Crystalline Component Identification From Simulated Powder X-Ray Diffraction Patterns

Industry Sector

Pharmaceutical

Organization

Bristol-Myers Squibb

Key Product

Crystal diffraction tools

Researchers at the Pharmaceutical Research Institute, Bristol-Myers Squibb, used crystal modeling tools to identify the crystalline components of bulk materials - e.g. pharmaceuticals.

The study illustrated the use of simulated powder X-ray diffraction patterns as reference standards for phase identification and quantitative phase analysis.

In the pharmaceutical industry, the identification of the crystalline components of bulk materials is essential. This comes as no surprise as the crystal structure of the active pharmaceutical ingredient (API) can determine vital properties including safety, efficacy, and unit processes. Understanding the nature of crystalline materials and whether the API is a single phase is vital. Powder X-ray diffraction (PXRD) is the principal method of characterization.

PXRD, the traditional technique used to identify the crystalline components of bulk materials, relies on the comparison of experimental data with reference patterns. These reference standards can be experimental patterns archived in a database or collected in a local synthesis laboratory. Alternatively, powder patterns expected for homogenous bulk sample can be simulated by standard algorithms from atomic parameters when single crystal structures are known. Such simulated patterns can be used as the 'gold standard' for unambiguous phase identification.

Researchers at Bristol-Myers Squibb used crystal diffraction software tools to simulate PXRD patterns as reference standards for individual crystal forms (such as polymorph, solvates, and salts).[1,2] The team observed that the small differences between observed and simulated PXRD patterns, such as the appearance of new peak(s), additional shoulders, shifts in the peak position, or abnormal intensity distribution, can indicate the presence of different forms (e.g. polymorphs, solvates), or a preferred orientation, or improperly calibrated instruments.

Accelrys Corporate Headquarters
9685 Scranton Road
San Diego, CA 92121–3752, USA
Tel: +1 858 799 5000

Accelrys European Headquarters
334 Cambridge Science Park
Cambridge, CB4 0WN, UK
Tel: +44 1223 228500

Accelrys Asia Headquarters
Nishi-shimbashi TS Bldg 11F
Nishi-shimbashi 3-3-1, Minato-ku,
Tokyo, 105-0003, Japan
Tel: 81 3 3578 3861

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In addition, a so-called 'hybrid' Rietveld Refinement method was used to circumvent problems caused by different temperatures for the single crystal structure determination and the PXRD experiments. The simulations were also used as reference standards for thermodynamic studies of bulk phase transformations by comparison to thermal and microscopic studies.

This study demonstrates that simulated PXRD patterns can be used effectively for phase identification. The approach is simple and fast, and should be viable for manufacturing process quality control and assurance.

References

1. S. Yin, R.P. Scaringe, J. Dimarco, M. Galella, J.Z. Gougoutas, *American Pharmaceutical Review,* 80-85, Summer 2003.

2. M. Davidovich, J. Z. Gougoutas, R. P. Scaringe, I. Vitez, S. Yin, Bristol-Myers Squibb Pharmaceutical Research Institute, *American Pharmaceutical Review,* 10-16, January/February 2004.