



DETERMINATION OF VORICONAZOLE METABOLISER PHENOTYPE IN THE ABSENCE OF GENETIC TESTING

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BACKGROUND AND IMPORTANCE

It is metabolized mainly by CYP2C19 → enzyme with a considerable genetic polymorphism → variable metabolism in the population



Its genotyping is expensive and inaccessible → Development of alternative methods to determine the patient's metaboliser phenotype

AIM AND OBJECTIVES

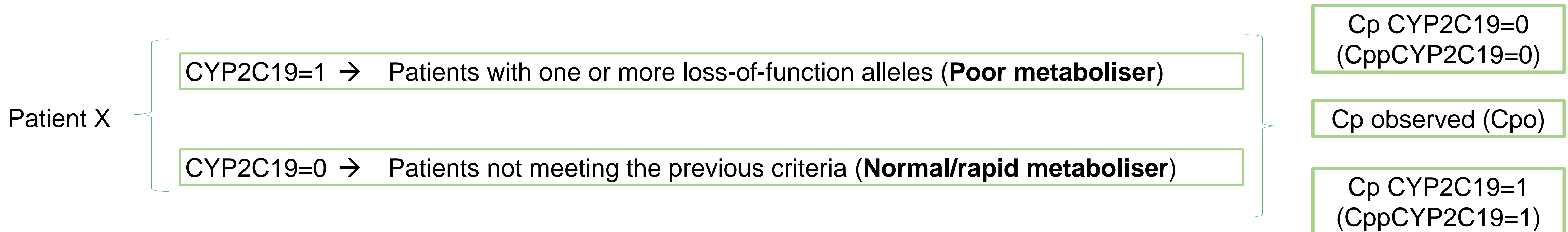
To determine the metaboliser phenotype according to plasma concentrations (Cp) of voriconazole using a population pharmacokinetic model

MATERIALS AND METHODS

Observational, descriptive, retrospective study of patients treated with intravenous and oral voriconazole in a second level hospital from 01/2016 to 06/2024.

1. Clinical data collection: medical history number, weight, posology, route and rate of administration, Cp and concomitant treatments with prednisone, methylprednisolone, dexamethasone, carbamazepine, phenytoin, ritonavir and St. John's wort.

2. Application the Dolton pharmacokinetic model to each patient using NONMEM software through Pirana



3. Deduction of metaboliser phenotype

C _{po} value closest to C _{pp} CYP2C19=1	→	Poor metaboliser
C _{po} value closest to C _{pp} CYP2C19=0	→	Normal/rapid metaboliser
Values very different or very similar to each other	→	Not possible to determine the metaboliser phenotype

RESULTS

Metaboliser phenotype	Number of patients (%)
Normal/rapid	30 (63.9%)
Poor	3 (6,4%)
Not determined	14 (29,7%)

Patients= 47 → Cp voriconazole= 85

CONCLUSION AND RELEVANCE

The metaboliser phenotype could be estimated in 70,3% of patients.

The application of the Dolton pharmacokinetic model to the Cp of voriconazole obtained could be a useful tool, in the absence of genetic studies, to determine the metaboliser phenotype of our patient.