Poster Presentation

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Understanding complex phase transition mechanism by crystal structure analysis

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Xylazine hydrochloride (2-(2,6-xylidino)-5,6-dihydro-4H-1,3-thiazine hydrochloride) is an adrenergic α-agonist used as a sedative, analgesic, and muscle relaxant in veterinary medicine. It has four polymorphous forms (A, Z, M and X), monohydrate (H), hemihydrate and solvates with dichloromethane and 2-propanol. It has been reported that the polymorph X is thermodynamically the least stable of these polymorphs, while the A is the most stable form at temperatures above 50 °C. The X forms only in H dehydration process, and at elevated temperature X transforms to polymorph A [1]. The crystal structures of the polymorphs A and X as well as hydrate H have been reported. Crystal structure of A and X have been determined from the powder X-ray diffraction data (PXRD), whereas that of hydrate have been determined from single crystal X-ray diffraction data [2-3]. In this study structure of A have been determined from single crystal data and compared to that determined by PXRD data. Crystal structures of A, X and H have been compared and analysed. Molecule conformation in crystal structure of all three forms is the same and molecular packing is similar. However, that in monohydrate H and polymorph X is basically the same and the only difference is the inclusion of the water molecules next to the chlorine anions, whereas relative xylazine moiety orientation and arrangement of the chlorine anions is different in the structure of polymorph A. The structural similarity or differences between all three forms noted above were also approved by the 2D-fingerprint plots of the Hirshfeld surfaces. Analysis of all three form crystal structures allowed to better understand complex solid-state phase transition from xylazine hydrochloride polymorph X to polymorph A during and after the dehydration of it monohydrate H.

[1] *A. Bērziņš, K. Krūkle, A. Actiņš, and J. P. Kreišmanis, Pharm. Dev. Technol., 2010, 2, 217–222,* ***[2]*** *M. V Veidis, L. Orola, and R. Arajs, Acta Crystallogr. Sect. E., 2008, 6, o1062,* ***[3]*** *A. Zvirgzdins, A. Mishnevs, and A. Actiņš, Acta Crystallogr. Sect. B., press in progress*

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