



Figure 1 MADRS scores during the observation period (week 0 corresponds to VNS device reactivation).

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Clinical perspective on antipsychotic receptor binding affinities

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The interactions between antipsychotic drugs and cell receptors can be measured as binding affinity values, expressed in terms of the dissociation constant, K_d ; the inhibition constant, pK_i ($-\log K_i$); and the half-maximal inhibitory concentration, IC_{50} . The affinity constant values (K_i) of each ligand are experimentally measured, calculated from the Cheng-Prusoff equation: $K_i = IC_{50}/(1 + C/K_d)$, where C is the concentration of ligand and K_d is its

dissociation constant. Each medication included in the antipsychotic class has a unique receptor-binding profile. This profile, the magnitude of the bond between ligand and targets (binding affinity or K_i), and the type of pharmacodynamic action (inverse agonism, antagonism, partial agonism, agonism) all converge to determine a specific pharmacological response. A lower K_i value indicates greater ability to bind to receptors and is associated with a more potent pharmacological action. The K_i value may be calculated from pK_i :

$$pK_i = -\log K_i \rightarrow -pK_i = \log K_i \rightarrow 10^{-pK_i} = K_i$$

Thus, higher pK_i values correspond to lower K_i values, and vice versa.¹ However, we suppose that sometimes a mix-up can occur between different measures of receptor-binding affinity. For instance, in a review² published in 2010, K_i values for asenapine are reported as follows: D2 (8.9), 5-HT1A (8.6), 5-HT2A (10.15), 5-HT2C (10.46), α_1 (8.9), H1 (9.0), M1 (5.09), while in a previous paper³ the same numerical values described in the review mentioned above are presented as pK_i , not K_i : D2 (8.9), 5-HT1A (8.6), 5-HT2A (10.2), 5-HT2C (10.5), α_1 (8.9), H1 (9.0), M1 (5.09). Also, it is important to keep in mind that K_i values may be obtained under heterogeneous laboratory conditions (e.g., different tissue sources, species, and radioligands).

The purpose of our Letter is to briefly highlight the utmost importance of correctly understanding and reporting data on binding affinities and how they determine the clinical role of each antipsychotic drug. Proper knowledge of binding affinity profiles is decisive to:

- i) predicting the specific efficacy of a drug on positive (e.g., antagonism and low K_i to D2), negative (e.g., high 5-HT2A/D2 ratio), and cognitive (e.g., antagonism and low K_i to 5-HT7) symptoms of schizophrenia;
- ii) considering a dimensional pharmacotherapeutic approach, rather than a strictly categorical one;
- iii) detecting specific propensity to trigger extrapyramidal symptoms, hyperprolactinemia, sexual dysfunctions, sedative/metabolic, and antiadrenergic/anticholinergic/antihistaminergic effects;
- iv) defining the best switching strategies between different antipsychotics, choosing among abrupt switch, taper switch, cross-taper switch, or plateau-cross-taper switch;
- v) predicting dopaminergic/adrenergic/cholinergic/serotonin/histamine rebound;
- vi) determining the potential pharmacodynamic synergy of antipsychotic polypharmacy to choose a suitable complementary affinity profile;

- vii) applying results of preclinical pharmacology studies to humans;
- viii) using pharmacoepidemiologic-pharmacodynamic methods to investigate the mechanisms of adverse drug reactions recorded in pharmacovigilance databases;
- ix) understanding the pharmacodynamic factors involved in pharmacogenomic-directed therapeutics; and
- x) orientating clinicians toward precision medicine.¹⁻⁵

We hope that clarifying the difference between pK_i and K_i will prevent perpetuation of potential incorrectness in the scientific literature. Furthermore, some of our considerations may be applied to other drugs. We believe that having this topic clear in mind may be of crucial importance both for clinical and research purposes.

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Disclosure

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