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Synergistic interaction between antifungal agents against Candida guilliermondii using pharmacodynamics-modelling approach

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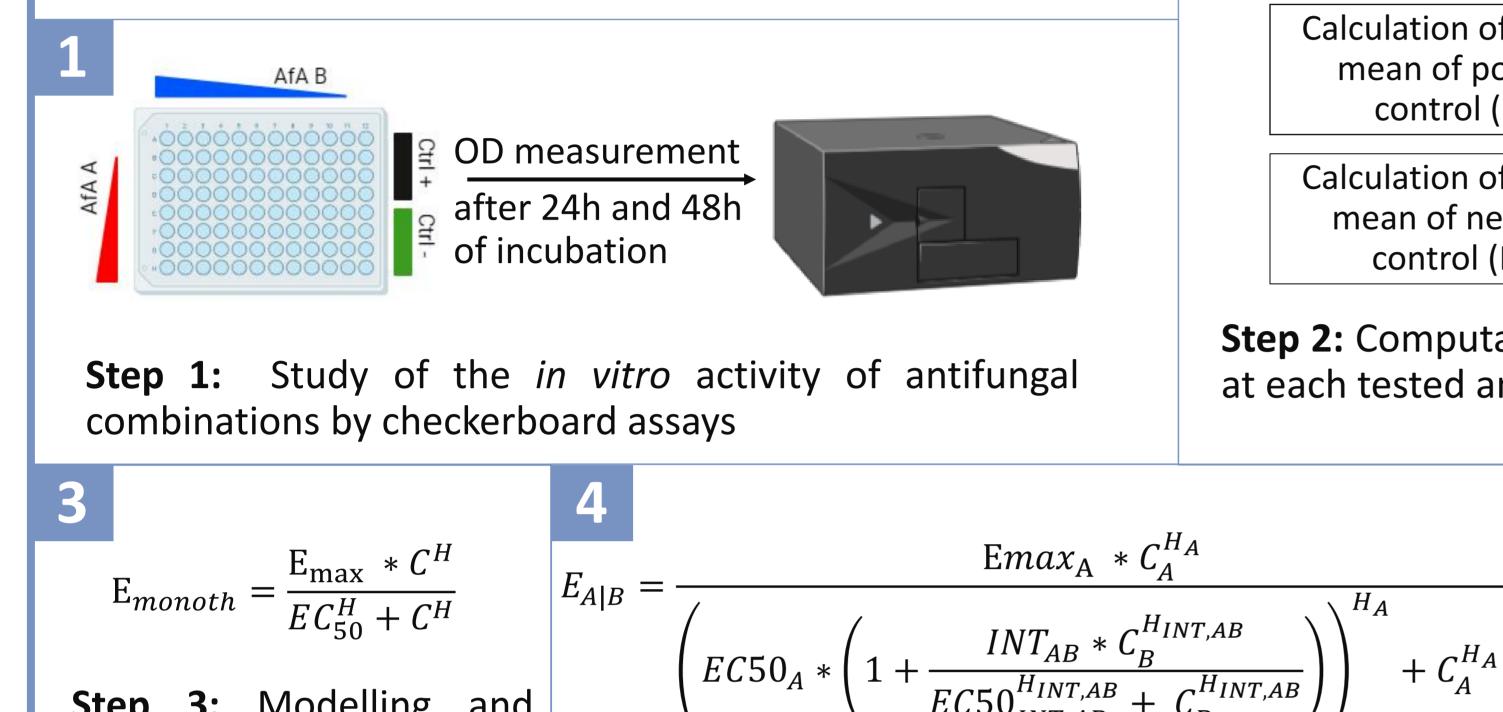
Introduction

Candida guilliermondii is a yeast species involved in candidemia. It presents high MICs for echinocandins, the first-line treatment, and several strains showed tolerance to amphotericin B (AmB). The objective of this study was to test in vitro combinations of antifungal agents against clinical isolates of C. guilliermondii by using an innovative pharmacodynamics-modelling approach to evaluate the interactions between antifungal agents. This approach is used to replace the fractional inhibitory combination index (FICI), which is unusable due to the varied definitions of MIC (Minimum Inhibitory Concentration) for antifungal agents, such as 90% or 50% growth inhibition.

Materials and methods

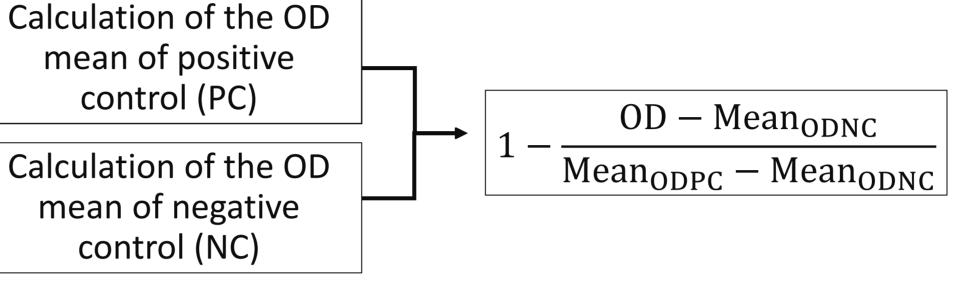


Microbiological materials: Checkerboard assays were performed



$$\left(EC50_A * \left(1 + \frac{INI_{AB} * C_B}{EC50_{INT,AB}} + C_B^{H_{INT,AB}} \right) + C_B^{H_{INT,AB}} + C_B^{H_{IN$$

Step 4: Modelling and simulation of the combination effect for all antifungals, strains, time, concentration combination



Step 2: Computation of the growth inhibition percentage at each tested antifungal agent(s) concentrations¹

 $Effect improvement = E_{AandB} - \max(E_A, E_B)$

Step 5: Computation of the difference effect (effect improvement = of increase of growth inhibition) between combination and the best the monotherapy effect of the same combination

using RPMI medium and 5 different antifungal combinations :

- AmB/micafungine (MICA)
- AmB/fluconazole (FLU)
- AmB/voriconazole (VORI)
- MICA/FLU
- MICA/VORI

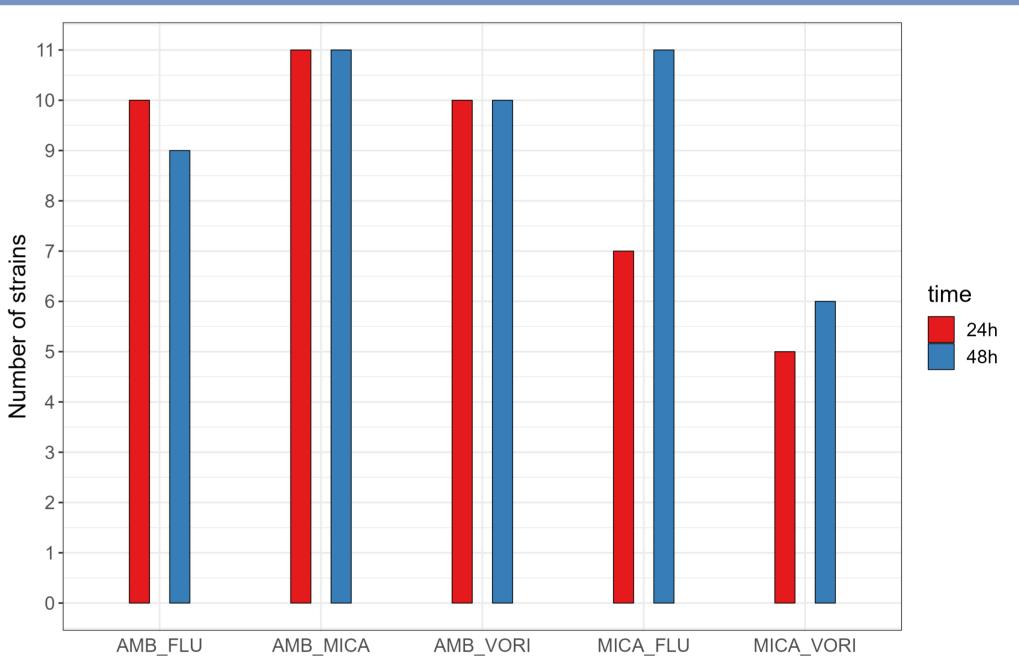
11 C. guilliermondii strains were tested, ATCC 6260 and 10 clinical isolates including 3 azole-resistant strains $(MIC_{FIU} > 16 \text{ mg/L} \text{ and } MIC_{VORI} > 0,25)$ mg/L).

Mathematical methods and software:

An Emax model fitted to was monotherapy data. It was modified following the GPDI² method to fit combination data. Modelling and simulation were performed with R³ version 4.3.2.

Results

We developed models that successfully described the effect of the five combination therapies at 70 different concentration combinations against the 11 strains. From the final models, we were able to quantify the improvement of the effect of the combination in comparison to the most efficient monotherapy at equivalent concentrations. Representative data for one strain are showed in Figure 1.



After data analyzing, synergy was defined as an improvement of at least 20% for the concentration combination in comparison to the most efficient monotherapy.

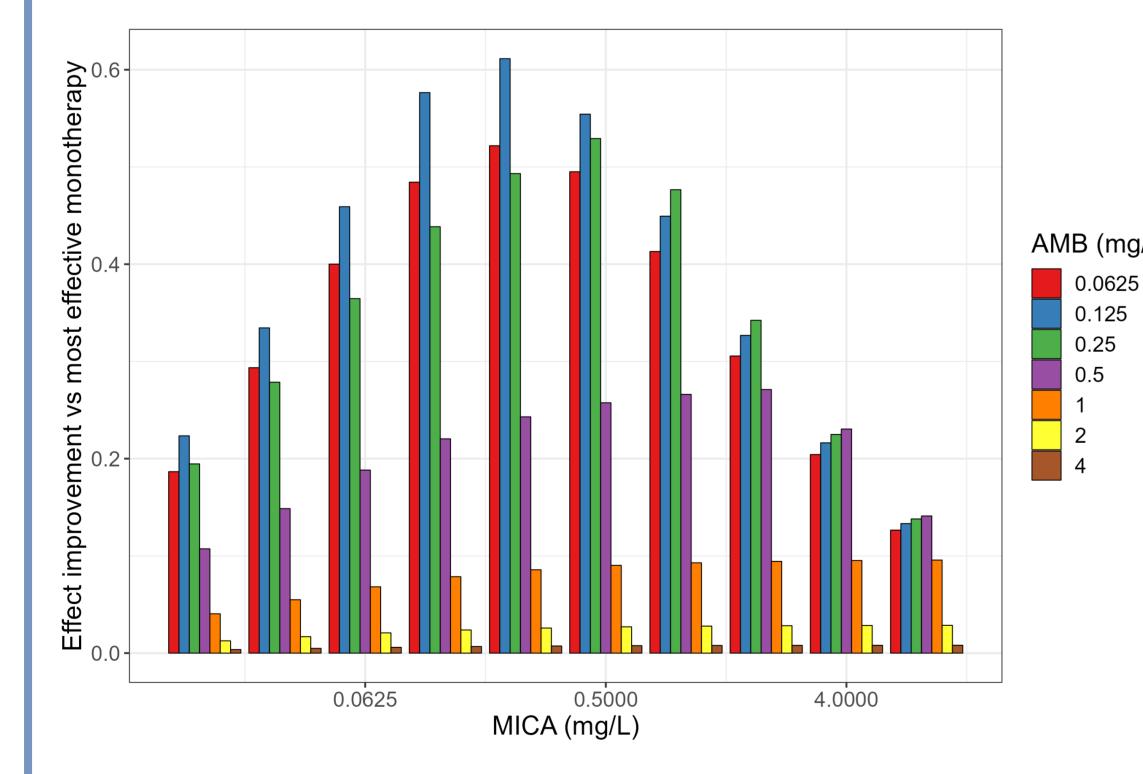


Figure 1: Representative data for one combination (AMB/MICA) against one strain (G9) at one time (48h).

The model suggested synergy for (Figure 2) :

- The majority of strains for the **AmB/azole** combinations, including azole-resistant strains.
- AMB (mg/L) Every strains for **AMB/MICA combination** at both 24h and 48h.
 - Several strains for MICA/FLU combination.

AMB/MICA combination the The was combination with the highest number of concentration combinations that showed synergy (Figure 3).

Figure 2: Number of strains with at least one synergistic concentration combination.

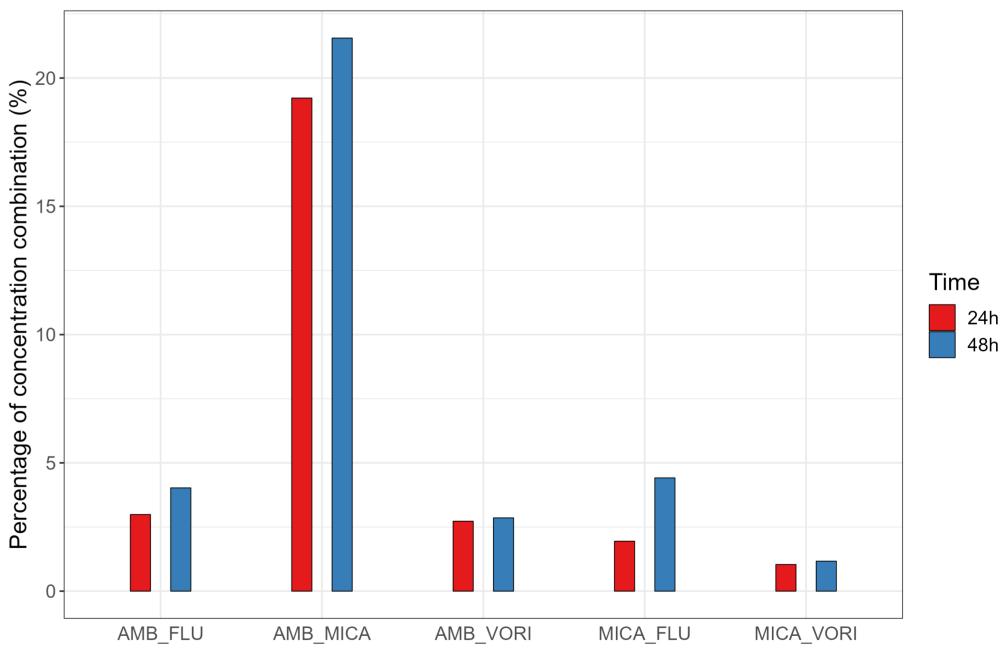


Figure 3: Percentage of synergistic concentration combinations for every strains.

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Conclusion

The pharmacodynamics-modelling approach allowed us to evaluate combined effect of antifungal agents without the need to binarize our results as necessitated by traditional methods such as the fractional inhibitory combination index (FICI). The model suggested synergy for the majority of strains for the AmB/azole (9/11 strains) and AmB/MICA (11/11 strains) combinations, including azole-resistant strains. The model suggested that AMB/MICA was the combination with the most effective concentration combinations against the tested strains. No tested combination exhibited antagonism.

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References

1) EUCAST_E.Def_7.4_Yeast_definitive_revised_2023 2) Wicha et al. <u>10.1038/s41467-017-01929-y</u>

3) R Core Team (2023) https://www.R-project.org/



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