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Growth hormone decreases muscle glutamine production and stimulates protein synthesis in hypercatabolic patients

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Biolo, Gianni, Fulvio Iscra, Alessandra Bosutti, Gabriele Toigo, Beniamino Ciocchi, Onelio Geatti, Antonino Gullo, and Gianfranco Guarnieri. Growth hormone decreases muscle glutamine production and stimulates protein synthesis in hypercatabolic patients. *Am J Physiol Endocrinol Metab* 279: E323–E332, 2000.— We determined the effects of 24-h recombinant human growth hormone (rhGH) infusion into a femoral artery on leg muscle protein kinetics, amino acid transport, and glutamine metabolism in eight adult hypercatabolic trauma patients. Metabolic pathways were assessed by leg arteriovenous catheterization and muscle biopsies with the use of stable amino acid isotopes. Muscle mRNA levels of selected enzymes were determined by competitive PCR. rhGH infusion significantly accelerated the inward transport rates of phenylalanine and leucine and protein synthesis, whereas the muscle protein degradation rate and cathepsin B and UbB polyubiquitin mRNA levels were not significantly modified by rhGH. rhGH infusion decreased the rate of glutamine de novo synthesis and glutamine precursor availability, total branched-chain amino acid catabolism, and nonprotein glutamate utilization. Thus net glutamine release from muscle into circulation significantly decreased after rhGH administration (~50%), whereas glutamine synthetase mRNA levels increased after rhGH infusion, possibly to compensate for reduced glutamine precursor availability. We conclude that, after trauma, the anticatabolic action of rhGH is associated with a potentially harmful decrease in muscle glutamine production.

stable isotopes; competitive polymerase chain reaction; amino acid transport; glutamine synthetase; trauma patients

PATIENTS SUFFERING FROM MAJOR INJURY have a rapid and progressive loss of skeletal muscle protein that can be reduced only partly by nutritional support (5, 14, 30). The administration of recombinant human growth hormone (rhGH) as adjunctive therapy has been shown to be effective in slowing the loss of muscle mass in patients (8, 16, 17, 28, 37, 38), despite the fact that it may have some secondary harmful effects (31, 37). Changes in protein mass derive from a balance between protein synthesis and degradation, which in turn can be influenced by the rate of transmembrane amino acid transport. Evidence indicates that stimulation of protein synthesis is a primary mechanism of rhGH action on muscle (12, 13). However, the hormone effects on protein degradation and amino acid transport have not been clarified.

Besides an anticatabolic effect, rhGH action on muscle also involves a suppression of glutamine efflux, which is much greater than that expected on the basis of the hormone's effects on protein metabolism (4, 28). Such a decrease in glutamine efflux can result from changes in glutamine de novo synthesis and/or outward transmembrane transport. Glutamine is the most abundant free amino acid in the body. It is a precursor of many compounds (e.g., glucose, glutathione, and nucleic acids) and a major fuel for rapidly dividing cells (intestinal mucosa, immune system, and wound tissue). Glutamine is synthesized primarily in skeletal muscle and released into the bloodstream to serve as an interorgan vehicle for carbon and nitrogen. The key enzyme for glutamine synthesis is glutamine synthetase, whereas precursor substrates are glutamate, α-ketoglutarate, free ammonia, and amino-nitrogen derived from the catabolism of the branched-chain amino acids (9). In skeletal muscle, there is a large intracellular pool of preformed free glutamine that serves as a reservoir for any increased glutamine requirement in extramuscular tissues. A decline in muscle free glutamine has consistently been observed in trauma patients (5).

The aim of this study was to define the mechanisms of the rhGH-mediated changes in muscle glutamine and protein kinetics in severely traumatized patients during combined enteral and parenteral nutrition. Leg arteriovenous catheterization, muscle biopsy, and stable isotopic tracer of amino acids were used to determine the rates of muscle protein synthesis, proteolysis, glutamine de novo synthesis, nonprotein utilization of glutamate (mainly to form glutamine) and the branched-chain amino acids (catabolism), as well as transmembrane transport of glutamine and selected essential amino acids (2–4, 6). Competitive RT-PCR was used to determine muscle mRNA levels of key

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enzymes for glutamine synthesis (glutamine synthetase) and for myofibrillar (ubiquitin) and nonmyofibrillar (cathepsin B) protein degradation (7, 15, 27, 34, 35).

METHODS

Patients

Eight adult patients (6 males, 2 females; age 39 ± 5 yr, weight 74 ± 4 kg, height 172 ± 3 cm) with multiple injuries (APACHE II score 15 ± 1) were studied between *days 7* and *12* after admission to the Intensive Care Unit of the University Hospital of Cattinara, Trieste, Italy. Leg volume (8,603 ± 520 ml) was estimated by use of an anthropometric approach (21). Informed consent was obtained from the patients' close relatives. The protocol was approved by the competent hospital authority. All patients received continuous combined intravenous (80% of total energy as amino acids, glucose, and lipids) and enteral [20% of total energy: Nutrisond (Nutricia, Zoetermeer, Netherlands) or Sondalis ISO (Clintec, Rome, Italy)] nutrition providing 35 kcal · kg^{-1} · day^{-1} with 250 mg of nitrogen · kg^{-1} · day^{-1}. Nutrient administration was constant for ≥2 days before and during the study.

Experimental Protocol

Each patient was studied twice. Two leg muscle metabolic studies (which included determination of protein and glutamine metabolism by stable isotopes and competitive RT-PCR) were performed 24 h apart during rhGH administration or saline infusion (control study). To account for time-related changes of muscle metabolism after trauma and for potential interference between two close stable isotope infusions, the control study was performed either before (*protocol 1*) or after (*protocol 2*) rhGH infusion. Patients were randomly assigned to *protocol 1* (n = 4, 3 males, 1 female, age 42 ± 6 yr, weight 74 ± 6 kg, height 171 ± 5 cm; APACHE II score 15 ± 2) or to *protocol 2* (n = 4, 3 males, 1 female, age 36 ± 5 yr, weight 75 ± 6 kg, height 174 ± 4 cm; APACHE II score 15 ± 2). Seven to twelve days after trauma, patients were in relatively stable clinical and metabolic conditions. A continuous infusion of either saline (*protocol 1*) or rhGH (0.10 μg · kg^{-1} · min^{-1}; Genotropin, Pharmacia and Upjohn Stockholm, Sweden; *protocol 2*) was started at 1 PM and continued for 24 h. rhGH was infused directly into the femoral artery to reduce systemic hormone effects. The next day, a leg muscle metabolic study was performed from 8 AM to 1 PM. Thereafter, in the four patients previously infused with saline, rhGH infusion was started into the femoral artery and was continued for 24 h. In the other four patients previously treated with rhGH, a 24-h saline infusion was commenced and then the second metabolic study was performed during the last 5 h of either rhGH or saline administration.

Leg Metabolic Study

Indwelling catheters were placed in a central vein (subclavian or internal jugular) for isotope infusion and in the femoral artery and vein of one leg for blood sampling. The femoral artery catheter was also used for continuous infusion of rhGH and for primed continuous infusion of indocyanine green (Infracyanine, SERB, Paris, France) to measure leg blood flow (2–4, 6, 22). Indocyanine green recycling was assessed by measuring dye concentration in the left antecubital vein. Most of the catheters were placed for clinical purposes. At *hour 19* (8 AM) femoral venous blood samples were obtained to measure background amino acid enrichments and indocyanine green concentration. Then a primed continuous infusion of L-[5-^{15}N]glutamine (MassTrace, Woburn, MA) was started, followed at *hour 21* by L-[*ring*-$^{2}H_5$]phenylalanine (MassTrace) and L-[1-^{13}C]leucine (MassTrace). Tracer infusions were maintained constant throughout the experiment. The following tracer infusion rates(IR) and priming doses (PD) were used: L-[*ring*-$^{2}H_5$]phenylalanine: IR = 0.05 μmol · kg^{-1} · min^{-1}, PD = 2 μmol/kg; L-[1-^{13}C]leucine: IR = 0.08 μmol · kg^{-1} · min^{-1}, PD = 4.8 μmol/kg; L-[5-^{15}N]glutamine: IR = 0.35 μmol · kg^{-1} · min^{-1}, PD = 63 μmol/kg. Isotope infusions were not started simultaneously, because the equilibration period of each tracer varied (2). L-[5-^{15}N]glutamine required 5 h to reach steady state in muscle (2). L-[*ring*-$^{2}H_5$]phenylalanine and L-[1-^{13}C]leucine were infused for 3 h.

To measure leg blood flow, at *hour 23* a primed continuous infusion of indocyanine green dye (IR = 0.5 mg/min; PD = 5 mg) into the femoral artery was started and maintained for 30 min. During the last 15 min of indocyanine green infusion, four blood samples were taken every 5 min from the femoral and left antecubital vein for spectrophotometric determination of steady-state dye serum concentrations. The rate of leg plasma flow was calculated at steady state from the ratio between the dye infusion rate and the difference between serum dye concentrations in femoral and antecubital veins. Leg blood flow was calculated from the hematocrit. During the last 30 min of the intra-arterial rhGH or saline infusion, four blood samples were taken every 10 min from the femoral artery and vein to determine amino acid enrichments and concentrations. To allow sampling from the femoral artery, the rhGH or the saline infusion was stopped for <10 s and then quickly resumed. Blood samples were also taken from the femoral and left antecubital veins to determine local and systemic growth hormone concentrations, respectively. Insulin and insulin-like growth factor I (IGF-I) concentrations were measured in blood samples taken from the left antecubital vein. At *hour 24*, after the last blood sample was taken and before stopping the tracer and the rhGH or saline infusions, a muscle biopsy was taken to measure enrichments and concentrations of free amino acids and mRNA levels of cathepsin B, ubiquitin, and the glutamine synthetase enzyme. The biopsy was taken from the lateral portion of the vastus lateralis muscle ~20 cm above the knee with a Bergström biopsy needle (Stille, Stockholm, Sweden) (2–4, 6). Approximately 80–100 mg of muscle tissue were obtained with each biopsy. This procedure yields a sample of mixed skeletal muscle. Blood, visible fat, and connective tissue were quickly removed from the specimen, and the tissue was immediately frozen in liquid nitrogen and stored at −80°C for later analysis. Thereafter, in the four patients previously infused with saline, an rhGH infusion was started into the femoral artery and continued for 24 h. In the other four patients previously treated with rhGH, a 24-h saline infusion was commenced. During the last 5 h of either rhGH or saline administration, tracer infusion was performed, leg blood flow was measured, and blood samples and muscle biopsies were taken, as described.

Amino Acid Enrichments and Concentrations

Blood samples taken from the femoral artery and vein to determine amino acid enrichments and concentrations were collected in preweighed tubes containing 1% saponin. Simultaneously, a known amount of a homoserine solution was

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added to the tube as internal standard and thoroughly mixed. The blood was then precipitated with 15% sulfosalicylic acid (SSA). The tubes were weighed again, and the difference was recorded as blood volume after subtraction of the internal standard and SSA volumes. The supernatant was frozen for later analysis. To determine tracer enrichments, the *t*-butyldimethylsilyl derivatives were prepared as described (2).

Each tissue sample was weighed, and muscle protein was precipitated with 15% SSA. A known amount of a homoserine solution was added as internal standard and thoroughly mixed. The tissue was then homogenized and centrifuged, and the supernatant was collected. This procedure was repeated twice more. The pooled supernatant was frozen for later analysis. Muscle and whole blood SSA extracts were processed to determine free amino acid enrichments and concentrations by gas chromatography-mass spectrometry (Incos XL, Finnigan, Bremen, Germany) and HPLC (Beckman, Berkeley, CA), respectively. Mass spectrometry analysis was performed by electron impact ionization and selected ion monitoring for the *t*-butyldimethylsilyl derivatives of leucine ([mass-to-charge ratios (*m/e*) 302 and 303], phenylalanine (*m/e* 234 and 239) and glutamine (*m/e* 431 and 432). Data were expressed as a tracer-to-tracee ratio. Concentrations (nmol/ml) of free amino acids in blood and total muscle water were calculated as referenced (2). Measured values of enrichment and concentrations relative to total tissue water were corrected (2, 18) to obtain intracellular values. These corrections required the knowledge of amino acid concentration and enrichment in the interstitial fluid, as well as knowledge of the proportion between intra- and extracellular water in muscle. We assumed that amino acid enrichment and concentrations in the interstitial fluid equaled blood values in the femoral vein and that the ratio between intra- and extracellular water in muscle was 0.16, as previously determined in humans by the chloride method (2).

Calculation of Kinetic Parameters

At the whole body level, amino acid rates of appearance (R_a) were calculated by dividing isotope infusion rates by arterial enrichments. Because amino acid intakes were identical in the control studies and during rhGH infusions, changes in the R_a of the essential amino acids phenylalanine and leucine can be considered as markers of changes in whole body proteolysis. Whole body glutamine clearance was calculated by dividing the glutamine R_a by the arterial glutamine concentration.

The net leg balance for amino acids was calculated from the Fick principle

$$\text{net balance} = (C_A - C_V) \cdot \text{BF} \quad (1)$$

where C_A and C_V are whole blood amino acid concentrations in femoral artery and vein, respectively; BF is leg blood flow. A positive value indicates net uptake, whereas a negative value indicates net release. Skeletal muscle is considered to account largely for amino acid metabolism in the whole leg (2). In the steady-state condition of muscle free amino acid concentrations, amino acid uptake or release across the leg reflects the balance between intracellular production and disposal for that particular amino acid. Thus net phenylalanine, tyrosine, and lysine release from leg muscle are markers of net protein catabolism, because these amino acids are not synthesized or oxidized in muscle tissue (1, 26, 36). Furthermore, phenylalanine is not hydroxylated to tyrosine in muscle (1, 26, 36), whereas the kidney and the splanchnic bed together account for all of the whole body hydroxylation of this amino acid (32). In contrast, skeletal muscle is the main site of catabolism of the branched-chain amino acids leucine, valine, and isoleucine, and of synthesis of alanine from pyruvate and of glutamine from glutamate. We assumed that amino acids are released from proteolysis in proportion to their relative content in muscle protein (2–4, 6, 24). Thus the net rates of release from protein catabolism of glutamate, glutamine, alanine, and the branched-chain amino acids can be calculated from the net rate of phenylalanine release, corrected for the molar ratios glutamate/phenylalanine (1.87), glutamine/phenylalanine (2.05), alanine/phenylalanine (2.35), leucine/phenylalanine (3.10), isoleucine/phenylalanine (2.55), and valine/phenylalanine (1.77) determined in mixed human muscle protein (2, 24). Then, the rates of net alanine and glutamine synthesis (i.e., the differences between the rates of synthesis and nonprotein utilization of the amino acids) of net nonprotein disposal of glutamate (mainly to form glutamine) and of branched-chain amino acid catabolism can be calculated by subtracting from the total release or uptake of these amino acids the component accounted for by protein catabolism

$$\text{net alanine synthesis} = -[\text{net alanine balance} - (\text{net phenylalanine balance} \times 2.35)] \quad (2)$$

$$\text{net glutamine synthesis} = -[\text{net glutamine balance} - (\text{net phenylalanine balance} \times 2.05)] \quad (3)$$

$$\text{net nonprotein glutamate disposal} = [\text{net glutamate balance} - (\text{net phenylalanine balance} \times 1.87)] \quad (4)$$

$$\text{leucine catabolism} = [\text{net leucine balance} - (\text{net phenylalanine balance} \times 3.10)] \quad (5)$$

$$\text{isoleucine catabolism} = [\text{net isoleucine balance} - (\text{net phenylalanine balance} \times 2.55)] \quad (6)$$

$$\text{valine catabolism} = [\text{net valine balance} - (\text{net phenylalanine balance} \times 1.77)] \quad (7)$$

$$\text{total branched-chain amino acid catabolism} = \text{leucine catabolism} + \text{isoleucine catabolism} + \text{valine catabolism} \quad (8)$$

This calculated rate of branched-chain amino acid catabolism (i.e., nonprotein branched-chain amino acid disposal) is not equivalent to the actual rate of branched-chain amino acid oxidation; in fact, branched-chain amino acids are deaminated to the corresponding ketoacids before undergoing irreversible decarboxylation and oxidation. Some of these ketoacid molecules could escape intracellular metabolism and be released into the bloodstream. In our study, we did not measure the arteriovenous balance of branched-chain ketoacids across the leg to directly determine branched-chain amino acid oxidation. Nonetheless, the difference between the rates of branched-chain amino acid catabolism and oxidation is likely to be very small for two reasons. First, the arteriovenous difference across the leg of the leucine ketoacid α-ketoisocaproate is usually very small (33). Second, during leucine tracer infusion, there is a net uptake across the leg of the α-ketoisocaproate tracer derived from deamination of the leucine tracer (33).

Inward and outward amino acid transports are calculated as the rates of net amino acid movements from the femoral artery to muscle and from muscle to the femoral vein (2, 3, 6), respectively

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$$\text{inward amino acid transport} = \{[(E_M - E_V)/(E_A - E_M)] \times C_V + C_A\} \times BF \quad (9)$$

$$\text{outward amino acid transport} = \{[(E_M - E_V)/(E_A - E_M)] \times C_V + C_V\} \times BF \quad (10)$$

where E_A, E_V and E_M were amino acid enrichments in the femoral artery, femoral vein, and muscle, respectively.

Muscle protein synthesis and proteolysis were calculated as rates of intracellular phenylalanine disposal and appearance (2, 3, 6), respectively

$$\text{protein synthesis} = [(C_{A(PHE)} \times E_{A(PHE)} - C_{V(PHE)} \times E_{V(PHE)})/E_{M(PHE)}] \times BF \quad (11)$$

$$\text{proteolysis} = \{[(C_{A(PHE)} \times E_{A(PHE)} - C_{V(PHE)} \times E_{V(PHE)})/E_{M(PHE)}] - (C_{A(PHE)} - C_{V(PHE)})\} \times BF \quad (12)$$

where (PHE) indicates the values of phenylalanine concentrations and enrichments.

The absolute rate of glutamine de novo synthesis was calculated from the rate of total intracellular glutamine appearance and glutamine appearance from proteolysis. The latter is calculated from the rate of intracellular phenylalanine appearance from proteolysis (*Eq. 12*) and the molar ratio glutamine/phenylalanine in mixed muscle proteins (2)

$$\text{glutamine de novo synthesis} = \{[(C_{A(GLN)} \times E_{A(GLN)} - C_{V(GLN)} \times E_{V(GLN)})/E_{M(GLN)}] - (C_{A(GNL)} - C_{V(GNL)})\} \times BF - \{[(C_{A(PHE)} \times E_{A(PHE)} - C_{V(PHE)} \times E_{V(PHE)})/E_{M(PHE)}] - (C_{A(PHE)} - C_{V(PHE)})\} \times 2.05 \times BF \quad (13)$$

where (GLN) indicates the values of glutamine concentrations and enrichments.

Determination of Specific mRNA Levels

Muscle mRNA levels of cathepsin B (7), UbB polyubiquitin (7, 35), and glutamine synthetase (34) were determined by competitive RT-PCR (15). Ubiquitin is encoded in the human genome as a multigene family (35). Among the different ubiquitin genes, we assessed the UbB polyubiquitin gene, which codes for three direct repeats of the ubiquitin sequence (7, 35). Total RNA was extracted from 20–30 mg of muscle tissue by the guanidine thiocyanate procedure (7, 15). The quality and integrity of total RNA and its approximate concentration were evaluated by denaturing agarose gel electrophoresis and ethidium bromide staining. The presence of contamination from genomic DNA in the extracted total RNA was checked by amplification with primers for glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (see below). If contamination was detected, the samples were treated with RNase-free DNase I (10 U/μl) (Boehringer Mannheim, Mannheim, Germany) and extracted with phenol-chloroform-isoamylic alcohol.

Approximately 5 μg of the extracted total RNA were incubated with 100 ng of oligonucleotide NOT I-$(dT)_{18}$ (Pharmacia) for 10 min at 68°C. Then reverse transcription was performed at 42°C for 1 h using murine myeloblastosis virus reverse transcriptase (GIBCO BRL Life Technologies, Paisley, Scotland) in the presence of ribonuclease inhibitor RNASE BLOCK (Stratagene, La Jolla, CA).

Amplification of GAPDH cDNA was performed using the primers 5′ CCATCACCATCTTCCAGGAGCG 3′ (nucleotides 278–299 of file M33197 in GenBank) for the sense strand and 5′ ACGGAAGGCCATGCCAGTGA 3′ (762–743) for the antisense strand. Amplification of cathepsin B cDNA was performed using the primers 5′ GGGCACAACTTCTACAACGTGG 3′ (nucleotides 307–328 of file L16510 in GenBank) sense and 5′ GTGTGGATGCAGATGCGGTCA 3′ (551–531) antisense. The sense strand primer for UbB polyubiquitin cDNA amplification was 5′ CAGTCATGGCATTCGCAGTGCC 3′ (nucleotides 1789–1810 of file X04803 in GenBank), whereas oligonucleotide NOT I-$(dT)_{18}$ was used directly as antisense primer. The sense strand primer for glutamine synthetase cDNA was 5′ GACTTTGGAGTGATAGCAACC 3′ (nucleotides 810–830 of file Y00387 in GenBank) and primer 5′ GCAGTTGGCAGAGGGGCGACGA 3′ (1136–1157) for the antisense strand. Competitors for cathepsin B, UbB polyubiquitin, and glutamine synthetase were constructed by a recombinant PCR methodology, as already described for cathepsin B and UbB polyubiquitin (7, 15). Each competitor corresponding to the sequence amplified by the primers reported above, plus an insertion of 26 bp in the middle, was constructed by two separate PCR amplifications. The sequences of the internal primers for the glutamine synthetase competitor were as follows: 5′ CTTCGGAGAGAATCCCCTCAGCGGGAGGAGGCCATTGAGAAAC 3′ for the sense strand and 5′ CCGCTGAGGGGATTCTCTCCGAAGGATGTACTTCAGACCATTC 3′ for the antisense strand. The competitor for GAPDH quantification was the plasmid pBluGAPDH 260 (kindly donated by Prof. F. E. Baralle, ICGEB, Trieste, Italy) obtained from the pBluescript II KS vector (Pharmacia) (7, 15).

Quantitative PCR amplifications were performed by mixing scalar amounts of competitor DNA to the target cDNA followed by PCR amplification with the appropriate primer pairs. All amplifications were conducted in PCR buffer containing the two primers, the four dNTPs, 2.5 U of Taq DNA polymerase (Boehringer), 1 μl of cDNA, and 1 μl of appropriately diluted competitor DNA, using a DNA Thermo Cycler (Perkin-Elmer Cetus). Samples were submitted to 38 cycles of amplification. After amplification, PCR products were resolved on an 8% nondenaturing polyacrylamide gel, visualized under ultraviolet light after ethidium bromide staining, and photographed. Quantification of the amplification products was obtained by densitometric scanning on photographs of the ethidium bromide-stained gels. According to the principles of competitive PCR, the ratio between the amount of the PCR products for the target cDNA and that of the competitor DNA is linearly correlated with the initial amount of cDNA in the reaction. To verify such a linear correlation, we plotted the densitometric ratios between the PCR products of scalar amounts of competitor DNA (0 pg, 0.1 pg, 0.5 pg, 1 pg, 2 pg) and fixed amounts of target glutamine synthetase cDNA with the initial amount of competitor DNA in the reaction. The correlation coefficient (r^2) was 0.9989, and the equation was $y = 2.55 \times +0.04$.

Cathepsin B, UbB polyubiquitin, and glutamine synthetase mRNA levels were calculated from the ratios between cathepsin B and GAPDH cDNA, between UbB polyubiquitin and GAPDH cDNA, and between glutamine synthetase and GAPDH cDNA quantities in the same sample. The units of cathepsin B, UbB polyubiquitin, or glutamine synthetase mRNA content are expressed as %GAPDH mRNA

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levels. It is assumed that rhGH administration does not modify GAPDH mRNA levels in skeletal muscle of trauma patients (19, 25). The variation coefficient for GAPDH mRNA content for four different samples from the same muscle specimen was 3.2% of the mean when the samples were processed on the same day and 4.3% of the mean when the samples were processed on different days. The two muscle samples from a single subject, whether studied in basal conditions or during rhGH infusion, were always processed together.

Data Presentation and Statistics

All data are expressed as means ± SE. Because the values of leg blood flow, amino acid concentrations, and kinetics were not significantly different in the control studies performed before rhGH infusion (*protocol 1*) and 24 h after rhGH discontinuation (*protocol 2*), the results obtained in the two control studies were pooled together. Then, the values of leg blood flow, amino acid concentrations, and kinetics obtained during rhGH infusions (*protocols 1* and *2*) were compared with those in the control studies (*protocols 1* and *2*) by means of Student's *t*-test for paired samples. The effects of rhGH infusion (*protocol 1*) and rhGH discontinuation (*protocol 2*) on muscle levels of selected mRNAs were assessed separately in the two protocols by means of Student's *t*-test for paired samples. $P < 0.05$ was considered statistically significant.

RESULTS

Before rhGH infusion, plasma growth hormone concentration was 3 ± 1 ng/ml (*protocol 1*) and increased to 91 ± 9 ng/ml in the femoral vein and to 39 ± 3 ng/ml in the antecubital vein during rhGH infusion (*protocols 1* and *2*). After rhGH discontinuation, plasma growth hormone concentration decreased to 3 ± 1 ng/ml (*protocol 2*). Plasma insulin concentration increased ($P < 0.05$) during rhGH infusion (*protocol 1*) from 77 ± 22 to 141 ± 20 μU/ml. Insulin concentration did not change significantly after rhGH discontinuation (*protocol 2*) (from 131 ± 22 to 122 ± 33 μU/ml). Mean values of insulin concentrations were not significantly different in the pooled control studies (99 ± 20 μU/ml) and during rhGH infusions (136 ± 14 μU/ml; *protocols 1* and *2*). Plasma IGF-I concentration tended to increase ($P = 0.08$) during rhGH infusion (*protocol 1*) from 93 ± 14 to 153 ± 27 ng/ml. IGF-I concentration did not significantly change after rhGH discontinuation (*protocol 2*; from 188 ± 15 to 187 ± 17 ng/ml). Mean values of IGF-I concentrations were not significantly different in the pooled control studies (140 ± 21 ng/ml) and during rhGH infusions (170 ± 16 ng/ml; *protocols 1* and *2*).

Leg blood flow was similar in the control studies (5.25 ± 0.62 $ml \cdot min^{-1} \cdot 100$ ml leg vol^{-1}) and during rhGH infusions (5.01 ± 0.83 $ml \cdot min^{-1} \cdot 100$ ml leg vol^{-1}). The values of amino acid concentrations in femoral artery and vein were not significantly different in the control studies and during rhGH infusion (Table 1). In skeletal muscle, intracellular concentrations of most amino acids tended to decrease during rhGH infusion. Intramuscular glutamine concentrations decreased ($P = 0.07$) by ~10%. Table 2 shows the values of amino acid balance across the leg in the control studies and during rhGH infusion. In the basal studies, the net balance of most amino acids was negative and significantly different from zero. Total amino acid release from leg muscle decreased after rhGH infusion by ~55%. In particular, net phenylalanine, tyrosine, and lysine release, which are markers of net muscle protein catabolism, significantly decreased by ~45–55% during rhGH infusion. Glutamine release also decreased significantly after rhGH infusion.

Table 3 shows the effects of rhGH infusion on selected parameters of muscle amino acid metabolism derived from leg arteriovenous balance of unlabeled amino acids (see *Calculation of Kinetic Parameters*). rhGH decreased the rates of net nonprotein glutamate

Table 1. *Amino acid concentrations in femoral artery and vein and in leg muscle during saline and rhGH infusion*

	Femoral Artery		Femoral Vein		Leg Muscle	
	Saline	rhGH	Saline	rhGH	Saline	rhGH
Nonessential amino acids						
Glutamine	430 ± 36	437 ± 31	478 ± 34	464 ± 30	4573 ± 320	4090 ± 395
Glutamate	231 ± 20	229 ± 21	209 ± 19	208 ± 22	2545 ± 445	2218 ± 342
Alanine	231 ± 14	239 ± 22	274 ± 12	280 ± 22	1644 ± 145	1591 ± 172
Asparagine	58 ± 3	57 ± 2	64 ± 3	61 ± 2	300 ± 45	248 ± 40
Aspartate	92 ± 6	93 ± 5	97 ± 8	97 ± 6	370 ± 47	340 ± 44
Glycine	336 ± 25	327 ± 31	358 ± 24	337 ± 31	1281 ± 69	1259 ± 120
Serine	114 ± 8	118 ± 5	118 ± 7	119 ± 5	531 ± 28	477 ± 32
Tyrosine	52 ± 4	50 ± 5	58 ± 4	54 ± 4	146 ± 11	129 ± 13
Arginine	291 ± 44	370 ± 8	308 ± 45	369 ± 7	196 ± 24	206 ± 34
Histidine	61 ± 3	59 ± 4	69 ± 2	63 ± 4	207 ± 12	216 ± 52
Essential amino acids						
Isoleucine	82 ± 4	82 ± 4	85 ± 5	83 ± 4	219 ± 14	198 ± 17
Leucine	140 ± 10	135 ± 12	139 ± 10	133 ± 10	263 ± 28	226 ± 25
Valine	236 ± 17	201 ± 12	227 ± 15	193 ± 10	323 ± 27	272 ± 21
Phenylalanine	94 ± 8	89 ± 10	100 ± 8	92 ± 10	186 ± 6	167 ± 6
Threonine	136 ± 13	120 ± 14	153 ± 11	132 ± 13	559 ± 58	482 ± 60
Lysine	164 ± 14	141 ± 12	182 ± 13	152 ± 11	494 ± 42	483 ± 57

Values are means ± SE. Units are nmol/ml whole blood or intracellular water. rhGH, recombinant human growth hormone.

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Table 2. *Leg balance of amino acids during saline and rhGH infusion*

	Saline	rhGH
Nonessential amino acids		
Glutamine	−258 ± 44*	144 ± 29*†
Glutamate	131 ± 13*	103 ± 15*
Alanine	−221 ± 29*	−200 ± 33*
Asparagine	−32 ± 8*	−22 ± 6*†
Aspartato	−27 ± 9*	−20 ± 13*
Glycine	−106 ± 7*	−55 ± 16*†
Serine	−18 ± 4*	−4 ± 5
Tyrosine	−34 ± 8*	−14 ± 5*†
Arginine	−82 ± 17*	12 ± 39
Histidine	−40 ± 9*	−22 ± 7*
Essential amino acids		
Isoleucine	−14 ± 5*	−7 ± 7
Leucine	7 ± 19	3 ± 12
Valine	−4 ± 18	−9 ± 11
Phenylalanine	−28 ± 4*	−15 ± 3*†
Threonine	−79 ± 16*	−51 ± 16*
Lysine	−82 ± 23*	−45 ± 20†
Total amino acids	−854 ± 105*	−389 ± 124*

Values are means ± SE and are expressed as nmol · min^{-1} · 100 ml leg vol^{-1}. Negative numbers indicate net release. *Significantly different from zero; †$P < 0.05$ rhGH vs. saline.

disposal (mainly to form glutamine) and of net glutamine synthesis from glutamate, whereas the hormone infusion did not change the rate of net alanine synthesis. rhGH infusion decreased the rates of catabolism of the branched-chain amino acids leucine (from 93 ± 18 to 49 ± 12 nmol · min^{-1} · 100 ml leg vol^{-1}; $P < 0.05$), valine (from 46 ± 18 to 18 ± 8 nmol · min^{-1} · 100 ml leg vol^{-1}; $P < 0.05$), and isoleucine (from 57 ± 11 to 31 ± 5 nmol · min^{-1} · 100 ml leg vol^{-1}; $P < 0.05$). The rate of catabolism of total branched-chain amino acids decreased by ~50% during rhGH infusion (Table 3).

Table 4 shows the values of amino acid enrichments in femoral artery and vein and in muscle tissue. rhGH infusion tended to increase amino acid enrichments in all sampled compartments. rhGH administration significantly ($P < 0.001$) decreased the rate of whole body phenylalanine R_a from 1.34 ± 0.07 to 1.17 ± 0.08 μmol · kg^{-1} · min^{-1} and tended to decrease the rate of whole body leucine R_a from 2.92 ± 0.26 to 2.72 ± 0.22 μmol · kg^{-1} · min^{-1}. rhGH administration tended also to decrease the rates of whole body glutamine R_a (from 8.01 ± 0.90 to 6.95 ± 0.73 μmol · kg^{q-1} · min^{-1}) and clearance (from 194 ± 24 to 167 ± 24 ml · kg^{-1} · min^{-1}).

Figure 1 shows the rates of intracellular phenylalanine disposal for protein synthesis and release from protein degradation during saline and rhGH infusions.

Table 3. *Selected parameters of leg muscle amino acid metabolism during saline and rhGH infusion*

	Saline	rhGH
Net alanine de novo synthesis	156 ± 28	165 ± 29
Net glutamine de novo synthesis	201 ± 43	113 ± 26*
Net nonprotein glutamate disposal	197 ± 20	139 ± 22*
Total branched-chain amino acid catabolism	196 ± 41	98 ± 20*

Values are means ± SE and are expressed as nmol · min^{-1} · 100 ml leg vol^{-1}. *$P < 0.05$ rhGH vs. saline.

Table 4. *Amino acid enrichments in femoral artery and vein and in leg muscle during saline and rhGH infusion*

	Femoral Artery	Femoral Vein	Leg Muscle
Phenylalanine			
Saline	0.0381 ± 0.0021	0.0344 ± 0.0019	0.0248 ± 0.0025
rhGH	0.0442 ± 0.0031*	0.0383 ± 0.0024*	0.0326 ± 0.0027*
Leucine			
Saline	0.0291 ± 0.0027	0.0236 ± 0.0015	0.0165 ± 0.0021
rhGH	0.0307 ± 0.0025	0.0237 ± 0.0024	0.0208 ± 0.0031*
Glutamine			
Saline	0.0468 ± 0.0040	0.0337 ± 0.0031	0.0252 ± 0.0030
rhGH	0.0535 ± 0.0043	0.0439 ± 0.0044*	0.0299 ± 0.0039

Values are means ± SE and are expressed as tracer/tracee ratio. *$P < 0.05$ rhGH vs. saline.

rhGH almost doubled the rate of protein synthesis, whereas the hormone infusion did not significantly change the rate of protein degradation. Also, the rate of intracellular leucine release from protein degradation was not significantly different during saline (220 ± 40 nmol · min^{-1} · 100 ml leg vol^{-1}) and rhGH (240 ± 42 nmol · min^{-1} · 100 ml leg vol^{-1}) infusions. In addition, muscle mRNA levels of cathepsin B and UbB polyubiquitin did not significantly change after rhGH infusion (*protocol 1*; from 17 ± 2 to 19 ± 9% of GAPDH mRNA and from 4.9 ± 1.8 to 4.0 ± 0.2% of GAPDH mRNA, respectively) and after rhGH discontinuation (*protocol 2*; from 24 ± 9 to 28 ± 9% of GAPDH mRNA and from 10.0 ± 1.8 to 8.7 ± 3.4% of GAPDH mRNA, respectively).

Table 5 shows the rates of inward and outward transport of phenylalanine, leucine, and glutamine in skeletal muscle during saline and rhGH infusions. rhGH significantly increased the rates of inward transport of the essential amino acids leucine and phenylalanine, whereas the rates of glutamine transport were decreased by rhGH in both the outward and the inward directions. Figure 2 shows the isotopically derived rates of intramuscular glutamine de novo synthesis during saline and rhGH infusions. The absolute rate of glutamine de novo synthesis was 44 ± 11% lower

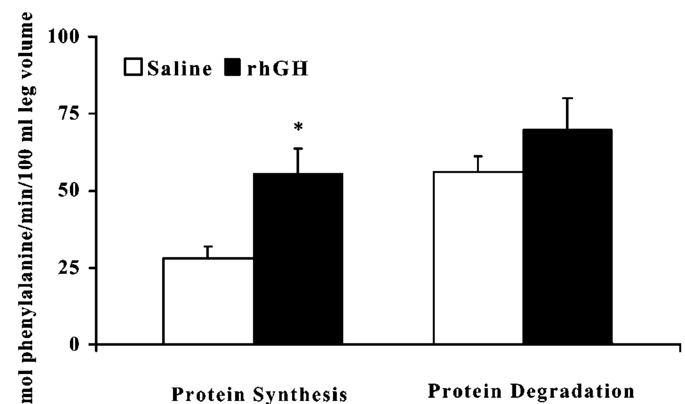

Fig. 1. Rates of protein synthesis and degradation in leg skeletal muscle of trauma patients during saline or recombinant human growth hormone (rhGH) infusion. *$P < 0.05$ rhGH vs. saline.

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Table 5. *Transmembrane amino acid transport*

	Phenylalanine	Leucine	Glutamine
Inward transport			
Saline	119 ± 20	303 ± 68	1316 ± 276
rhGH	228 ± 53*	558 ± 117*	848 ± 170*
Outward transport			
Saline	147 ± 19	296 ± 73	1574 ± 314
rhGH	243 ± 53	556 ± 122*	992 ± 192*

Values are means ± SE and are expressed as $nmol \cdot min^{-1} \cdot 100$ ml leg vol^{-1}. $*P < 0.05$ rhGH vs. saline.

during rhGH than during saline infusions (*protocols 1* and *2*). In contrast, rhGH infusion (*protocol 1*) significantly ($P = 0.03$) increased glutamine synthetase mRNA levels from 26 ± 14 to 51 ± 12% of GAPDH mRNA. In the patients studied according to *protocol 2*, glutamine synthetase mRNA did not change significantly after rhGH discontinuation (from 22 ± 6 to 27 ± 12% of GAPDH mRNA).

DISCUSSION

In skeletal muscle of hypercatabolic traumatized patients, 24-h rhGH infusion *1*) increased muscle protein synthesis without significantly affecting protein degradation, *2*) suppressed the rates of branched-chain amino acid catabolism, *3*) increased the rates of transmembrane transport of the essential amino acids leucine and phenylalanine, whereas it decreased membrane transport of glutamine, *4*) decreased the rates of de novo synthesis of glutamine, and *5*) decreased the rates of release of total essential and nonessential amino acids from skeletal muscle.

Patients were studied during the second week after trauma in relatively stable clinical and metabolic conditions. They were hypercatabolic, as shown by the net efflux of essential amino acids from skeletal muscle despite a continuous combined parenteral and enteral artificial nutrition. We have shown that rhGH administration significantly reduces the net muscle protein loss of patients. This anticatabolic effect of rhGH is completely accounted for by an acceleration of protein synthesis. Previous studies have demonstrated a selective increase in muscle protein synthesis induced by rhGH administration in humans (12, 13). It is possible, however, that many of the observed anabolic effects of rhGH are mediated via the stimulation of endogenous IGF-I synthesis, which may exert its effects via endocrine and/or paracrine mechanisms. In humans, IGF-I administration promoted protein anabolism both by stimulating protein synthesis and by inhibiting protein degradation both in muscle and at the whole body level (10, 11). In our study, rhGH administration did not result in significant modifications of the rates of muscle protein degradation. The effects of rhGH on protein degradation were evaluated with different approaches. Stable isotopes and mass spectrometry techniques were used to measure the rate of protein degradation in skeletal muscle as the rate of appearance of the essential amino acids phenylalanine and leucine in muscle cells.

With competitive PCR, we determined in skeletal muscle the mRNA levels of cathepsin B and ubiquitin as markers of nonmyofibrillar and myofibrillar protein degradation, respectively. It is known that growth hormone has the potential to decrease proteolysis, possibly through stimulation of IGF-I synthesis (10, 11). In this study, we did not observe any decrease in muscle proteolysis: we observed a substantial stimulation of protein synthesis and a tendency toward decreasing intracellular concentration of total amino acids. It is likely that the rate of degradation was maintained and possibly increased to prevent a further decrease in amino acid concentrations.

In contrast to the rhGH effects on muscle proteolysis, at the whole body level, the rate of phenylalanine appearance was significantly lower during the hormone infusion. Such a decrease of a marker of whole body proteolysis clearly indicates a systemic effect of the intra-arterial rhGH infusion. In fact, in the systemic circulation, not only growth hormone but also insulin and IGF-I increased during the local rhGH infusion. It is likely that such a decrease of whole body proteolysis could have been mediated by insulin and/or IGF-I. Furthermore, such systemic hormonal changes could also have contributed to the stimulation of muscle protein synthesis observed in our study (3, 6, 11).

In agreement with previous observations in animals (20, 23), this study shows that rhGH infusion in traumatized patients accelerates the rates of transmembrane transport of the essential amino acids leucine and phenylalanine. This effect was independent of changes of leg blood flow and arterial amino acid concentrations. This rhGH-mediated increased ability of transmembrane systems to transport essential amino acids confirms previous observations in vitro (20, 23) and represents a novel observation in vivo. This acceleration of transport of essential amino acids may have contributed to the anabolic effect of rhGH by increasing intracellular amino acid availability for protein synthesis. However, the slight decrease in intracellular amino acid concentrations suggests that the stimulation of amino acid transport is not the primary mechanism for stimulation of synthesis. In contrast, transport acceleration may represent a compensatory

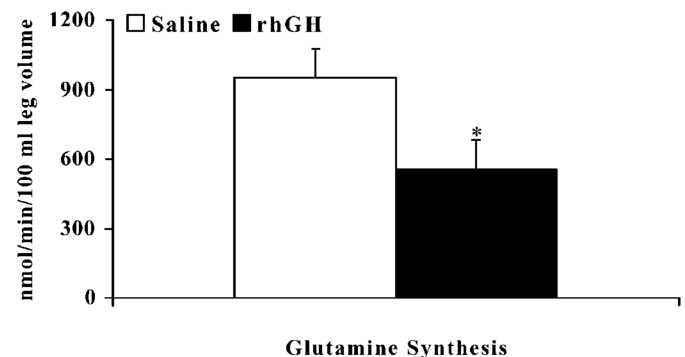

Fig. 2. Absolute rate of de novo glutamine synthesis in leg skeletal muscle of trauma patients during saline or rhGH infusion. $*P < 0.05$ rhGH vs. saline.

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mechanism to prevent depletion of intracellular amino acid pools.

Besides stimulating protein synthesis, growth hormone suppressed the rate of catabolism of the branched-chain amino acids leucine, isoleucine, and valine. This effect has been reported by several other authors using isotopic tracers of leucine at the whole body level (8, 12).

In this study, the anticatabolic growth hormone effects on protein and branched-chain amino acid metabolism were paralleled by a suppression of the rate of de novo muscle glutamine production. De novo muscle glutamine production was determined either as absolute intracellular synthesis by stable isotopes or as net rate of synthesis appearing in the circulation without stable isotopes. With both methods, muscle glutamine production decreased by ~50% during rhGH infusion. Immediate precursors of glutamine synthesis are glutamate and free ammonia, whereas precursors for glutamate synthesis are α-ketoglutarate and amino-nitrogen from the branched-chain amino acids (9). The rates of branched-chain amino acid catabolism and of nonprotein utilization of glutamate, which is mainly for glutamine synthesis, decreased after rhGH infusion. Thus a decreased glutamine de novo synthesis could be secondary to a decreased glutamate availability from reduced transamination of the branched-chain amino acids with α-ketoglutarate. The fact that mRNA levels of glutamine synthetase (the key enzyme for glutamine synthesis) were found to be increased after rhGH infusion in the present study, as well as in previous studies in animals (29), supports the hypothesis that the growth hormone-mediated decrease in glutamine synthesis was determined by decreased precursor availability. Gene expression of glutamine synthetase may increase after rhGH infusion to compensate for reduced glutamine precursor availability.

In our study, besides a suppression of the rate of glutamine production, we observed a decrease of glutamine transmembrane outward transport from skeletal muscle, which prevented excessive depletion of the intracellular glutamine pool in skeletal muscle. Previously, Hammarqvist et al. (17) showed that rhGH administration prevented the decrease in muscle free glutamine typically observed after surgical trauma. We may speculate that, in their study, an rhGH-mediated decrease of outward glutamine transport prevailed over the effect on glutamine production. Consequently, glutamine concentration tended to increase during rhGH administration.

Glutamine and alanine constitute the major carriers of nitrogen among body tissues (2). In skeletal muscle, these amino acids are constantly being synthesized and released into the bloodstream (2). In severe trauma, alanine release from muscle is greatly accelerated, whereas glutamine release was found to be increased or unchanged (5). Our results indicate that rhGH administration selectively decreases the rates of synthesis and release of glutamine, whereas alanine synthesis did not change during the hormone administration.

In our experimental protocol, the control study was performed either before rhGH administration (*protocol 1*) or 24 h after the hormone discontinuation (*protocol 2*). This approach was adopted to account for time-related changes of muscle metabolism after trauma and for potential interference between two close stable isotope infusions. However, in the control studies of *protocols 1* and *2*, the whole body hormonal pattern tended to be different. In *protocol 1*, local rhGH infusion tended to increase systemic concentrations of both insulin and IGF-I; in the control study of *protocol 2*, despite the fact that circulating growth hormone returned to basal levels, both insulin and IGF-I concentrations failed to decline after rhGH discontinuation. However, this does not seem to constitute a problem for evaluating the rhGH effects on muscle protein and glutamine kinetics. In fact, the values of amino acid concentrations and kinetics were not significantly different in the control studies performed before rhGH infusion (*protocol 1*) and 24 h after rhGH discontinuation (*protocol 2*). Furthermore the rhGH-mediated changes of amino acid kinetics were similar in *protocols 1* and *2*. Protein synthesis increased by 137 ± 0.68% after rhGH infusion (*protocol 1*) and decreased by 113 ± 0.42% after rhGH discontinuation (*protocol 2*). Branched-chain amino acid catabolism decreased by 41 ± 7% after rhGH infusion (*protocol 1*) and increased by 42 ± 12% after rhGH discontinuation (*protocol 2*). Glutamine de novo synthesis decreased by 58 ± 14% after rhGH infusion (*protocol 1*) and increased by 31 ± 15% after rhGH discontinuation (*protocol 2*). It is likely, therefore, that the observed changes of protein and glutamine kinetics were directly mediated by an increase of growth hormone concentration and not by a secondary stimulation of insulin and IGF-I secretions.

In contrast to the rhGH-mediated changes in amino acid kinetics, muscle mRNA levels of glutamine synthetase significantly increased after rhGH infusion (*protocol 1*) but failed to decline after rhGH discontinuation (*protocol 2*). Several potential explanations may account for such a discrepancy between *protocols 1* and *2*. *1*) Growth hormone induction of the glutamine synthetase gene may continue for many hours after the infusion has been discontinued. *2*) Glutamine synthetase mRNA could be very stable. *3*) Induction of the glutamine synthetase gene might be mediated by the secondary stimulation of insulin and/or IGF-I secretion, which also failed to decline in *protocol 2*. Finally, *4*) a hormone-mediated change of the housekeeping gene GAPDH is unlikely, because this change would have also affected the determination of mRNA levels of cathepsin B and of UbB polyubiquitin, which did not change after rhGH infusion in either *protocol 1* or *protocol 2*. Whatever the reason for the discrepancy between *protocols 1* and *2*, the results of *protocol 1* confirm the ability of the growth hormone to induce in human skeletal muscle the glutamine synthetase gene previously shown in different animal tissues (29).

To calculate intracellular enrichments and concentrations in skeletal muscle, we assumed a ratio of 0.16

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between the extra- and intracellular spaces in muscle samples. This value had been obtained previously in normal human subjects (2). Nonetheless, despite the fact that none of our patients showed clinical evidence of changes in fluid retention during the study, we cannot exclude the possibility that growth hormone could have slightly increased extracellular space volume in muscle tissue. In fact, sodium and water retention are well recognized side effects of rhGH administration (16). We therefore evaluated the potential effects of changes in the ratio between the extra- and intracellular compartments on the calculated kinetic parameters of protein and glutamine metabolism. When such a ratio was increased by 100% over the assumed initial value of 0.16, the changes in protein synthesis and degradation, glutamine de novo synthesis, and amino acid transport were $<5\%$. It is unlikely, therefore, that growth hormone-mediated changes in extracellular fluid in muscle could have affected the conclusions of our study.

Takala et al. (31) recently reported the results of two large multicenter studies indicating an increased morbidity and mortality in critically ill patients treated with high doses of growth hormone. Multiple organ failure and septic shock or uncontrolled infections were the main causes of death, suggesting that a modulation of the immune system or gut function was involved. However, the reason for such a deleterious effect of growth hormone is unclear. Our study describes a potential side effect of rhGH administration in critically ill patients. In these patients, glutamine is an essential substrate for rapidly dividing cells in the immune system and in the intestinal mucosa, as well as for glutathione synthesis in the liver. Skeletal muscle is the main tissue involved in glutamine de novo synthesis. In our patients, whole body skeletal muscle released ~19 g of glutamine per day into the bloodstream before rhGH administration [to extrapolate the data to whole body skeletal muscle (33), the data for one leg were multiplied by four]. After rhGH administration, glutamine release from skeletal muscle decreased by ~50%, whereas at the whole body level, glutamine clearance tended to decrease by ~15%, despite the fact that the highest growth in hormone levels was achieved in only one leg. We may speculate, therefore, that in a clinical setting, rhGH therapy could decrease systemic glutamine availability and have negative effects on the immune system and gut function. The obvious solution for this potential side effect of growth hormone treatment in critically ill patients is to simultaneously administer exogenous glutamine to offset the decreased availability of the endogenous amino acid.

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