Background: Discovery of the central role of hepcidin in body iron regulation has shed new light on the pathophysiology of iron disorders. Information is lacking on newer analytical approaches to measure hepcidin in serum and urine. Recent reports on the measurement of urine and serum hepcidin by surface-enhanced laser-desorption/ionization time-of-flight mass spectrometry (SELDI-TOF MS) necessitate analytical and clinical evaluation of MS-based methodologies.

Methods: We used SELDI-TOF MS, immunocapture, and tandem MS to identify and characterize hepcidin in serum and urine. In addition to diagnostic application, we investigated analytical reproducibility and biological and preanalytical variation for both serum and urine on Normal Phase 20 and Immobilized Metal Affinity Capture 30 ProteinChip arrays. We obtained samples from healthy controls and patients with documented iron-deficiency anemia, inflammation-induced anemia, thalassemia major, and hereditary hemochromatosis.

Results: Proteomic techniques showed that hepcidin-20, -22, and -25 isoforms are present in urine. Hepcidin-25 in serum had the same amino acid sequence as hepcidin-25 in urine, whereas hepcidin-22 was not detected in serum. The interarray CV was 15% to 27%, and interspot CV was 11% to 13%. Preliminary studies showed that hepcidin-25 differentiated disorders of iron metabolism. Urine hepcidin is more affected by multiple freeze-thaw cycles and storage conditions, but less influenced by diurnal variation, than is serum hepcidin.

Conclusion: SELDI-TOF MS can be used to measure hepcidin in both serum and urine, but serum requires a standardized sampling protocol.

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**Materials and Methods**

**STUDY PARTICIPANTS**

Study participants included a control population of healthy volunteers (laboratory personnel), hereditary hemochromatosis (HFE<sup>+</sup> C282Y homozygous) patients cross-sectionally selected from a family screening program (various stages of phlebotomy treatment), iron deficiency anemia patients (Hb ≤ 8.3 mmol/L men, ≤ 7.3 mmol/L women; mean corpuscular volume ≤ 80 fl; ferritin ≤ 10 μg/L), and thalassemia major patients treated with chelation therapy. The patients were recruited by their physicians during outpatient clinic visits (all in Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands, except for the thalassemia major patients, who were in Ospedale Sant'Eugenio, Rome, Italy). Endotoxemia samples from volunteers injected with lipopolysaccharide were selected from a human endotoxemia project (10). Written informed consent was obtained from all study participants, according to the Declaration of Helsinki. Characteristics of the study participants are shown in Table 1. In addition, collaborators from several medical centers in The Netherlands provided urine and serum samples from 3 patients with distinct forms of hereditary hemochromatosis not associated with the hemochromatosis (HFE) gene [Online Mendelian Inheritance in Man (OMIM) type 2a, homozygous G320V HJV variation (11); OMIM type 4, N144H-caused ferroportin disease (12)]. Characteristics of these patients are shown in Table 1 in the Data Supplement that accompanies the online version of this article at http://www.clinchem.org/content/vol53/issue4.

*<sup>4</sup> Human gene: HFE, hemochromatosis.*

We collected samples randomly between December 2005 and June 2006, at no specified time of day, except from the endotoxemia patients, from whom samples were collected according to a tight time schedule (10, 13). Urine and blood samples were centrifuged immediately after collection, divided into aliquots to avoid multiple freeze-thaw cycles, and stored at −80 °C. We performed the hepcidin assay within 2 months after collection.

**LABORATORY MEASUREMENTS**

Using an Abbott Aeroset analyzer, we measured total serum iron and latent iron binding capacity by the ascorbate/FerroZine colorimetric method, urine creatinine by enzymatic/colorimetric detection (Roche Diagnostics), and C-reactive protein by immunologic agglutination detection with latex-coupled polyclonal anti-C-reactive protein antibodies (Abbott Laboratories). We quantified serum ferritin by a solid-phase, 2-site chemiluminescent immunometric assay (Immulite 2000 and 2500, Diagnostic Products Corp.) and routine hematology characteristics by use of a Sysmex XE-2100 analyzer.

**SELDI-TOF MS**

We performed nonblinded hepcidin measurements by use of SELDI-TOF MS as previously reported (8). In brief, a 5-μL sample was applied to Immobilized Metal Affinity Capture 30 (IMAC30), Normal Phase 20 (NP20), or cation exchange ProteinChip arrays (CM10), all equilibrated with appropriate buffers according to the manufacturer’s instructions (Ciphergen Biosystems). Loaded arrays were incubated in a humidity chamber for 30 min and then washed according to the manufacturer’s instructions and

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**Table 1. Characteristics of participants who provided sample material for assay validation.**

<table>
<thead>
<tr>
<th>n</th>
<th>Control</th>
<th>Endotoxemia (model)</th>
<th>Iron deficiency anemia</th>
<th>Thalassemia major&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Hereditary hemochromatosis&lt;sup&gt;c&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex (male:female)</td>
<td>20</td>
<td>28</td>
<td>6</td>
<td>5</td>
<td>14</td>
</tr>
<tr>
<td>Age, years</td>
<td>44 (24–62)</td>
<td>47 (14–61)</td>
<td>35 (25–44)</td>
<td>56 (23–82)</td>
<td></td>
</tr>
<tr>
<td>Hemoglobin, mmol/L</td>
<td>8.7 (7.8–11.0)</td>
<td>NA</td>
<td>6.3 (6.1–7.3)</td>
<td>9.3 (7.5–12.0)</td>
<td></td>
</tr>
<tr>
<td>MCV, fL</td>
<td>88 (84–93)</td>
<td>NA</td>
<td>77 (76–79)</td>
<td>86 (78–88)</td>
<td></td>
</tr>
<tr>
<td>Serum iron (Fe), μmol/L</td>
<td>19 (9–38)</td>
<td>6 (4–7)</td>
<td>52 (47–62)</td>
<td>22 (10–48)</td>
<td></td>
</tr>
<tr>
<td>Fe/TIBC, TS, %</td>
<td>35 (14–73)</td>
<td>8 (5–10)</td>
<td>98 (93–100)</td>
<td>56 (21–100)</td>
<td></td>
</tr>
<tr>
<td>Ferritin, μg/L</td>
<td>60 (11–191)</td>
<td>6 (6–10)</td>
<td>784 (272–1710)</td>
<td>64 (28–1361)</td>
<td></td>
</tr>
<tr>
<td>C-reactive protein, mg/L</td>
<td>&lt;5</td>
<td>&lt;5</td>
<td>&lt;5</td>
<td>&lt;5</td>
<td></td>
</tr>
<tr>
<td>Urinary hepcidin-25 (NP20), M Int/mmol Cr</td>
<td>0.52 (0.09–2.97)</td>
<td>0.01 (0.01–0.02)</td>
<td>0.21 (0.04–0.98)</td>
<td>0.15 (0.02–1.25)</td>
<td></td>
</tr>
<tr>
<td>Urinary hepcidin-25 (IMAC30), M Int/mmol Cr</td>
<td>1.45 (0.52–7.83)</td>
<td>0.10 (0.01–0.19)</td>
<td>0.59 (0.24–2.96)</td>
<td>0.66 (0.08–4.50)</td>
<td></td>
</tr>
<tr>
<td>Serum hepcidin-25 (IMAC30), M Int/L</td>
<td>4.38 (0.58–9.95)</td>
<td>0.41 (0.35–0.60)</td>
<td>0.28 (0.18–2.42)</td>
<td>1.60 (0.19–9.39)</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> Data are median (range).
<sup>b</sup> Cross-sectional selection of thalassemia major patients with variable transfusion history and treated with different iron chelators (desferrioxamine and/or deferiprone).
<sup>c</sup> Cross-sectional selection of homozygous C282Y patients from family study; 11 patients are under phlebotomy treatment.
<sup>d</sup> NA, not available; TIBC, total iron binding capacity; M Int/mmol Cr, megaintensity/mmol creatinine.
air-dried for 15 min. Finally, 1 μL energy-absorbing matrix (EAM), made up of a 12.5 g/L solution of sinapinic acid in 500 mL/L acetonitrile (ACN) containing 5 mL/L trifluoroacetic acid (TFA), was applied twice onto each spot surface with the use of polymer-free polypropylene pipette tips and allowed to air-dry for 5 min. Mass-to-charge (m/z) spectra were generated using a Ciphergen Protein Biology System llc TOF mass spectrometer at laser intensity 180 (NP20 and CM10) or 175 (IMAC30); detector sensitivity 9; high mass to acquire 50 kDa; optimization interval 1500 to 10 000 Da. External mass calibration was performed with a mixture of synthetic human hepcidin-25 peptide (2789.4 Da, Peptides International), hepcidin-22, and hepcidin-20 (2436.1 and 2191.8 Da, respectively; kindly provided by E. Nemeth, University of California, Los Angeles). Peak annotation was performed with Ciphergen ProteinChip Software version 3.2.0. From unpublished experiments we found that for serum and urine, normalization to total ion current (TIC) did not improve the hepcidin measurements and was therefore not applied in this study. Urine hepcidin measurements showed a relationship with TIC and total peptide content, which was predominated by hepcidin under the applied experimental conditions and instrumental settings (data not shown). Consequently, normalization of urine hepcidin values to TIC leads to loss of differentiation between samples. In contrast, due to the relatively stable protein content of serum samples, the serum hepcidin concentrations did not significantly change upon normalization to TIC (unpublished observations). Although the reabsorption and excretion characteristics of hepcidin are unclear, we used urinary creatinine to normalize all peak intensities for hepcidin-25 in urine. Normalization on creatinine is a prerequisite for comparison of urine hepcidin measurements because it is the best method to correct for the highly fluctuating concentration differences between urine samples. Relative concentrations were expressed as mega-intensity units per millimole of creatinine. Relative concentrations of serum hepcidin-25 were expressed as mega-intensity units per liter. Information on the assay can be found on: www.UMCN.NL/Hepcidin.

IDENTIFICATION OF PEPTIDES BY TANDEM MASS SPECTROMETRY
We analyzed peptides of interest for the presence of disulfide bonds. Aliquots of the 30% ACN fractions were air-dried on an NP20 array. A solution containing 10 mmol/L dithiothreitol (DTT) in 50 mmol/L ammonium bicarbonate, and the sample loaded arrays, was preheated to 70 °C. Then we loaded 10-μL aliquots of the DTT solution onto the spots and air-dried them at 70 °C. After complete evaporation of solutions and cooling to room temperature, we applied EAM. We acquired single MS spectra for unreduced and DTT-reduced samples by use of a Q-STARXL MS/MS (Applied Biosystems) equipped with a Ciphergen PCI-1000 ProteinChip Interface. We used the reduced samples to acquire tandem mass spectrometry (MS/MS) spectra. We subjected the ions of interest (m/z values of 2198 for hepcidin-20, 2442 for hepcidin-22, and 2796 for hepcidin-25) to collision-induced dissociation and submitted the results to the database-mining tool Mascot (Matrix Science) for peptide identification.

IMMUNOCAPTURE
We captured hepcidin from urinary samples by use of Protein G coupled to IDM beads (Ciphergen Biosystems) and polyclonal rabbit antihepcidin serum (generous gift from E. Nemeth and T. Ganz, University of California, Los Angeles). We performed all incubation steps at room temperature. Protein G beads were first incubated with rabbit antiserum diluted 20 times in 0.01 mol/L phosphate-buffered saline (PBS; Sigma-Aldrich Chemie BV) supplemented with 0.1% Triton X-100 (PBS-Tx). We washed the beads 3 times with PBS-Tx to remove unbound serum proteins and resuspended the beads in urine, diluted 20 times in PBS containing a final concentration of 0.25 mol/L NaCl and 0.1% Triton X-100 (PBS0.25-Tx). We washed the beads 6 times with PBS0.25-Tx to remove unbound and nonspecifically bound proteins. Finally, we eluted bound proteins with 500 mL/L ACN containing 3 mL/L TFA. To obtain profiles of Protein G–captured proteins, we applied eluates to a CM10 array equilibrated with 0.1 mol/L ammonium acetate (pH 3) and incubated them for 30 min in a humidity chamber. To obtain reference spectra, we diluted untreated urine samples once in equilibration buffer before on-spot incubation. Spots were washed, allowed to air-dry, and followed by sinapinic acid application.

ANALYTICAL ASSAY CHARACTERISTICS
We performed spot-to-spot precision for hepcidin-25 on NP20 and IMAC30 ProteinChip array with 2 human urine samples with medium and high hepcidin concentrations. Both samples were applied onto the first 6 positions of the 8-spot array, followed by addition of the EAM. The last 2 spots were used for control samples. For serum, we followed the same procedure for a single sample.
We used the same urine and serum samples for a chip-to-chip reproducibility study. We collected single measurements for serum and urine on NP20 and IMAC30 array types from randomized chip positions for 10 days (8 days for serum application on NP20 arrays). Every day a new sample aliquot was thawed, and freshly prepared EAM was applied. From these data, we calculated means, SDs, and CVs.

We measured linearity of peak intensities by dilution of the urine and serum samples used for the reproducibility tests with human urine or serum (dilution samples) from a patient with hepcidin concentrations below those detectable by SELDI-TOF MS. Immediately before sample application, we diluted 1 to 18 μL sample in a polypropylene microcentrifuge container to a 20 μL end volume with the dilution sample. After pipette mixing, 5 μL of the diluted sample was spotted on the array.

We created standard curves of synthetic hepcidin-25 for both serum and urine applications. After dissolving the lyophilized peptide in distilled water (100 μmol/L), the peptide was diluted 4500-fold with dilution sample for serum or urine (22.2 nmol/L). Dilutions of 18, 16, 12, 8, 4, 2, and 1 μL of the 22.2 nmol/L solution with the dilution sample to the final volume of 20 μL yielded a standard curve ranging from 22.2 to 1.11 nmol/L.

PREANALYTICAL AND BIOLOGICAL INTERFERENCES

We evaluated the influence of multiple freeze-thaw cycles for both serum and urine using IMAC30 arrays. Five sera and 4 urine samples from different participants and different intensity concentrations underwent 4 freeze-thaw cycles. After every cycle, we analyzed hepcidin batchwise by single measurement.

We studied the existence of a circadian rhythm for hepcidin in serum and urine by performing a 24-h time course in 3 healthy volunteers (1 man, 2 women). Blood and urine were collected every 3 h for analysis of routine iron measurements and serum and urine hepcidin (IMAC30 array), starting at 6:00 AM with fasting blood and urine samples, after which the fasting state was ended. All samples were processed as described above and stored at −80 °C before analysis (batchwise by single measurement).

STATISTICAL ANALYSIS

We performed statistical analyses with GraphPad Prism software, version 4.0. Pearson correlation was used for comparison studies. P values <0.05 were considered significant.

**Results**

HEPCIDIN IDENTIFICATION AND CHARACTERIZATION

The presence of hepcidin-25 in human urine (8) and serum (9) has been demonstrated. Our current investigation revealed that, in addition to hepcidin-25, hepcidin-20 can be verified in both urine and serum with the use of a purified synthetic reference human hepcidin peptide, whereas hepcidin-22 can be identified only in urine (Fig. 1A). This supports the hypothesis that both the 20- and 25–amino acid peptides are secreted in the circulation after production in hepatocytes, whereas the 22–amino acid peptide merely is a urinary degradation product of hepcidin-25 (14).

In addition to mass tracing, we investigated immuno-capture of all 3 known forms of hepcidin from urine. Immunoaffinity assays using polyclonal rabbit antihepcidin antibodies [the same as those used in hepcidin dotblot assay (7)] showed that the 3 peaks annotated as hepcidin-25, -22, and -20 can be specifically captured from a human urine sample of a healthy individual (Fig. 1B). MS/MS analysis of peptides in a urine sample from an endotaxemia patient confirmed that the peaks with m/z of 2198, 2442, and 2796 corresponded to hepcidin-20, -22, and -25, respectively (see Fig. 1A in the online Data Supplement). Similarly, we identified the m/z 2796 peak in serum as hepcidin-25. Notably, single MS spectra of urine and serum samples displayed a mass shift of +8 Da for all hepcidin forms after reduction with DTT, as exemplified for urine hepcidin-25 (see Fig. 1B in the online Data Supplement). This observation confirms the presence of 4 disulfide bonds in these peptides, which is a typical characteristic of hepcidin (15). Finally, the MS/MS spectra for serum and urine peptides with m/z of 2796 displayed mostly the same fragment ions, strongly suggesting that both parent ions corresponded to the same peptide hepcidin-25 (see Fig. 1C in the online Data Supplement).

ANALYSIS OF SERUM AND URINE HEPCIDIN-25 ON NP20 AND IMAC30 PROTEINCHIP ARRAYS

Because the roles of hepcidin-20 and -22 in iron metabolism are unclear (2, 14), hepcidin-25 is used for optimization of serum and urine hepcidin measurements. To evaluate the effect of ProteinChip array type on the performance of the hepcidin-25 assay, we analyzed 73 serum and urine sample pairs from controls and patients with various iron metabolism disorders using the previously reported NP20 and IMAC30 arrays (8, 9). Although hepcidin concentrations measured using NP20 arrays are lower than those measured with IMAC30 arrays, both arrays correlate for the urinary application (R = 0.928, P <0.0001; Pearson correlation; Fig. 2A). Sensitivity was higher with the use of IMAC30 compared with the NP20 arrays, likely because of highly specific binding of hepcidin to the IMAC-Cu surface. In contrast to the IMAC30 arrays, NP20 arrays did not bind detectable concentrations of serum hepcidin-25; therefore, we could not perform correlation analyses for serum and urine on NP20 arrays. In contrast, IMAC30 arrays showed a significant correlation (R = 0.822, P <0.0001; Pearson correlation; Fig. 2B).

Chip-to-chip variation of the urine application for IMAC30 ranged from 22% at a high intensity of 48 to
27.5% at a lower intensity of 20 (Table 2), whereas NP20 variation reached 34% for the same samples. Precision was also better for urine hepcidin measurements using the IMAC30 chip (CVs 11% and 13%) compared with the NP20 chip (CVs of 16% and 23%; Table 2).

For serum, the reproducibility was strongly affected by differences in protein binding capacity of both arrays. Intensities measured from the same sample differed, from an intensity of 5 with relatively high CVs on NP20 array to an intensity of 50 with low CVs on IMAC30 array. We checked the linearity of the urinary and serum hepcidin application on IMAC30 array by measuring a dilution series of urine and serum samples from an inflammation patient (single measurements). Fig. 2, A and B, in the online Data Supplement shows a high degree of linearity for both urine and serum ($R = 0.993$ and 0.971, respectively). Intensity values $>55$ seem to deviate from linearity, perhaps because of MS detector saturation. Therefore, an intensity value of 55 was considered to be the upper level of detection.

The construction of a calibration curve with synthetic human hepcidin-25 showed that both NP20 and IMAC30 arrays are capable of producing a 6-point calibration curve based on a urine matrix (see Fig 2, C and D, in the online Data Supplement). Again, intensity values $>55$ deviated from linearity and therefore were considered as exceeding the upper level of detection. Construction of
the same concentration interval on IMAC30 array in a serum matrix showed hepcidin-25 only for a concentration of 22.2 nmol/L and above (results not shown).

We categorized urine and serum sample pairs into 5 groups after clinical diagnosis. Fig. 3 shows that, despite the variation within each group and a slight overlap, differentiation between inflammation-induced and iron deficiency anemia is clear for both serum and urine hepcidin concentrations measured on IMAC30 array. The results are comparable with the results obtained with NP20 and consistent with previous reports (7, 8). The broad ranges of the thalassemia group and the hemochromatosis group are in accordance with the individual heterogeneity in genetic makeup, extent of anemia, and treatment (16–18).

In this study, we found serum and urine hepcidin concentrations close to zero in 2 brothers treated for juvenile hemochromatosis (OMIM type 2a) and values in

<table>
<thead>
<tr>
<th>Table 2. Reproducibility of hepcidin-25 analysis by SELDI-TOF MS in NP20 and IMAC30 chip arrays in both serum and urine.</th>
</tr>
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<tbody>
<tr>
<td></td>
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<tr>
<td></td>
</tr>
<tr>
<td>Urine application</td>
</tr>
<tr>
<td>Chip-to-chip*</td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>SD</td>
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<td>CV, %</td>
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<tr>
<td>Level II</td>
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<tr>
<td>Mean</td>
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<tr>
<td>SD</td>
</tr>
<tr>
<td>CV, %</td>
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<tr>
<td>Spot-to-spotb</td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>SD</td>
</tr>
<tr>
<td>CV, %</td>
</tr>
<tr>
<td>Serum application</td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>SD</td>
</tr>
<tr>
<td>CV, %</td>
</tr>
</tbody>
</table>

* Ten-day single measurement with randomized chip position.

b One chip (6 replicates).

* Eight-day single measurement (NP20 array) and 10-day single measurement (IMAC30 array) with randomized chip position.
the upper level of the reference range for a patient treated for ferroportin disease (OMIM type 4; see Table 1 in the online Data Supplement). These data confirm the potential of hepcidin analysis in prescreening for the presence of non-HFE hemochromatosis.

PREANALYTICAL AND BIOLOGICAL DETERMINANTS THAT INFLUENCE HEPcidIN-25 MEASUREMENTS IN SERUM AND URENE

Decreases in hepcidin concentrations in serum samples due to multiple freeze-thaw cycles is of minor importance compared with those in urine (see Fig. 3 in the online Data Supplement). Preliminary results from urine samples stored at −80 °C and −20 °C during a 6-month course showed that (a) hepcidin was stable only at −80 °C and (b) addition of protease inhibitor phenylmethylsulfonyl fluoride (19) had no beneficial effect (unpublished observations).

Hepcidin concentrations in serum follow a clear circadian rhythm, such that the concentrations were 2- to 6-fold higher at 1500 than at 0600. Urinary concentrations, however, show a more blunted response, and thus less
diurnal variation. The course of serum iron shows an inverse association with serum and urine hepcidin values (Fig. 4).

Discussion

The IMAC30 array–based urinary hepcidin assay correlated significantly with the previously described urinary hepcidin MS application using NP20 arrays (8) and showed greater sensitivity and reproducibility, resulting in improved analytical performance. The increase in protein-binding capacity of the IMAC30 array makes it particularly suitable for serum analysis and measurement of low hepcidin concentrations in urine.

The total assay variation includes analytical variation, biological or diurnal variation, and preanalytical variation, all contributing to the widening of ranges of the clinical utility clusters. In the future, we plan to routinely perform duplicate measurements and investigate isotope dilution (20) or hepcidin derivatives as internal standards to reduce analytical variability.

Biological variation in hepcidin concentrations due to a circadian rhythm correlated inversely with daily variations in serum iron concentrations (21), in accordance with previous reports that transferrin receptors 1 and 2 on the outer hepatocyte membrane act as sensors of circulating iron and T5, thereby linking low serum iron with increased hepcidin synthesis (22, 23). Circadian rhythm may also lead to important variation in outcome if sampling time is not standardized, thereby contributing to the wide variation in hepcidin concentrations of the control population (Fig. 3C). Sampling according to protocol led to decreased variation in hepcidin concentrations within the lipopolysaccharide group. The low variation within the iron deficiency anemia group is likely to be due to the dominant down-regulating influence of an iron-deficient erythropoiesis on hepcidin that prevents circadian increases.

Variation in hepcidin results is also attributable to preanalytical conditions. According to our preliminary results, urine samples are more susceptible than serum to variation from multiple freeze-thaw cycles, which should be avoided, and urine samples should be stored at −80 °C as soon as possible (24, 25).

Measurement of serum and urine hepcidin by the same technique, and under the same circumstances, enabled comparison of serum with urinary values. Although their association was strong, confirming the previously reported correlation between hepcidin mRNA expression in liver cells and urinary hepcidin excretion (26), differences in serum and urine composition prohibit absolute comparison of analytical characteristics such as binding competition on the array surface and flight behavior during SELDI-TOF MS analysis (27). Aspects such as ionization efficiency or ion suppression also can play a role and should be investigated in future studies. Meanwhile, differences in specimen behavior preclude calculations of the kinetics of hepcidin release by hepatocytes and its excretion from the blood into the urine. Construction of a calibration curve by addition of the same amount of hepcidin-25 to serum or diluted urine confirms this effect, leading to speculation that a binding protein in serum prevents the binding of free hepcidin on the chip surface at low concentrations (27). To circumvent differences in binding characteristics or possible matrix interferences, methodologic approaches such as plasma fractionation (27) or the use of magnetic reversed-phase beads (28) have to be investigated for utility on hepcidin measurements.

Our reported SELDI-TOF MS method detected all 3 isoforms of hepcidin, improved urinary hepcidin analysis, and enabled measurement of serum hepcidin by IMAC30 array. We show for the first time a high correlation of concentrations measured in corresponding serum and urine samples. Selection of the optimal body fluid for analysis, however, is influenced by preanalytical, analytical, and biological variations that effect serum and urine differently. Urine is more vulnerable to multiple freeze-thaw cycles and storage temperatures other than −80 °C but less influenced by diurnal variation. Serum is more susceptible to circadian variation, and therefore standardization of sampling time is needed in clinical studies with serum. Serum is likely to be more sensitive than urine, however, for monitoring short-term kinetics of body hepcidin concentrations. Therefore, the specimen of first choice depends on study design and practical aspects such as availability of materials and equipment. The ability to measure hepcidin in both serum and urine confirms that the learning process on hepcidin characteristics, kinetics, and clinical utility has only just begun.

We thank Elizabeta Nemeth and Tomas Ganz (University of California, Los Angeles) for kindly providing samples of synthetic hepcidin-20 and -22 and polyclonal antihepcidin rabbit serum. We thank Henk Engel (Isala Klinieken, Zwolle, The Netherlands), as well as Omer Njajou, Cornelia van Duijn, and Leon Testers (Erasmus Medical Center, Rotterdam, The Netherlands), for providing sample material of 2 HJV G320V patients and a FPN N144H patient, respectively, and Peter Pickkers for sharing the endotoxemia samples. We thank Giuliana Zanninelli (Ospedale Sant’Eugenio, Rome, Italy) for selection and collection of sample material of thalassemia major patients. We also thank Mirian Janssen, Esther Jacobs, Lammy Elving, and all other physicians involved in selection and collection of samples.

References