

Structural characterization and immunogenicity in wild-type and immune tolerant mice of degraded recombinant human interferon Alpha2b

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Purpose

This study was conducted to study the influence of protein structure on the immunogenicity in wild-type and immune tolerant mice of well-characterized degradation products of recombinant human interferon alpha2b (rhIFN α 2b).

Methods

RhIFN α 2b was degraded by metal-catalyzed oxidation (M), cross-linking with glutaraldehyde (G), oxidation with hydrogen peroxide (H), and incubation in a boiling water bath (B). The products were characterized with UV absorption, circular dichroism and fluorescence spectroscopy, gel permeation chromatography, reverse-phase high-pressure liquid chromatography, sodium dodecyl sulfate polyacrylamide gel electrophoresis, Western blotting, and mass spectrometry. The immunogenicity of the products was evaluated in wild-type mice and in transgenic mice immune tolerant for hIFN α 2. Serum antibodies were detected by enzyme-linked immunosorbent assay or surface plasmon resonance.

Results

M-rhIFN α 2b contained covalently aggregated rhIFN α 2b with three methionines partly oxidized to methionine sulfoxides. G-rhIFN α 2b contained covalent aggregates and did not show changes in secondary structure. H-rhIFN α 2b was only chemically changed with four partly oxidized methionines. B-rhIFN α 2b was largely unfolded and heavily aggregated. Nontreated (N) rhIFN α 2b was immunogenic in the wild-type mice but not in the transgenic mice, showing that the latter were immune tolerant for rhIFN α 2b. The anti-rhIFN α 2b antibody levels in the wild-type mice depended on the degradation

product: M-rhIFN α 2b > H-rhIFN α 2b \sim N-rhIFN α 2b \gg B-rhIFN α 2b; G-rhIFN α 2b did not induce anti-rhIFN α 2b antibodies. In the transgenic mice, only M-rhIFN α 2b could break the immune tolerance.

Conclusions

RhIFN α 2b immunogenicity is related to its structural integrity. Moreover, the immunogenicity of aggregated rhIFN α 2b depends on the structure and orientation of the constituent protein molecules and/or on the aggregate size.

About this Article

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