

## Pirinixic Acid Derivatives as Potent Dual Agonists of the Peroxisome Proliferator Activated Receptor Alpha and Gamma

Manfred SCHUBERT-ZSILAVECZ

Schubert-Zsilavec@pharmchem.uni-frankfurt.de

Johann Wolfgang Goethe University Frankfurt,  
Institute of Pharmaceutical Chemistry/ZAFES  
Max-von-Laue-Straße 9, D-60438 Frankfurt am Main, Germany

Peroxisome proliferator-activated receptors (PPARs) comprise a three-member subgroup ( $\alpha$ ,  $\gamma$ ,  $\beta/\delta$ ) within the nuclear hormone receptor family of ligand-activated transcription factors that have been the focus of extensive research during the past decade. Being activated by the fibrate and glitazone types of drugs, PPAR  $\alpha$  and PPAR  $\gamma$  are among the major targets for the treatment of dyslipidemia and type 2 diabetes. Dual PPAR  $\alpha$ ,  $\gamma$  agonists are currently under investigation for the combined treatment of both diseases, which, furthermore, are frequently associated. In addition, PPAR is gaining more and more evidence to be an anti-inflammatory target.

Pirinix acid (WY-14643), which is a common research tool for PPAR  $\alpha$ , was developed in the 1970s as an antihypercholesterolemic agent and was found to be a peroxisome proliferator, whereas the target of pirinix acid, the peroxisome proliferator activated receptor, was discovered in 1990, which led to the discovery of the PPAR  $\alpha$  and the less known PPAR  $\gamma$  agonism of pirinix acid.

Starting with pirinix acid which is a moderately active dual PPAR  $\alpha$ ,  $\gamma$  agonist we improved potency at the human PPAR  $\alpha$  and PPAR  $\gamma$  by substituting the  $\alpha$ -position with an aliphatic chain. The maximal effect was achieved at a chain length of four and six carbon atoms respectively, leading to an activity induction by factor 36 at PPAR  $\alpha$  and 18 at PPAR  $\gamma$  respectively.

Our lead structure optimisation program also revealed that the mere substitution of the dimethyl aniline moiety of pirinix acid by quinoline leads to a total loss of PPAR  $\alpha$ ,  $\gamma$  agonism, whereas concomitant  $\alpha$ -substitution with n-butyl or n-hexyl groups restores and even enforces PPAR activation, leading to potent dual PPAR  $\alpha$ ,  $\gamma$  agonists. Molecular docking of those compounds suggests a binding mode resembling to that of tesaglitazar.

### References

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