The Spectral and Thermodynamic Properties of Staphylococcal Enterotoxin A, E, and Variants Suggest That Structural Modifications Are Important to Control Their Function*

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The superantigens staphylococcal enterotoxin A and E (SEA and SEE) can activate a large number of T-cells. SEA and SEE have approximately 80% sequence identity but show some differences in their biological function. Here, the two superantigens and analogues were characterized biophysically. SEA was shown to have a substantially higher thermal stability than SEA. Both SEA and SEE were thermally stabilized by 0.1 mM Zn\(^{2+}\) compared with Zn\(^{2+}\)-reduced conditions achieved using 1 mM EDTA or specific replacements that affect Zn\(^{2+}\) coordination. The higher stability of SEE was only partly caused by the T-cell receptor (TCR) binding regions, whereas regions in the vicinity of the major histocompatibility complex class II binding sites affected the stability to a greater extent. SEE exhibited a biphasic destabilizaton between pH 5.0–6.5, influenced by residues in the TCR binding regions. Interestingly, enzyme-linked immunosorbent assay, isoelectric focusing, and circular dichroism analysis indicated that conformational changes had occurred in the SEA/E chimerical constructs relative to SEA and SEE. Thus, it is proposed that the Zn\(^{2+}\) binding site is very important for the stability and potency of SEA and SEE, whereas residues in the TCR binding site have a substantial influence on the molecular conformation to control specificity and function.

Superantigens (SAgs)\(^1\) such as the staphylococcal enterotoxins (SE) are very potent T-cell-activating proteins known to cause food poisoning or toxic shock (1). SEs bind as unprocessed proteins to MHC class II molecules and activate T-cells displaying certain V\(\beta\) regions of T-cell receptor (TCR) (2, 3). Because the number of V\(\beta\)-genes is limited, a much larger fraction of the T-cells is activated by SAgs than by normal antigens (2, 4). The strong cytotoxicity induced by these enterotoxins has been explored for cancer therapy by fusing them to tumor-reactive antibodies (5, 6).

Nine different SEs have been identified and these are designated SEA-SEE and SEG-SEJ. The sequence identity of these SAgs with SEA ranges from 20% for SEG to 82% for SEE (described in greater detail in Refs. 7 and 8). The binding to MHC class II of both SEA and SEE is known to be Zn\(^{2+}\)-dependent (9). Both SEA and SEE have two MHC class II binding sites, one close to the N terminus with low affinity for MHC class II and one close to the C terminus with moderate affinity. These two sites may cooperate and cross-link MHC class II molecules with a higher affinity (10, 11). In addition the ability to cross-link two neighboring MHC class II molecules may stimulate secretion of inflammatory cytokines, such as interleukin-6, interleukin-8 (12), and interleukin-13 (13). One of these interactions is stabilized by a Zn\(^{2+}\) ion, coordinated by His187, His225, and Asp227 in SEA (14) and His81 in the MHC class II \(\beta\)-chain (15). Replacing any of the residues Asp227, His-225, and His-187 with Ala dramatically decreases the affinity for Zn\(^{2+}\) and subsequently MHC class II (10). SEA and SEE behave similarly in many functional assays, for example human T-cell proliferation and MHC class II-dependent cytotoxicity assays (16). However, the V\(\beta\) specificity (2, 16, 17) differs slightly between SEA and SEE, and in contrast to SEE, SEA can induce a strong MHC class II-independent T-cell response. This indicates that presentation on MHC class II is more important for optimal activation of T-cells with SEE (16). As a consequence, these intrinsic differences in the TCR binding sites of SEA and SEE indicate that the affinity of SEA for the TCR may be different compared with SEE.

In this study, the differences in stability between SEA and SEE were studied and compared with functional data. To address differences on the molecular level, engineered chimeras as well as variants with specific replacements were investigated. Exchanging parts of the SEA amino acid sequence for the corresponding sequence from SEE or vice versa induces conformational changes in the tertiary structure that could be important for the T-cell-activating properties. Also, the influence of the Zn\(^{2+}\) binding site, which is important for MHC class II binding, on the structural stability of the SAgs was investigated.

EXPERIMENTAL PROCEDURES

Materials—Horseradish peroxidase-labeled goat anti-human IgG (\(\gamma\)-specific), Sigma Fast\textsuperscript{TM} OPD peroxidase substrate tablets, and t-methionine sulfoximine were purchased from Sigma. Purified IgG pool was from Pharmacia & Upjohn AB (Stockholm, Sweden). Dry milk (fat-free) was from Semper AB (Stockholm, Sweden) and horseradish peroxidase-labeled rabbit anti-SEA antibodies were from Toxin Technology (Sarasota, FL). Na\(_2\)CrO\(_4\) was from Amersham Pharmacia Biotech. The restriction enzymes BglII and HindIII were from Roche Molecular Biochemicals and Life Technologies, Inc., respectively, and T4 ligase was from Roche Molecular Biochemicals.

RPMI 1640 cell growth medium and HEPES were from Bio Whitaker (Verviers, Belgium) and Hank’s balanced salt solution without phenol red was from Life Technologies, Inc. R10 fetal bovine calf serum was from Flow Laboratories (McLean, VA). 51CrO\(_4\) was from Amersham...
Characterization of SEA and SEE

was from Hy-Clone Laboratories Inc. (Logan, UT). Gentamicin sulfate was from Biological Industries (Kibbutz Beit hemeek, Israel), and [3H]thymidine was from NEN Life Science Products. 1-[4,5-3H]Leucine for metabolic labeling of cells was from Moravek Biochemicals Inc. (Brea, CA), and SPA-polyvinyl toluen e beads were from Amersham Pharma- cia Biotech.

**Thermal Denaturations**—The thermal denaturations were carried out using a HP 8453 UV diode-array spectrophotometer with a heating cell (Hewlett-Packard, Waldbronn, Germany). The spectrum was monitored between 190 and 1100 nm. Before measurement the cuvette was cleansed with 6× guanidine-HCl and Millipore water. SAg solution was added to the cuvette and diluted with 20 mM phosphate buffer to give a final concentration of 0.1 mg/ml. If the temperature was increased in steps of 0.5 °C, and at every temperature the sample solution was left to equilibrate before the absorbance measurement. The typical temperature interval was 40–75 °C. The denaturation was visualized by plotting the absorbance change per gram of protein at every temperature and the denaturation temperatures were defined as the EC50 value.

**Expression and Purification of SEA/E Chimeras**—The different supra- peppers were expressed constitutively in the Echerichia coli strain UL 635 (sul-7, ara-14, T4, ΔompT) using a vector (10, 19) with a staphylococci promotor A promoter, a signal peptide, and a kanamycin resistance gene. In the Fab-SAg vector (5, 6), expression was controlled by a lacUV5 promoter. The SAg's (Table I) were expressed using either shaker flasks or fermenters (Belach Biotechnik, Sweden), whereas the C215Fab-SAg’s (Table I) were produced in fermenters. When using shaker flasks bacteria containing the respective production plasmid (Table I) were cultivated for approximately 18 h in 500 ml of 106 cells/ml of growth medium. The sample was eluted with an ammonium acetate buffer gradi- mens/cm, adjusted to pH 5.0, and applied on a 1-ml Resource-S column (Amersham Pharmacia Biotech). The flow rate of 5 ml/min. To wash the column between samples. 30 ml of 1 × 104 M NaOH was used. The purified SAg was concentrated to at least 1 mg/ml by ultrafiltration (Centriprep 10, Amicon Inc., Beverly, MA).

The Fab-SAGs were purified using protein G affinity chromatography and ion-exchange chromatography (6). Typical yields for the SAG chimeras were 5 mg/l in shaker flasks and 50 mg/l or more in fermenters. The yield for the Fab-SAGs in fermenters was typically 50–400 mg/l.

**Analytical Procedures**—SDS-polyacrylamide gel electrophoresis was carried out using precast 10–15% polyacrylamide gradient gels in the PhastSystem Pharmacia Biotech) and isoelectric focusing with gels ranging from pH 3 to 9. For staining, Coomassie Blue was used. The purity of the samples was visually estimated from the SDS-polyacrylamide gel electrophoresis. The protein concentration of the product solutions was determined with a UV-spectrophotometer (Hewlett-Packard) at 280 nm. Mass spectrometry was carried out on a Lasermet 2800 laser desorption/ionization mass spectrometer (Finnigan Mat ltd, Hemel Hempstead, United Kingdom) with a matrix con- sisting of 10 mg/ml sinapinic acid (20%) in 30% acetoni trile with 0.1% trifluoroacetic acid.

**CD Measurements**—Both the far UV and near UV CD spectra were recorded in a 20 mM NaH2PO4 buffer, pH 6.0, using a Jasco J720 (Japan Spectroscopic Co. Ltd., Hachioji City, Japan). The path length of the cuvettes used for far and near UV measurements were 0.1 and 1 cm respectively. The concentration of the protein solutions used for near UV CD was approximately 0.8 mg/ml and for far UV CD it was approxi- mately 0.2 mg/ml (21). Corrections were made in the CD spectra for concentration differences between samples.

**Enzyme-linked Immunoassortent assay Analysis of C215Fab-SAGs**—Flat bottomed high binding EIA/RIA 96-well plates (Corning Costar Co., Cambridge, MA) were coated with SEA/E solution, which was stored at 4 °C using 100 μl of 1 μg/ml goat anti-mouse k chain in 50 mM NaHCO3, pH 9.6. Residual binding sites were blocked using 3% fat-free dry milk in PBS-Tween, 200 μl/well for 1 h. To each well 100 μl of the respective C215Fab-SAg solution, 0.5 μg/ml in PBS-Tween, was added and incubated for 1 h. As a negative control, 100 μl of 0.5 μg/ml C215Fab was used. The final steps were carried out using either human or rabbit antibodies. Using human antibodies, 100 μl of purified IgG pool at different concentra- tions in 3% fat-free dry milk in PBS-Tween was added to the wells and incubated for 2 h, and 100 μl of 1.66 μg/ml horseradish peroxi- dase-labeled goat anti human IgG (γ-specific) were added and incubated for 1 h. Alternatively horseradish peroxidase-labeled rabbit anti-SEA at different concentrations, diluted in blocking solution, was added and and incubated for 2 h. The plates were developed with the Sigma Fast™ OPD peroxidase substrate tablet as recommended by the supplier. Between each step of the assay the wells were washed four times with PBS-Tween.

**T-Cell Proliferation**—The growth medium used was RPMI 1640 with 10% fetal calf serum, 50 μ g/ml 2-mercaptoethanol, and 0.1 mg/ml genta- mycin sulfate. Spleen cells from C57B1/6 mice were obtained in mouse as a suspension in growth medium. The cells, 2 × 106/well as deter- mined by counting in Burker chambers using trypan blue viability staining, were incubated in 96-well flat bottomed plates (Nalgene Nunc International, Denmark). The SAgs used were analyzed in triplets in a concentration interval 0.01–100 μg/ml. After incubation for 3–4 days the cells were pulsed with 10 μg of [-H]thymidine (0.05 μCi), and the DNA of the cells was harvested after 4 h with a Micro Cell Harvester (SKATRON, Dalsletta, Norway). The radioactivity of the sample was measured with a 1205 Bepitplate Liquid Scintillation Counter (Wallac Sverige AB, Solentuna, Sweden).

**Scintillation Proximity-based Binding Assay—**Chinese hamster ovary cells transfected with human CD80 and HLA-DR4 were cultured in RPMI 1640 supplemented with 10% fetal calf serum, 0.1 mg/ml gentamycin sulfate, and 1 mM 1-themione sulfonamide. CHO-CD80-DR4 cells, resuspended to a density of 5 × 106 cells/ml in l-leucine-deficient (Leu-) medium (l-leucine-free RPMI 1640 medium supplemented with 2 mg/ml l-glucose, 0.24 mg/ml l-arginine, 0.035 mg/ml 1-iso-inositol, 0.015 mg/ml l-methionine, 0.596 mg/ml disodium cysteine, 0.01 mg/ml l-lysine, 2% (v/v) fetal bovine serum, 0.1 mg/ml gentamycin sulfate, and 1% (v/v) 1-themione sulfonamide), were labeled overnight at 37 °C in a CO2 incubator with 0.2 μCi of l-[4,5-3H]leucine/106 cells. The next day, [3H]CHO-CD80-DR4 cells were resuspended to a density of 3 × 105 cells/ml in assay buffer (Hank’s balanced salt solution without phenol red supplemented with 25 mM HEPES, pH 6.8, and 1% (w/v) bovine serum albumin).

The affinity was estimated by calculating half-maximal binding (B50) from the saturation curve. The C215Fab moeity was used to attach the C215Fab-SEA to the SPA beads coated with anti-mouse antibodies. Fifty microliters of C215Fab-SEA (at different concentra- tions) and 50 μl of anti-mouse SPA-polyvinyl toluen e beads (40 mg/ml in assay buffer without bovine serum albumin) were mixed for 5 min in a microtiter plate (OptiPlate, Packard, Greve, Denmark), covered with a plastic film, and incubated for 30 min to 2 h at 4 °C (depending on the time needed for the preparation of the cells). The 3H-labeled cells were added to the microtiter plate with preincubated C215Fab-SEA-SPA beads at a density of 1.5 × 105 cells/50 μl/well. The plate was sealed by a plastic film, mixed for 1 min on an orbital shaker platform, and incubated in the dark for 8 h at room temperature. The radioactivity in each well was measured during 3 min/well using a β-top counter (Pack-ard). As a negative control, C215Fab was used.

**RESULTS**

**Denaturations of SEA and SEE**—To investigate the stability of SEA and SEE and understand how it depends on variables such as pH, salt concentration, and various additives, thermal
denaturations were carried out using a UV spectrophotometer with a heating cell and a diode array detector. The sample consisted of 0.1 mg/ml SAg dissolved in 20 mM phosphate buffer of varying pH. At denaturation the UV absorbance spectra are changed, because buried residues become exposed. The denaturation was monitored by measuring the difference in absorbance at 286 and 264 nm, because drastic changes in the absorbance difference of these two wavelengths occur upon denaturation (18). After denaturation, the SAgs usually precipitated.

The melting points for SEE were generally 5–15 °C higher compared with SEA. Notably, a biphasic denaturation was observed for SEA between pH 5.0 and pH 6.5, but at a higher pH the denaturation was monophasic (Fig. 1). A possible biphasic denaturation was observed for SEA at pH 5.0. At pH 4.0–5.0 for SEA and 4.0 for SEE, the melting was less distinct suggesting unfolding in a more complex way. At pH 4.0, both SEA and SEE remained soluble after denaturation while precipitating at the other pHs.

Denaturations were also carried out with SEA and SEE at pH 4.0–9.0 with the addition of 150 mM NaCl, which substantially reduced the stability of both SEA and SEE at lower pH by approximately 6 °C, while increasing the thermal stability of SEE at higher pH with 2–5 °C (data not shown).

To see whether SEE could obtain its original structure from the partially unfolded state, the temperature gradient was stopped there, and the sample slowly cooled. However, during this procedure most material precipitated.

Denaturations of SEA and SEE in guanidine-HCl monitored by far and near UV CD measurements showed that the tertiary structure unfolds with midpoints at 1.52 M for SEA and 1.96 M for SEE (Fig. 2). The secondary structure for SEA and SEE is lost at 5.10 and 4.14 M, respectively (Fig. 2). Thus, at pH 6.0 the tertiary structure of SEE is more resistant than SEA to chemical denaturants, whereas the opposite is true for the secondary structure.

In conclusion SEE has a substantially more stable structure than SEA, and the melting points differ up to 15 °C. At a lower pH the denaturation of SEA and SEE was less distinct.

Zn$^{2+}$ Dependence of the Thermal Stability of SEA and SEE—To investigate the importance of Zn$^{2+}$ binding for thermal stability of SEA and SEE, denaturations were made with buffers containing 1 mM EDTA to bind Zn$^{2+}$ ions or buffers containing 0.1 mM ZnCl$_2$ to saturate the SAgs with Zn$^{2+}$. Compared with conditions with no Zn$^{2+}$, accomplished by the addition of 1 mM EDTA, the increase in melting points for SEA with Zn$^{2+}$ addition was up to 6 °C (Fig. 1). The stabilizing effect of Zn$^{2+}$ for SEA was larger at pH 6.0 compared with pH 7.0, but for SEE (Fig. 1) it was almost independent of pH at pH 5.0, 6.0, and 7.0. The melting points of SEA with the addition of 0, 0.01, and 0.1 mM ZnCl$_2$ increased almost linearly from 59.5 to 61.4 °C but no detectable increase in melting point occurred with the addition of 1.0 mM ZnCl$_2$ compared with 0.1 mM (data not shown) indicating Zn$^{2+}$ saturation of the SAgs at 0.1 mM ZnCl$_2$. In contrast 0.1 mM MgCl$_2$ or 0.1 mM CaCl$_2$ at pH 6.0 stabilized neither the SEA nor the SEE structure (data not shown).

With the Zn$^{2+}$ addition, SEE exhibited a biphasic denaturation at pH 5.0 and 6.0, as did SEA at pH 5.0 (Fig. 1). Interestingly, the denaturation curve of SEA at pH 5.0 was much less distinct than at pH 6.0 and 7.0, and no precipitate was formed. Unlike SEA, the EDTA-treated SEE showed a substantially less distinct denaturation behavior at pH 7.0 (Fig. 1).

Denaturations were also made on the mutants SEA$^{D227A}$,
SEAD227A, F47A, SEA H187A, SEE D227A, and des(1–5)SEA (Fig. 3, Table I). The residues Asp-227 and His-187 (10) are essential for coordination of Zn\(^{2+}\) in the MHC class II b-chain binding site. The residue Phe-47 is located in the MHC class II a-chain binding site, which is unlikely to be metal ion-dependent. Similarly Ser1 may be involved in the Zn\(^{2+}\) coordination (22) according to one crystal structure.

The replacement of the Zn\(^{2+}\) binding residues strongly affected the thermal stability of the SAgs. The melting point of SEAD227A was 1.8 °C lower than SEA at pH 6.0 and 6.3 °C at pH 7.0.

![Fig. 3. Guanidine denaturations of SEA and SEE. Denaturation of SEA (●) and SEE (□) using guanidine followed by CD at 280 nm (left) and 220 nm (right). Background signal subtracted.](image)

**Table I**

<table>
<thead>
<tr>
<th>SAg</th>
<th>Thermal melting points (°C)</th>
<th>dCharge from SEE</th>
<th>Proliferation (EC(_{50}) rel. to SEA)</th>
<th>Theoretical mol. mass</th>
<th>Observed mol. mass</th>
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<td>pH 7.0</td>
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<td></td>
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<tr>
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<td>6.9</td>
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<td>67.4</td>
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**FIG. 3. Thermal denaturations of SAg mutants.** Melting points (°C) for wild type SAgs (●) and the mutants SEA\(_{D227A}\) (■), SEA\(_{H187A}\) (■), SEA\(_{D47A}\) (■), SEE\(_{D227A}\) (■), SEE/A-a\(_{D227A}\) (■), and des(1–5)SEA (□). The melting temperatures for the variants with replacements in the MHC class II binding sites (Table I) were generally lower than those for wild type SAgs, although the difference was larger at pH 7.0 compared with pH 6.0.

**Characterization of SEA and SEE**
Characterization of SEA and SEE

The melting points of SEA and SEE were determined at pH 6.0 and 7.0 (Fig. 3). For SEA, the melting points at pH 6.0 and 7.0 were lowered 0.5 and 3.9 °C, respectively. Therefore, all denaturations were henceforth carried out in the presence of 0.1 mM ZnCl2.

In conclusion, the addition of Zn2+ to SEA and SEE increased the stability compared with Zn2+-free conditions. The substitution H187A in SEA and D227A in SEE, and SEE/A-a had a clear destabilizing effect, indicating that these residues are very important for the stability of the SAgs. The destabilizing effect was more pronounced at pH 7.0 than at pH 6.0. The substitution F47A in SEA stabilized the structure at both pH 6.0 and 7.0. Because of the substantial influence of Zn2+ on the stability of the SAgs, all denaturations were henceforth carried out in the presence of 0.1 mM ZnCl2.

Characterization of the SEA/E Chimeras—SEA and SEE have a sequence identity of approximately 80%. The main differences are found in eight different regions, four close to the two MHC class II binding sites and four in the vicinity of the TCR binding site (16). SEA/E-bdeg has the two MHC class II binding regions from SEE and the TCR binding region from SEA. To get an excess of Zn2+, avoiding differences in this important parameter, 0.1 mM ZnCl2 was added. The results of the thermal denaturation of these molecules are shown in Fig. 6 and Table I.

The melting points for the chimeras were all lower than for SEA, with the exception of SEE/A-a at pH 6.0 and 7.0 and SEE/A-h at pH 6.0 but substantially higher compared with SEA (Table I). Notably SEA/A-a and SEE/A-h, at pH 6.0, had higher melting points than SEE (Table I), whereas SEE/A-a had a lower melting point, indicating that a combination of these two stabilizing regions reversed this effect. Interestingly the chimeras where region h had been replaced, SEE/A-h and SEE/A-ah, were significantly stabilized by the lower pH contrasting the other chimeras.

The melting points of SEE/A-a and SEE/A-f increased from pH 6.0 to 7.0 with approximately 1 °C for SEE/A-a and 2 °C for SEE/A-f (Table I). For the chimeras SEA/A-h and SEE/A-ah the melting points decreased from pH 6.0 to 7.0 with approximately 11 °C for SEA/A-h and 3 °C for SEE/A-ah. The melting point for SEA/E-bdeg was approximately 68–69 °C at both pH 6.0 and 7.0. The differences in melting points between pH 7.0 and 6.0 could be caused by residues, which are important for the structural stability of the protein in the present conformation, becoming protonated between pH 7.0 and 6.0 and thereby acquiring a charge, which might change the stability of the structure. Biphasic denaturations were observed for SEA/E-bdeg at pH 6.0 and by SEE/A-h at pH 7.0. The denaturation behavior of SEE/A-h at pH 6.0 seems to be more complex with the SAg not precipitating at denaturation (Fig. 6). SEE/A-a, -f, and -ah showed no biphasic denaturation behavior.

Interestingly, SEA/E-bdeg composed of SEA with the two MHC class II binding sites from SEE was substantially more stable than SEA, indicating that several different regions contribute to the greater stability of SEE. Of the chimeras, SEA/A-h and SEA/E-bdeg showed biphasic denaturations.

In conclusion, most likely there are conformational differ-
ences between the SEA/E chimeras indicated by isoelectric focusing and near UV CD spectra as well as the low antibody binding properties of SEE/A-a and SEE/A-f. The thermal stability of all the chimeras was higher than for SEA with the highest melting points obtained for SEE/A-a and SEE/A-h, but a combination of these two chimeras, SEE/A-ah, was substantially less stable.

Binding of SE Fusion Proteins to MHC Class II-expressing Cells—The interaction between C215Fab-SEs and human MHC class II (HLA-DR4) presented on cells was studied using a binding assay based on the SPA technology. To detect the binding of SEs to HLA-DR4, the C215Fab-SEs was attached to SPA beads coated with anti-mouse Ig antibodies via the Fab moiety, whereas the cells expressing HLA-DR4 were labeled by the incorporation of [3H]leucine. The concentration yielding half-maximal binding ($B_{max} \%$) was used as an estimate of the binding affinity. $B_{max} \%$ concentrations for the different C215Fab-SEs analyzed (Fig. 7) were found to be approximately in the same range ($2 \times 10^{-5}$ M) (data not shown). This indicates a similar affinity for HLA-DR4, for SEA, SEE, and the chimeras. A striking difference, however, in the saturation amplitude was noticed for the C215Fab-SEs (Fig. 7). The highest amplitude was seen for C215Fab-SEE/A-h, which was about twice the height of the cluster obtained for the SEA, SEE, SEE/A-h, and SEE/A-ah C215Fab fusion proteins. C215Fab-SEE/A-f and C215Fab-SEA/-bdeg formed an additional cluster of C215Fab fusion proteins, with an amplitude half of that obtained for the C215Fab-SEA cluster. These results indicate that the replacement of region a, alone or together with region h, does not affect the number of binding sites, whereas replacement of region h doubles the number of binding sites compared with that for the SEA cluster. In the same way, a replacement of

FIG. 5. Far and near UV CD spectra of the SAgs. Far (A) and near (B) UV CD spectra of SEA ( ), SEE ( ), SEE/A-a ( ), and SEE/A-f ( ). The spectra are similar in the far UV region, whereas they differ markedly in the near UV region. This indicates that the SAgs have a similar secondary structure, although the tertiary structure differs.

FIG. 6. Thermal denaturations of the SEA/E chimeras. Thermal denaturation curves at pH 6.0 ( ) and 7.0 (—–) for the chimeras SEE/A-a, -f, -h, -ah, and SEA/E-bdeg. SEA/E-bdeg exhibits a biphasic denaturation at pH 6.0 and SEE/A-h at pH 7.0, but the denaturation process of SEE/A-h at pH 6.0 seems to be more complex.
Characterization of SEA and SEE

DISCUSSION

Several studies have speculated in the importance of conformational changes for superantigen function (24, 25). In this study we have investigated the structural properties of several SEA and SEE variants. The results clearly support the previous hypotheses. Although the amino acid sequences of SEA and SEE are very similar, there are differences in biological function. The Vβ-specificities for SEA and SEE differ (2, 17) as do their affinities to different MHC class II alleles (9), and SEA may also have a different affinity for the TCR than SEE (16). Interestingly, in many cases chimerical molecules of SEA and SEE acquire properties that are unique and not the predicted combinations between SEA and SEE (Figs. 5–7). Replacing Phe-47 with Ala reduces the number of Vβ’s that can be activated (25). This could be caused by the inability of this, more structurally stable variant (Fig. 3) to undergo a necessary conformational change.

These findings can be explained by the subtle differences in the tertiary structure between the SAgs (Fig. 5). The MHC class II binding regions in SEE are mostly responsible for this stabilization, whereas the TCR binding sites seem more flexible. Thus, it is likely that some side chains primarily contribute to tertiary interactions, e.g. by burying hydrophobic surface area in the core of the protein whereas others mainly stabilize secondary structure, and that SEE and SEA differ in both types of side chains. Interestingly, both guanidine-induced and thermal (data not shown) denaturations of SEA and SEE monitored using CD showed that the tertiary structure was unfolded before the secondary structure. Tertiary structure is generally lost before secondary structure when the two levels of structure do not disappear concomitantly, as in e.g. the molten globule, and indicates that the transition observed when performing UV monitored thermal denaturations is mainly an unfolding of tertiary structure.

The regions a, f, and h are important for the conformation of SEE, as suggested by isoelectric focusing, CD, antibody recognition, and MHC class II binding assays (Fig. 5 and 7, Table I). We therefore propose that the TCR binding site in SEEs can adopt different conformations that are controlled by subtle differences in this region. This is supported by observed differences in Vβ-specificity between SEA and SEE (2, 17) and the SEE/E chimeras (16). Thus, several of the residues in the TCR binding site have important functions in controlling the structure, such as the ability for structural modification upon receptor binding and affinity and specificity. Interestingly, these regions may also influence the stoichiometry in binding to MHC class II (Fig. 7), perhaps by having structures that facilitate or hinder binding via the low affinity binding sites.

At certain pH values a biphasic denaturation occurs indicating a partial unfolding in the SAgs. SEE/A-f and SEE/A-ah showed no biphasic denaturation, whereas SEE/A-f and SEE showed an approximately three times lower proliferating activity (Table I) as determined by EC50 values. Using human T-cells (16), SEE/A-f was less potent, whereas the proliferating activity for SEA was similar to the other SAgs.

At certain pH values a biphasic denaturation occurs indicating a partial unfolding in the SAgs. SEE/A-f and SEE/A-ah showed no biphasic denaturation, whereas SEE/A-a, SEE/A-h, and SEE/E-bdeg did. Because the biphasic melting is only observed at pH 5.0 and 6.0 but not at pH 7.0, it was hypothesized that it involved His residues getting ionized. Notably SEE/A-f, with two His residues replaced, lacks a biphasic melting suggesting a role for His-161 or His-164 in this local stabilization. Thus, at least one of these two His residues may form part of the flexible elements that control the structure of the TCR binding site. This hypothesis is further supported by the similar T-cell-proliferating properties of SEE/A-f and SEA. However, there is a biphasic denaturation with a larger absorbance difference in SEE/E-bdeg, which also lacks the two His-161 and His-164, indicating more complete unfolding or that another region is denatured. Therefore, biphasic melting occurs with certain combinations of residues that destabilize the structure.

Zn2+ is important for the MHC class II affinity of both SEA and SEE (9), as well as the reduction in monokine release triggered by SEA and SEE, but Zn2+ does not influence the Vβ-specific T-cell stimulation (26). Loss of Zn2+ coordination significantly lowers the potency of SEA (27). From the data presented here, it is clear that Zn2+ also stabilizes the structures of SEA and SEE, especially at physiological pH. Coordination of metal ions often leads to stabilized structures and can increase melting points with approximately 10 °C including both functional Mg2+ (28) and engineered Zn2+ binding sites (29, 30). The importance of the Zn2+ binding region for the thermal stability of SEA and SEE was further shown by the dramatic decrease in melting point at pH 7.0 for the SEA Zn2+ binding site mutants, such as SEA1227A. Although having a reduced Zn2+ binding, the variants were all stabilized by the addition of a high concentration of Zn2+ indicating that they
bind Zn\(^{2+}\) through the known site but with a significantly reduced affinity. Alternatively, an unknown Zn\(^{2+}\) binding site could exist (24). Because SEA\(_{D227A}\) was less stable than EDTA-treated SEA, this replacement destabilizes or affects the structure of this MHC class II binding site. This suggests that the very low affinity of this variant for MHC class II is caused by two independent mechanisms, removal of the coordinated Zn\(^{2+}\) ion and structural disturbance. In contrast SEA\(_{H187A}\) is more stable than SEA\(_{D227A}\) and has a much higher MHC class II affinity and activity (10, 11), indicating that here the structure is less affected. In the SEA crystal structure Asp-227 is less exposed compared with His-187 (22).

In conclusion residues in the Zn\(^{2+}\) binding site are very important for the stability and potency of SEA and SEE, whereas residues in the TCR binding site have a substantial influence on the molecular conformation, which may control specificity and function. Our findings will further guide us to understand how bacterial superantigens have evolved and how their potent T-cell stimulatory capacity is maintained on the molecular level. However, these finding will also help us to design superantigens that could have clinical benefits, such as cancer therapy (5, 31).

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