

Distinct roles of haptoglobin-related protein and apolipoprotein L-I in trypanolysis by human serum

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Apolipoprotein L-I (apoL-I) is a human high-density lipoprotein (HDL) component able to kill *Trypanosoma brucei brucei* by forming anion-selective pores in the lysosomal membrane of the parasite. Another HDL component, haptoglobin-related protein (Hpr), has been suggested as an additional toxin required for full trypanolytic activity of normal human serum. We recently reported the case of a human lacking apoL-I (apoL-I^{-/-}HS) as the result of frameshift mutations in both *apoL-I* alleles. Here, we show that this serum, devoid of any trypanolytic activity, exhibits normal concentrations of HDL-bound Hpr. Conversely, the serum of individuals with normal HDL-bound apoL-I but who lack Hpr and haptoglobin [Hp(r)^{-/-}HS] as the result of gene deletion (anhaptoglobinemia) exhibited phenotypically normal but delayed trypanolytic activity. The trypanolytic properties of Hp(r)^{-/-}HS were mimicked by free recombinant apoL-I, whereas recombinant Hpr did not affect trypanosomes. The lysis delay observed with either Hp(r)^{-/-}HS or recombinant apoL-I could entirely be attributed to a defect in the uptake of the lytic components. Thus, apoL-I is responsible for the trypanolytic activity of normal human serum, whereas Hpr allows fast uptake of the carrier HDL particles, presumably through their binding to an Hp/Hpr surface receptor of the parasite.

innate immunity | sleeping sickness | trypanolytic factor | haptoglobin receptor | *Trypanosoma brucei*

African trypanosomes, the prototype of which is *Trypanosoma brucei brucei* (*T. b. brucei*), are protozoan parasites transmitted by tsetse flies. Living extracellularly in the bloodstream of their mammalian hosts, they overcome host adaptive immunity by restricting their exposed immunogenic epitopes to a continuously changing coat of variant surface glycoprotein (1). Humans and some primates exhibit specific innate immunity that allows them to kill *T. b. brucei*, but not *Trypanosoma brucei gambiense* and *Trypanosoma brucei rhodesiense*. These last subspecies are responsible for the sleeping sickness disease, which affects >300,000 people per year in subtropical Africa.

The trypanosome lytic factor (TLF) of normal human serum (NHS) was found to be associated with a minor subclass of high-density lipoproteins (HDL) that contains both haptoglobin-related protein (Hpr) and apolipoprotein L-I (apoL-I) (2–4). Trypanolysis results from the endocytosis of these particles by the parasite (5–7). Initially, the lytic component of TLF was identified as Hpr, and its effect on trypanosomes was attributed to oxidative damage of the lysosomal membrane (8). More recently, apoL-I was shown to exert trypanolytic activity by forming pores into the lysosomal membrane of the parasite, triggering fatal osmotic ionic fluxes (9, 10). The role of apoL-I in trypanolysis could be evidenced with both native and recombinant apoL-I (9–12). In contrast, the involvement of Hpr in this process largely was deduced from indirect evidence resulting from the difficulty of producing recombinant heterodimeric Hpr. Nevertheless, recent work concluded that affinity-purified

Hpr was toxic for trypanosomes, leading to the reporting that apoL-I and Hpr are two inefficient toxins whose activities need to be combined to build the trypanolytic potential of NHS (11). However, this view was debated (12).

Apart from a proposed involvement in trypanolysis, the biological function of Hpr and apoL-I is not clear. Hpr shares 91% amino acid sequence identity with Hp, an abundant (0.2–2 mg/ml) acute-phase serum protein that binds free Hb with high affinity and allows its clearance from the blood (13). Recently, the capacity of Hpr to bind Hb was demonstrated (14). However, Hpr probably does not function to scavenge Hb because, in contrast to haptoglobin (Hp), this protein is not cleared from the circulation during intravascular hemolysis (13). In addition, Hpr and Hp strongly differ in their ability to associate with apolipoprotein A-I (apoA-I)-containing HDL particles (14, 15). ApoL-I is the only secreted member of a family that could be involved in programmed cell death (16). It contains a pore-forming domain resembling that of bacterial colicins and Bcl-2 family members, as well as a region necessary for the membrane insertion of this pore-forming domain (10, 12).

We describe the trypanolytic potential of mutant human sera lacking either Hpr or apoL-I. Human serum devoid of Hp and Hpr [Hp(r)^{-/-}HS] originates from anhaptoglobinemic patients lacking both Hpr and Hp as a result of homozygous gene deletion (~20 kb) from the *Hp* promoter region to exon 5 of *Hpr* (17). Human serum devoid of apoL-I (apoL-I^{-/-}HS) originated from an Indian patient found to be infected with trypanosomes closely related to *T. b. brucei* (*Trypanosoma evansi*) (18, 19). The absence of apoL-I resulted from two independent frameshift mutations in the *apoL-I* alleles (20). The analysis of these sera allowed us to discriminate the respective roles played by apoL-I and Hpr in trypanolysis.

Results

ApoL-I Is Necessary and Sufficient for Trypanosome Lysis. As shown in Fig. 1, apoL-I^{-/-}HS was devoid of apoL-I but contained normal amounts of Hpr. The fraction of Hpr bound to HDLs, as revealed by its association with the HDL-specific protein apoA-I, was similar between apoL-I^{-/-}HS and NHS (Fig. 1). Moreover, the sequence of the *Hpr* gene of the apoL-I^{-/-} individual, determined after PCR amplification of the full *Hpr* coding

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Abbreviations: TLF, trypanosome lytic factor; FCS, fetal calf serum; NHS, normal human serum; HDL, high-density lipoproteins; apoL-I, apolipoprotein L-I; Hpr, haptoglobin-related protein; Hp, haptoglobin; apoA-I, apolipoprotein A-I; Hp(r)^{-/-}HS, human serum devoid of Hp and Hpr; apoL-I^{-/-}HS, human serum devoid of apoL-I.

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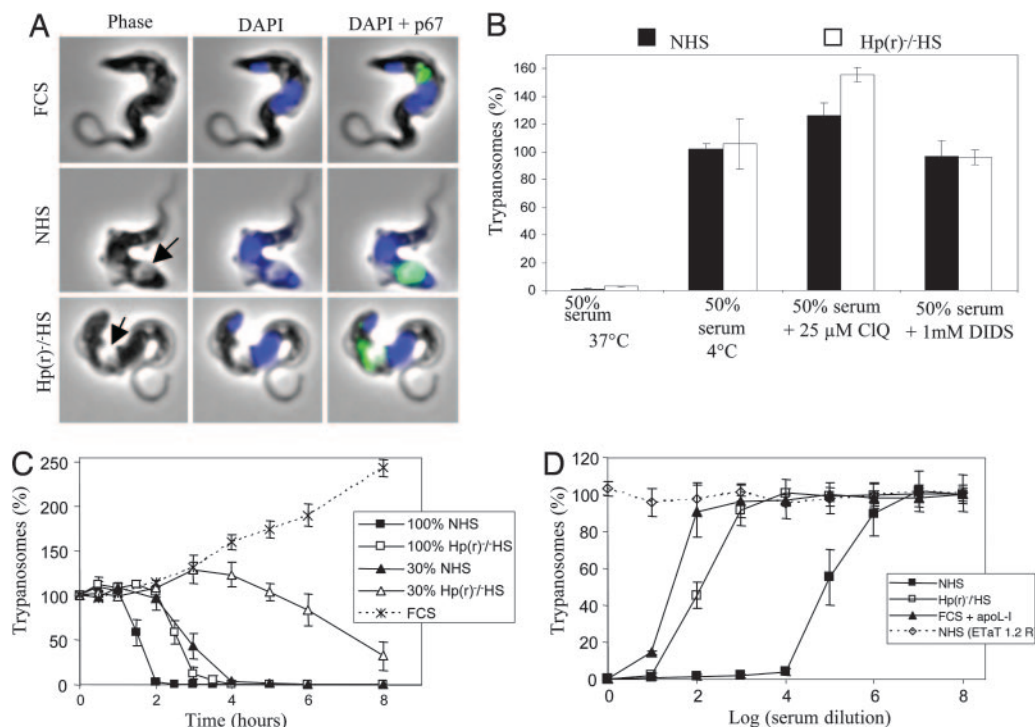


Fig. 3. Characteristics of trypanolysis by various sera. (A) *In situ* immunofluorescence of the lysosomal membrane protein p67 detected by Alexa 488 (green)-coupled antibodies in ETaT 1.2S trypanosomes incubated in 30% FCS, NHS, or Hp(r)^{-/-}HS. Large and small blue dots are DAPI-stained nucleus and kinetoplast, respectively. The arrows point to the swollen lysosome. (B) Inhibition of ETaT 1.2S lysis by 50% NHS or Hp(r)^{-/-}HS after incubation [3 h for NHS, 6 h for Hp(r)^{-/-}HS] at 4°C or at 37°C in the presence or absence of 25 μM chloroquine (ClQ) or 1 mM 4,4-diisothiocyanatostilbene-2,2-disulfonic acid (DIDS). (C) ETaT 1.2S lysis kinetics in various sera. (D) Survival percentage of ETaT 1.2S (solid curves) or ETaT 1.2R (dashed curve) trypanosomes incubated with log dilutions of the indicated sera for 24 h. In the undiluted FCS recombinant, apoL-I was supplemented at physiological concentration (8.5 μg/ml).

were conducted after preincubating the trypanosomes at 4°C, a temperature low enough to completely inhibit lysis and endocytosis (5). In the case of NHS, no significant difference in trypanolysis could be demonstrated after preincubation at either 37°C or 4°C. In contrast, in the case of Hp(r)^{-/-}HS, trypanolysis was no longer detectable after preincubation at 4°C (Fig. 4A). Similar results were obtained by using FCS supplemented with free recombinant apoL-I (Fig. 4A). These data revealed that the absence of Hpr prevents the binding of TLF to trypanosomes at 4°C, suggesting that Hpr is required for the binding of TLF to a specific surface receptor.

To assess this hypothesis, we tested the effect on trypanolysis of adding a constant amount of free Hp or Hpr (200 μg/ml) to various dilutions of NHS. As expected from previous reports analyzing the effect of Hp on the activity of purified lytic particles (21–23), an excess of Hp was able to inhibit some, but not all, trypanolytic activity of NHS (Fig. 4B). Very similar results were obtained with recombinant Hpr (Fig. 4B). Therefore, Hp and Hpr appeared to interfere with TLF activity only when present in large excess, as would occur if these proteins were competing with TLF for binding to the trypanosome surface. That this effect was specific was indicated by the lack of inhibition observed with both proteins added to Hp(r)^{-/-}HS (Fig. 4B). Thus, these results further suggested the involvement of Hpr in the binding of HDL to the trypanosome surface. Such a conclusion was independently reached previously (24) and also was supported by the monitoring of intracellular trafficking of free Hp (Fig. 5). Hp appeared to rapidly and efficiently accumulate in the endocytic pathway, contrasting with the inefficient uptake of bovine serum albumin (BSA), a protein not specifically recognized by the parasite (Fig. 5).

The Mechanism of Lysis Does Not Involve Hpr. To assess the hypothesis that apoL-I and Hpr act synergistically to generate full trypanolytic activity (11), we plotted the relationship between the time periods necessary in various NHS concentrations to achieve commitment to lysis (as determined by experiments involving preincubation with the lytic sera then incubation in nonlytic FCS; see Fig. 4A) and those necessary to observe complete lysis. The data, shown in Fig. 6, indicate that the time of lysis by NHS is related to the time required for commitment to lysis, both depending on the concentration of serum. This effect could be ascribed to later and longer times of lysosomal swelling when the number of internalized apoL-I molecules is reduced. This relationship also was measured for trypanolysis triggered by Hp(r)^{-/-}HS. As shown in Fig. 6, irrespective of the period required for cellular commitment to lysis, the time necessary for lysis after the commitment period was never longer in the absence of Hpr than in NHS. Again, similar results were obtained with FCS + recombinant apoL-I (Fig. 6). Thus, regardless of the presence or absence of Hpr, the lysis time could be predicted by that required for commitment to lysis, and the longer time of trypanolysis observed with Hp(r)^{-/-}HS could totally be assigned to slower uptake of the lytic component and not to the decrease in lytic activity. These data contradict the idea that apoL-I and Hpr work in synergy.

Discussion

The identification of the trypanolytic factor of NHS has been highly controversial. Two different HDL-bound serum proteins specific to humans, Hpr and apoL-I, successively have been proposed as trypanosome toxins, and the mechanisms by which these factors were thought to kill trypanosomes have varied from membrane lipid peroxidation to ionic pore-forming activity [for

proposed (24). A scavenger receptor for lipoproteins also has been suggested to be involved in TLF uptake (26). Because TLF binding to trypanosomes appeared to involve two receptors, one present in 350 copies exhibiting high affinity and another present in 60,000 copies binding with low affinity (24), a combination of specific and scavenger receptors could be required for optimal uptake of TLF. Only incomplete inhibition of trypanolysis was observed with large excess amounts of Hp or Hpr, but this finding cannot be simply explained by the existence of two different receptors. Indeed, a significant fraction of the lytic component that resisted excess Hp(r) actually depended on Hpr, as revealed with Hp(r)-free serum. The characteristics of this fraction evoke those of the lytic subfraction TLF2 (22, 23). How Hpr appears to be inaccessible to competing free Hp(r) within this subfraction remains a mystery.

The presence of an Hp receptor on the trypanosome surface would be useful for heme and iron uptake by the parasite because it would allow internalization of bound Hb. That this interpretation is plausible is indicated by results obtained when monitoring the growth of trypanosomes in transferrin-depleted medium. Indeed, trypanosomes thought to lack efficient TLF uptake, such as NHS-resistant clones of *T. b. rhodesiense* (27), do not tolerate deprivation of transferrin, in contrast to *T. b. brucei* parasites, which survive despite a strong reduction of growth (28). A possible explanation of this difference is that uptake of iron through the Hp receptor would compensate for the inability to capture iron from transferrin. The putative Hp receptor is expected to recognize Hpr-containing HDL particles, which also contain Hpr-bound Hb (14). Thus, the uptake of Hpr-Hb-containing HDL particles could contribute to providing a source of heme to the parasite, which lacks the pathway for heme biosynthesis (29). According to these views, internalization of apoL-I by the parasite would be a byproduct of heme uptake from Hpr-Hb-containing HDL particles.

The time necessary for complete lysis of trypanosomes by NHS could essentially be predicted by the time required to irreversibly commit them to lysis. As indicated by the lack of difference between 37°C and 4°C in the case of NHS, the period necessary to commit trypanosomes to death is likely to represent that required for binding and uptake of the lytic factor, the rest accounting for the lytic process itself. This interpretation is supported by the observation that the swelling of the lysosome always becomes detectable soon after the end of the period of commitment to death, irrespective of the length of this period (B.V., data not shown). The TLF uptake time increased with dilution of serum and was thus dependent on the relative abundance of TLF. Whereas TLF was taken up at a speed (2 min in 30% NHS) comparable with that of transferrin (30), the important increase of uptake time observed after dilution of serum (5 min in 10% NHS) suggests that TLF is not in excess in NHS and/or that the trafficking of TLF to the lysosome membrane is relatively inefficient. Presumably, many apoL-I molecules are degraded before reaching their target.

Regarding the lytic process, because apoL-I generates ionic pores that allow an influx of chloride ions into the lysosome (10), it is logical to assume that the greater the number of intracellular apoL-I molecules, the sooner and the faster lysosome swelling and cell lysis will be. It is likely that at high serum concentration the lytic process is initiated before the intracellular trafficking of apoL-I is complete because in >5% serum concentration the time for commitment to lysis was sharply shortened with respect to total lysis time. This view is actually supported by two observations: Preincubation of trypanosomes with NHS under conditions preventing full intracellular trafficking (that is, at 17°C) still allowed initiation of lysis (B.V., data not shown); moreover, the *T. b. rhodesiense* SRA protein was found able to block TLF activity upstream from the lysosomal compartment (31).

Taking these different parameters into consideration, we detailed the time period required to lyse trypanosomes with Hpr-free sera, either Hp(r)^{-/-}HS or FCS + apoL-I. The time of commitment to lysis by these sera (presumably the time required for TLF uptake) was clearly longer than in NHS, in full agreement with a putative absence of ligand normally involved in efficient binding of TLF to a specific surface receptor. However, in these sera the process of lysis was never slower than normal, as determined by plotting the lysis times against the times required for TLF uptake with different concentrations of serum. Thus, the delay of trypanolysis linked to the absence of Hpr could entirely be attributed to inefficiency of TLF uptake, contradicting the possibility that Hpr is required to synergize the lytic activity of apoL-I (11). In conclusion, within the trypanolytic HDL particles Hpr and apoL-I appear to be respectively involved in efficient uptake and lysis, and apoL-I is probably the sole trypanolytic factor of human blood.

Materials and Methods

Trypanolysis Assays. A NHS-sensitive clone of *T. b. rhodesiense* (ETat 1.2S) was used in all experiments. Trypanosomes, isolated from mice, were incubated at densities between 1.10^5 and 1.10^6 /ml in HMI-9 medium (32) at 37°C in a CO₂-equilibrated incubator. At the indicated times, living trypanosomes were counted in triplicate under the microscope (three independent experiments). The specificity of the lytic activity was systematically checked by verifying the absence of lysis in another clone expressing the same variant surface glycoprotein (ETat 1.2 R) but resistant to NHS because of the synthesis of SRA (33).

Kinetics of TLF Uptake. Trypanosomes, isolated from mice, were incubated at 1.10^6 /ml in HMI-9 or PSGS [2.5 mM NaH₂PO₄·H₂O/47.5 mM Na₂HPO₄·2H₂O/36.5 mM NaCl/1.5% (wt/vol) glucose/4.4% (wt/vol) sucrose, pH 8] under the indicated experimental conditions. Aliquots (100 μl) were centrifuged at $7,200 \times g$ for 2 min at either 37°C or 4°C. Pelleted cells carefully were washed twice with HMI-9 medium supplemented with 10% FCS, resuspended in 1 ml HMI-9 + 10% FCS, and incubated for 24 h at 37°C in a CO₂-equilibrated incubator before being counted in triplicate under the microscope.

ApoL-I Immunoaffinity Chromatography and Western Blotting. A total of 400 μg of rabbit anti-human apoA-I IgGs (Calbiochem, San Diego, CA) was incubated with 200 μl of washed Affi-Gel 10 (Bio-Rad, Hercules, CA) for 90 min at 4°C. Remaining active esters were blocked with 1 ml of 100 mM ethanolamine-HCl (pH 8) before extensive PBS washes. A total of 60 μl of gel was mixed with 400 μl of 20 × diluted NHS in PBS for 180 min at 4°C. Aliquots of unfractionated serum, flow-through, and bound fraction were subjected to SDS/PAGE. Western blots were incubated overnight at 4°C with a 1:100 dilution of a goat polyclonal monospecific anti-apoL-I antibody (Santa Cruz Biotechnology, Santa Cruz, CA) or with a 1:10,000 dilution of rabbit polyclonal anti-human Hp antibody (DAKO, Carpinteria, CA) in 150 mM NaCl/0.5% (wt/vol) Tween 20/20 mM Tris-HCl (pH 7.5) with 1% nonfat milk. The secondary antibodies were, respectively, peroxidase-conjugated mouse anti-goat IgGs (1:160,000; Sigma-Aldrich, St. Louis, MO) and peroxidase-conjugated mouse anti-rabbit IgGs (1:5,000; Promega, Madison, WI).

DNA Amplification and Sequencing. Genomic DNA was extracted from peripheral blood cells. Five different primer sets (from 5' to 3': CAGGTCCAAAGTTTGTAGACACAGG and TTTCTGCATCTGTACCAATGTATGC; GCATGTGCTGTGAAGCAGGGAGACC and CATCATGGAAATGTCA-GAGCAGGGG; TGCCTTCTCACTCTGCTCTGGGTGC and GAAGGCTGTGCCTCTAGGACGTTCC; TCACCCCTT-TCTCAGATGGAAAGGC and TGCAATCGTATTGGT-

