above results, only the GR3 molecules (GSTP-1, IL-1β, IL-6, H-FABP, TNF-α, IL-10, CCL8 and CXCL10) were selected for further analyses.

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Parasites in CNS and biomarker concentrations

GR3 molecule concentrations were classified according to the absence/presence of trypanosomes in CSF. GSTP-1, IL-1β, IL-6, H-FABP, TNF-α, IL-10, CXCL8 and CXCL10 concentrations were significantly increased in patients with parasites in CSF (Figure 2 and Table S1). The six biomarkers associated with inflammation had a lower \( p \) value (\(<0.0001\), Mann-Whitney U test) and higher AUC (ranging from 78% to 89%) than H-FABP and GSTP-1 (\(0.001<\text{\( p \)}<0.05\), Mann-Whitney U test, AUCs of 69% and 64% respectively). Additionally, when only S2 patients were analysed, CXCL10, IL-10 and TNF-α levels still demonstrated a significant difference between patients with or without trypanosomes in CSF (\(p<0.05\), Dunn’s post-hoc test, Table S1).

Neurological signs and biomarker concentrations

The patients were classified with respect to the neurological signs reported (absence, moderate or severe) (Figure 3). All the GR3 molecules except GSTP-1 showed a significant increase in concentration associated with higher severity of neurological signs \((p<0.05\), Kruskal-Wallis test). Indeed, CXCL10, CXCL8, IL-6, IL-10, IL-1β, and TNF-α concentrations were significantly different between patients without neurological signs and severe neurological signs \((p<0.05\), Dunn’s post-hoc test), as well as between patients with moderate and severe neurological signs \((p<0.05\), Dunn’s post-hoc test). H-FABP level was significantly different between patients without neurological signs and severe neurological signs \((p<0.05\), Dunn’s post-hoc test). Only the concentrations of CXCL10, IL-10 and TNF-α could distinguish...
between absence and moderate neurological signs (p<0.05, Dunn’s post-hoc test).

Panel selection

In an effort to improve the global sensitivity of molecules in the prediction of second stage HAT, the GR3 molecules were combined using the rule induction like (RIL) approach. This resulted in the identification of a three-molecule panel characterized by CXCL10, CXCL8 and H-FABP (cutoff values were set at 2080.0, 97.1 and 571.8 pg/mL, respectively). A positive test (leading to identification of S2 patient) was obtained as soon as one of the three molecules included in the panel was above its cutoff value (Table 3). The panel had a sensitivity of 97% (95% CI, 91–100%) and, by definition, a specificity of 100% (95% CI, 84–100%). This means that the panel could identify 77 out of 79 stage 2 patients, and ruled-out all the 21 stage 1 patients. Out of the 77 ruled-in S2 patients, 5 were CXCL10 positive only (≥2080.0 pg/mL), 6 CXCL8 positive only (≥97.1 pg/mL) and 3 H-FABP positive only (≥571.8 pg/mL). The rest of ruled-in S2 patients were identified with either 2 positive molecules (n = 23) or 3 positive molecules (n = 40). When this panel was applied on the intermediate stage patients (eight patients having ≥5 and ≤20 WBC/μL and no trypanosomes in CSF) only one patient gave a negative test response and thus 7 out of 8 patients were classified as S2.

Discussion

In this study, including early and late stage HAT patients (n = 100), we evaluated sixteen molecules as potential staging markers of HAT, to replace or complement trypanosome

Figure 2. Box-plot of GR3 molecules and WBC classified according to the presence of the parasite in CSF. Median and mean are represented as a solid line in the box and a diamond respectively. Whisks are defined as 5th–95th percentile without outliers. Half-width of the notch was calculated automatically by the software.
doi:10.1371/journal.pntd.0000459.g002
Figure 3. Box-plot of GR3 molecules and WBC classified according to the neurological signs. Median and mean are represented as a solid line in the box and a diamond respectively. Whisks are defined as 5th–95th percentile without outliers. Half-width of the notch was calculated automatically by the software. Neurological signs of two patients were not reported (n = 98).

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Table 3. Detailed results for the three molecule panel in respect with the stage of the disease.

| Markers                  | Number of negative test | Number of positive test | Mann-Whitney U test, p value | % AUC (ROC curve) | Panel cutoff | Sensitivity, % (95% CI)
|--------------------------|-------------------------|-------------------------|-----------------------------|-------------------|--------------|-----------------------------
| Panel CXCL10, CXCL8, H-FABP | 23                      | 77                      | <0.0001                     | 99                | ≥1 molecule above its cutoff value | 97 (91–100) |

*aSensitivity was set for a specificity of 100% (95% CI, 84–100).
bCutoff values: CXCL10 >2080.0 pg/mL, CXCL8 >97.1 pg/mL and H-FABP >571.8 pg/mL.
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Biomarkers for Staging HAT

CXCL10, also known as IP-10, is a pro-inflammatory chemokine with a central role in inflammatory responses [40]. The main effect of CXCL10 as a chemoattractant molecule is activation of T cell migration to the site of inflammation, after binding to its receptor, CXCR3 [41]. The involvement of this chemokine in different CNS disorders has been demonstrated, such as viral meningitis [42] and multiple sclerosis [43], where increased CXCL10 levels in the CSF correlated with tissue infiltration of T lymphocytes [44]. In our study, the concentration of CXCL10 increased with progression of the disease, and was highly correlated with the number of WBC in CSF. Many studies have pointed out astrocytes as the primary source of CXCL10 at the level of the CNS and showed that this molecule is responsible, as chemoattractant, for the influx of activated T lymphocytes in brain [43,45–47]. Indeed, there is a predominance of plasma cell infiltration in the brain of trypanosomiasis infected individuals. In addition, it has very recently been shown in a mouse model of HAT that CXCL10 may play an important role in T-cell recruitment into the brain parenchyma and is probably associated with brain invasion by trypanosomes [48]. Furthermore, the early activation of cytokine production (TNF-α, IL-6, and IFN-γ) by astrocytes and microglia in mice models infected with T. brucei was observed as a potential observation of an inflammatory response [49] has confirmed an important role of astrocyte activation in CNS inflammatory response. In consequence, early astrocyte activation, which induces CXCL10 production, is probably linked with BBB dysfunction and may occur before the inflammatory process. These hypotheses were supported by the increase CXCL10 concentration observed in patients having >5 and ≤20 WBC/μL but without trypanosomes detected in the CSF. The CXCL10 level was also demonstrated to be elevated in patients with cerebral malaria, and pointed out as potentially inducing apoptosis of endothelial cells leading to BBB breakdown [17]. Recent work has suggested that neuronal apoptosis associated with calcium dysregulation may be induced by CXCL10 [50]. Even if mechanisms of CXCL10 mediated neurotoxicity remain unclear, we showed that the concentration of CXCL10 was correlated to the severity of neurological signs, supporting a possible involvement of this protein in neuronal injury pathways. Thus, CXCL10 expression in late stage HAT patients may be associated with both cell death and inflammatory process. Finally, active tuberculosis and pregnancy, two exclusion criteria in this study, have also been reported as modulating the level of CXCL10 [51,52]. Although they have only been evaluated on serum and whole blood samples so far, it is not excluded that these criteria could potentially induce CXCL10 modulation in CSF. Nevertheless, our data demonstrated that CXCL10 is an efficient tool for staging patients, and suggested a potential role of CXCL10 as an early marker of parasite invasion into the CNS.

As the investigated proteins may be involved in different biological mechanisms, we evaluated in this study a strategy to combine results of each molecule, in order to find a panel able to discriminate more accurately early and late stage patients. This highlighted a panel of three molecules, including CXCL10 (the most promising single molecule), CXCL8 (another chemokine) and H-FABP (a marker of brain damage). With a specificity of 100%, this panel increased the sensitivity for staging of HAT patients up to 97% (compared to the 84% obtained with CXCL10
taken individually. Although the number of “intermediate” patients was small, the panel appeared to classify them rather as S2 patients (7/8 patients). This supports the current recommendation by WHO to consider such patients as S2 patients and treat them with drugs used for late stage disease. However, there is a need for more studies on T. b. gambiense and T. b. rhodesiense patients, before and after treatment, as well as on other parasitic diseases such as cerebral malaria, to verify these results and assess the feasibility of using the three-molecule panel as a complement to WBC count. There are obviously some drawbacks concerning this approach. Firstly the obtained panel is not 100% sensitive and thus some stage 2 patients will not be detected. The influence of other possible co-infections should also be evaluated in order to determine if they significantly modulate the evaluated molecules. Indeed, the three molecules included in the panel could potentially all be markers of other CNS disorders. It is also evident that the methods described in this study could not be implemented in such a way directly in the field and should be first transformed into a more simplified technique as for example a lateral flow immunosassay. Another limitation is the continued requirement of the invasive lumbar puncture since the molecules highlighted in this study have been evaluated on CSF samples.

In conclusion, the present study demonstrated the utility of inflammation-related proteins and brain damage markers as indicators of the second stage of HAT but potentially in other CNS disorders as well. We highlighted the value of CXCL10 as an efficient staging biomarker for T. b. gambiense infected HAT patients. Additionally, a combination of CXCL10 with CXCL3 and H-FABP resulted in a highly sensitive tool for identification of late stage HAT patients.

References


Supporting Information

Figure S1 ROC curves of GR3 molecules and the panel. *Cut-off value for each molecule [pg/ml] and for the panel is displayed by a point and the numeric value. In parenthesis, sensitivity (%) of each molecule was set for 100% specificity. Area under the ROC curve (AUC) is also given.

Found at: doi:10.1371/journal.pntd.0000459.s001 (1.37 MB TIF)

Figure S2 Box-plot of GR3 molecules classified according to the stage of the disease. *Median and mean are represented as a solid line in the box and a diamond respectively. Whisks are defined as 5th–95th percentile without outliers. Half-width of the notch was calculated automatically by the software.

Found at: doi:10.1371/journal.pntd.0000459.s002 (0.69 MB TIF)

Table S1 Detailed results for GR3 molecules in function of the presence of trypanosomes in CSF (according or not to the stage) and the neurological signs.

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Author Contributions

Conceived and designed the experiments: VL, JMN NT JCS. Performed the experiments: AH NT CF. Analyzed the data: AH NT XR FL MM NT JCS. Contributed reagents/materials/analysis tools: XR VL, DMN EM JCE JCS. Wrote the paper: AH NT JCS.