



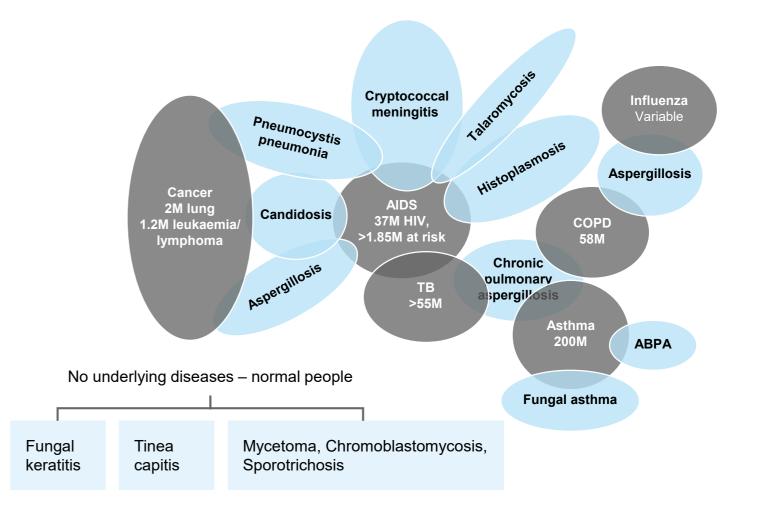
Evotec

Integrated Drug Discovery in Antifungal Research



Global burden of fungal disease

- Globally, over 300 million people are afflicted with a serious fungal infection and 25 million are at high risk of dying or losing their sight
- Estimates for the global burden of fungal diseases are based on population and disease demographics (age, gender, HIV infected, asthma etc.)
- Fungal diseases can be
 - Acute and severe (i.e. cryptococcal meningitis and fungal eye infection (keratitis)
 - Recurrent (i.e. *Candida* vaginitis or oral candidiasis in AIDS)
 - Chronic (i.e. chronic pulmonary aspergillosis or fungal hair infection (tinea capitis)

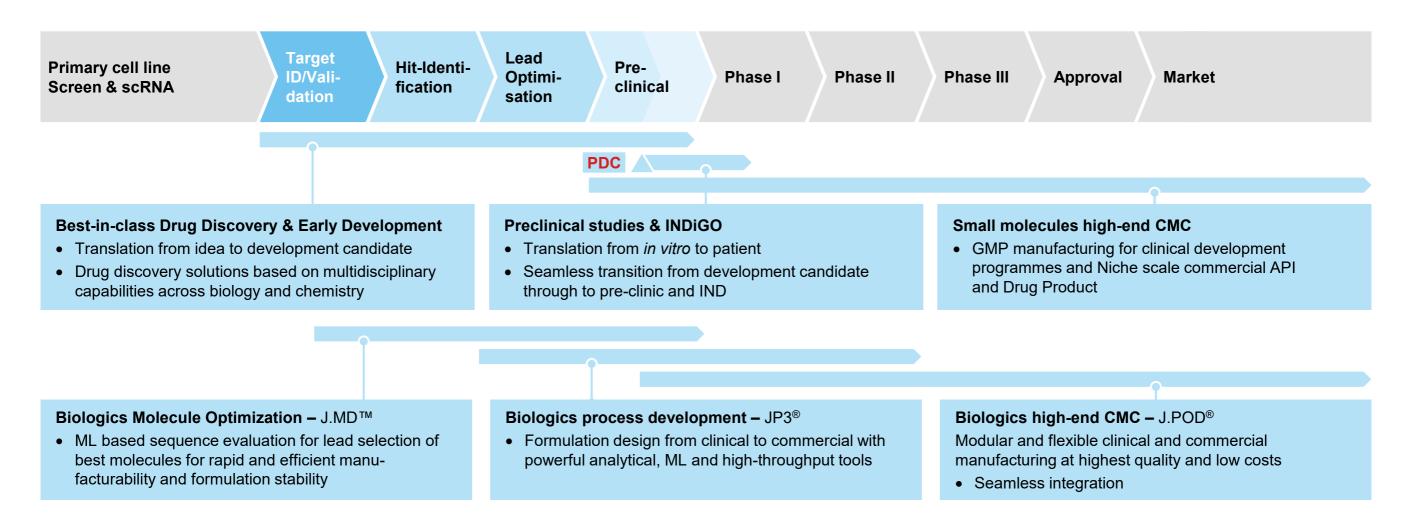


Gaffi - Global Action For Fungal Infections - https://gaffi.org/why/fungal-disease-frequency/



Relevant, seamless and state of the art

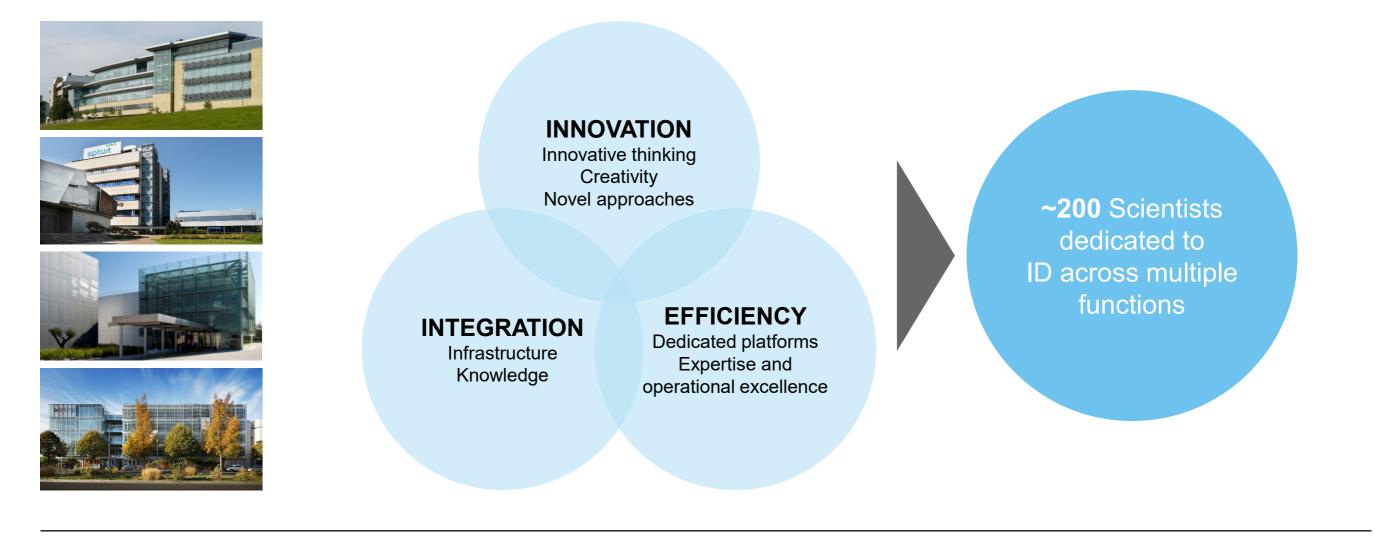
Integrated value chain





Evotec is confronting the renewed challenge in Infectious Diseases

Innovation and operational excellence





Fully integrated drug discovery and disease biology

Combining world-class expertise and platforms

- Deep rooted heritage in ID: High calibre scientists
- **Strong expertise:** Dedicated technologies and scientific platforms
- Global partner network: Foundations, BRIDGES, KOLs
- EvostrAIn[™]: Highly valuable collection of ~10,000 strains from clinic and reference collections including ~300 fungal isolates

 In vivo pharmacology and biomarker solutions: Efficacy, PK/PD, ex vivo platform

- Designing a TPP-driven strategy & screening cascade
 - From HTS to Lead identification and optimization
 - Clear criteria for progression
 - Link between in vitro activity and in vivo efficacy
- Supporting the development of multiple therapeutic modalities
 - From small molecules to biologics and large molecules
 - Traditional and non-traditional target
 - Full integration with DMPK, Immunology and Toxicology platforms
- Development of disease models representing pathological conditions
 - Use of clinical isolates from seriously ill patients
 - Qualify the model on the basis of host infection biomarkers
 - Apply imaging technologies for real time evaluation of progression and infection distribution



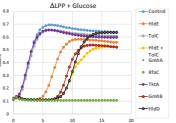
The anti-infective autobahn: from discovery biology to the clinic

Seamless program progression from discovery to development

Discovery biology

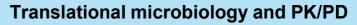
- Standard microbiology on a large strain collection (MIC, MIC₉₀, TKC, FoR, PAE, resistant mutants characterization, etc.)
- Target identification
- MoA/MoR determination and molecular profiling
- Omics and sequencing technologies
- Generation of engineered bacteria
- Target or Whole-cell based assay development

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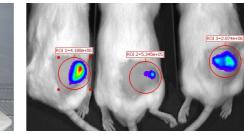


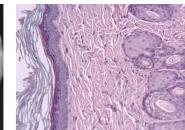
- Label-free bacterial intracellular compound accumulation assay
- Phenotypic screening (Biolog)
- Vivo-mimetic screening
- Target-based screening including fragment approaches
- Medicinal chemistry
- Computational chemistry and structure based drug design
- Highly efficient DMTA cycles



- State of the art in vivo DMPK
- In vivo microbiology for efficacy profiling
- In vivo and in vitro PK/PD platforms including Hollow fibre systems
- Mathematical modelling and simulations
- Translation of discovery data to the clinical setting









EvostrAIn™: a dedicated resource for AMR programs

Evotec's collection of characterised strains and clinical isolates

- Constantly evolving resource of thousands of primary clinical isolates and reference strains
- Broad collection of bacteria, fungi, viruses & parasites
 - ~10,000 strains from the clinic and culture collections
 - Global, recent sources with continual refreshment
 - High degree of characterisation (susceptibility profiles, mechanisms of resistance and in vivo drug response, genome sequences available)
 - Includes isogenic mutant strains and mutant libraries
- Used to establish spectrum of activity and potential clinical use of new antimicrobials
- Rapidly build bespoke panels
 - Guide SAR
 - MoA / MoR (target validation & identification)
 - TPP validation
 - Translational activities





EvostrAln™

Bacteria, fungi, viruses

Bacteria: Gram positive pathogens

- Staphylococcus aureus incl. MRSA, VISA & VRSA strains
- β-Haemolytic streptococci groups A, B, C & G
- Streptococcus pneumoniae (including penicillin, macrolide, fluoroquinolone, cephalosporin & MDRSP resistant strains)
- Vancomycin Resistant Enterococci (VRE)
- Bacillus species
- Listeria species
- Corynebacterium and Propionibacterium species
- *Clostridium difficile* (multiple ribotypes incl. 012, 027 & 078)
- Other *Clostridia* (including C. *perfringens*)
- Constituents of gut microbiota
- Mycobacteria (*Mtb* & non-*MTb*)

Bacteria: Gram negative pathogens

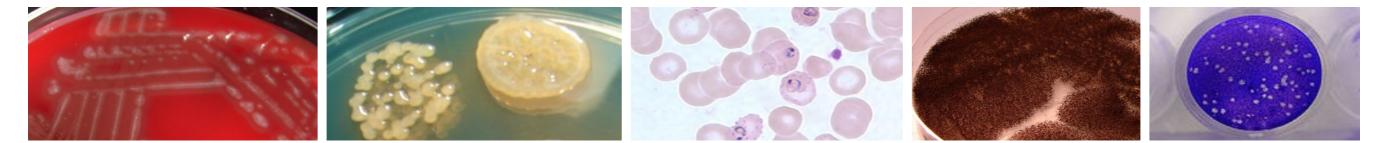
- E. coli including Extended Beta lactamase producing strains
- Klebsiella pneumoniae Carbapenemase producing strains (KPCs & MDR XDR)
- Acinetobacter baumannii incl. MDR XDR
- Pseudomonas spp. including MDR XDR
- Haemophilus influenzae
- Bacteroides spp.
- Neisseria gonorrhoeae and N. meningitidis
- Intestinal pathogens: *Vibrio* spp, *Campylobacter* spp incl. pylori, *Salmonella* spp, *Shigella* spp, *Yersinia* spp.
- Legionella spp. and Chlamydia (ongoing)
- Other Enterobacteriaceae: Enterobacter, Proteus, Citrobacter, Serratia, Prividencia & Moraganella
- Burkholderia and Stenotrophomonas

Fungi

- Aspergillus spp. (resistant to azoles, polyenes and echinocandins)
- *Candida* spp. (resistant to azoles, polyenes and echinocandins)
- Mucorales
- Cryptococcus
- Dermatophytes (Fusarium)

Viruses

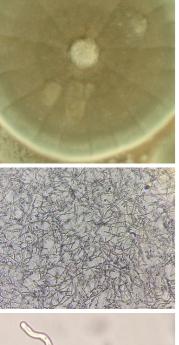
- SARS-CoCV2 (all VOC)
- Influenza virus
- Respiratory syncytial virus
- Human rhinovirus
- Human parainfluenza virus
- Human metapneumovirus
- Hepatitis B virus





Breadth and depth of microbiology expertise

Characterisation of microbiological activity





- Primary screening
- Panels of fully susceptible organisms and multidrug resistant strains that exhibit a broad range of resistant mechanisms and phenotypes. Clinically relevant and recently isolated bacterial, fungal and viral panels.
- Large and rapidly evolving collection of highly characterised clinical isolates and strains (EvostrAIn[™])
- Potencies of compounds (MIC/MFC/MPC/IC₅₀)
 - Standardised methods where available (CLSI, EUCAST), miniaturized methods when required (non CLSI)
 - Detailed screening against bespoke panels of pathogens
 - Additional visual endpoint for fungal MEC (minimum effective concentration), defined as lowest concentration in which abnormal, short, and branched hyphal clusters are observed.
 - Enzyme and cellular assays
 - Time Kill Curves
- Combination studies
 - Checkerboard assays to assess synergy, additive activity, and antagonism
 - Mathematical modelling of data





Testing of a panel of clinical *Candida* isolates

Case study

• Assessment of the In Vitro Antifungal Activity of SCY-078 Against a Panel of Susceptible and Resistant Clinical Candida Isolates from Europe

- Collaboration with University Hospital of South Manchester, Manchester, UK
- Evaluation of the in vitro antifungal activity of SCY-078 against a panel of recent clinical Candida isolates from the EU
- A panel of 270 clinical *Candida* strains isolated from referring hospitals throughout the was tested for sensitivity against SCY-078, Amphotericin B, Anidulafungin, Micafungin, Caspofungin, Fluconazole, Voriconazole and Posaconazole
- Panel composition: C. albicans (n=99), C. glabrata (n=72), C. guilliermondii (n=17), C. krusei (n=14), C. lusitaniae (n=10), C. parapsilosis (n=41), C. dubliniensis (n=6), C. inconspicua (n=1), C. kefyr (n=2) and C. tropicalis (n=9)
- SCY-078 demonstrated potent, broad spectrum activity against a panel of clinical *Candida* isolates. Notably, SCY-078 retained activity against all of the echinocandin- and azole-resistant *C. glabrata* isolates tested.

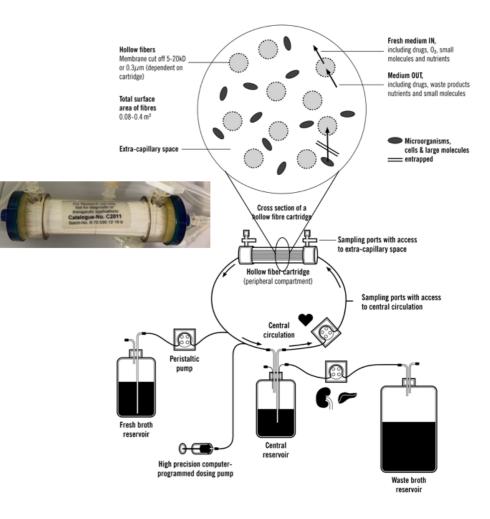
SCY-078 MICs vs DRUG RESISTANT <i>C. glabrata</i>						
<i>C. glabrata</i> Isolates	Total (N=72)	Anidulafungin Resistant (N=64)	Micafungin Resistant (N=43)	Anidulafungin and Micafungin Resistant (N=41)	Fluconazole Resistant (N=7)	
SCY-078 MIC (µg/mL)	$MIC_{50} = 1$ $MIC_{90} = 1$ Range 0.125 - 2	MIC ₅₀ = 1 MIC ₉₀ = 1 Range 0.25 - 2	MIC ₅₀ = 1 MIC ₉₀ = 1 Range 0.25 - 2	MIC ₅₀ = 1 MIC ₉₀ = 1 Range 0.25 - 2	Range 0.25 - 1	



Hollow Fibre Infection Model (HFIM)

Understanding the PK/PD relationship

- The Hollow Fibre Infection Model provides a dynamic *in vitro* method of assessing the impact of a time course of drug exposure(s) on a cell or combination of cells
- The most capable *in vitro* model for evaluating PK/PD indices and optimising dosing regimens for bacterial or fungal killing and suppressing the amplification of drug resistant mutant subpopulations
- Two principal compartments:
 - Central reservoir and associated tubing which constitutes a circulating system
 - A hollow fibre cartridge containing thousands of permeable capillaries, sealed at both ends within a tubular polycarbonate shell. The extracapillary space (ECS) outside the fibres but within the cartridge housing contains the target organism.
- Drug-infused growth medium in the central reservoir is continuously pumped to the hollow fibre cartridge, rapidly passes through the capillaries and equilibrates with medium in ECS. Nutrients and oxygen are continuously refreshed, waste products are removed
- Using infusion and clearance pumps any PK profile (animal, human) including drug combinations can be simulated
- System can also be applied to determine resistance development
- HFIM study designs can be tailored to specific requirements or bespoke client protocols



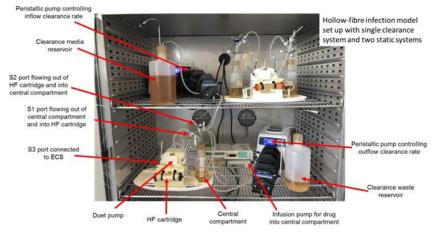


Hollow Fibre Infection Model

Capabilities, capacity and experience at Evotec

- Experience at Evotec with HFIM for:
 - Mycobacterium tuberculosis H37Ra
 - Bacteria: Acinetobacter baumannii, Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa, ...
 - Fungi: Aspergillus fumigatus
- Containment level 2 laboratory space dedicated to running HFIM studies
- Up to 34 hollow fibre cartridges¹⁾ can be operated in parallel for different organisms, using variable drug infusion and clearance rates, with study durations ranging from hours to 6 weeks
- Dedicated team of scientists trained to operate the system
- Full range of microbiology support including alternative endpoints, whole-genome sequencing and bioinformatics services to support resistance characterisation studies, and mechanism of action determination
- Bioanalysis facilities for LC-MS analysis of PK samples
- A dedicated PK/PD modelling team
 - Experimental design for single- and multiple-drug experiments
 - Generation of infusion parameters (duration, rates, frequency) to reproduce specific PK profile
 - Mathematical models for interpretation of pharmacokinetic and pharmacodynamic data

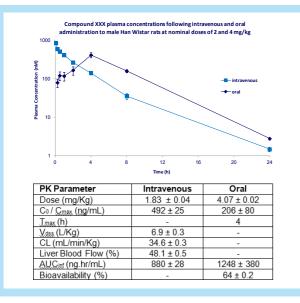






Pharmacokinetic profiling in anti-infective drug discovery

From in vivo characterisation to bioanalysis and biomarker assessment



- Standard and specialised PK studies in multiple rodent species:
 - Administration routes; intravenous (prolonged infusion), per oral, intraperitoneal, subcutaneous, intra cerebrospinal, intramuscular, pulmonary (nebulized, aerosolized), iPrecio & Alzet pumps
- Sampling types: jugular vein cannulation, cardiac puncture, tail vein microsampling
- Matrices: blood, plasma, CSF, BALF, whole tissues, bile, urine and faeces
- PK in infected animals assessing impact of disease state on drug exposure
- Data directly translated into efficacy studies to optimise outcomes
- PK experiments designed to accompany PK/PD profiling programmes



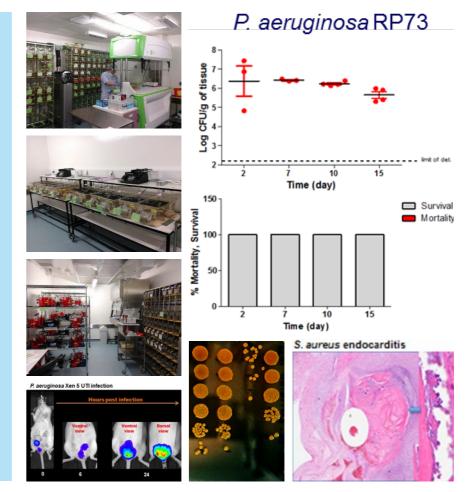
- State-of-the-art bioanalytics
 - Highly sensitive biophysical methods including LC-MSMS
 - Bioassay techniques: tracking biological activity
- Biomarker quantification: pathogen/infection specific and host response



Comprehensive translational microbiology platform

Integrating *in vivo* pharmacology and DMPK

- State-of-the-art animal facilities (**BSL 2 & 3**) to house rodents, immunocompromised animals, and multiple backgrounds (incl. dogs and monkeys AAALAC accredited)
- Target validation, tolerability studies, DMPK studies, PK/PD studies, *in vivo* MoA studies, efficacy screening
- Multiple hosts and fully validated models of infection: Rat, mouse, guinea pig, hamster, cotton rat, rabbit
- Multiple routes of infection include: lung, thigh, blood (sepsis), skin, urinary tract, GI tract, vagina, bone
- Full range of endpoints: pathogen burden (culture, qPCR, biomarkers), host response
- Real time imaging of microbes during infection: IVIS, MRI, CAT, PET
- New model development programme
- Invertebrate screening model for bacteria & fungi (wax moth larva rapid screening models)



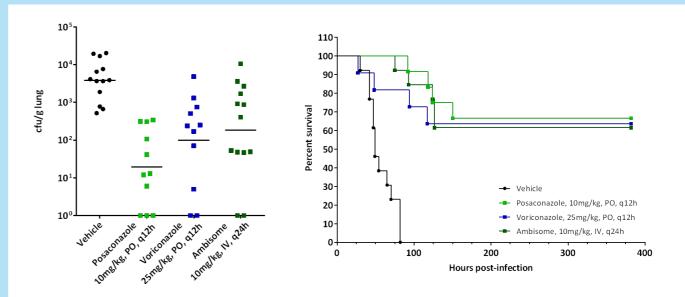


Breadth of in vivo models of fungal infection

Summary and Aspergillus lung infection as example

Model	Pathogen	Animal species	lmmune system
	A. fumigtaus, A. flavus, A. terreus	Mouse	neutropenic
Acuto Soncia	C. albicans, C. glabrata, C. tropicalis	Mouse	neutropenic
Acute Sepsis	C. auris	Mouse	neutropenic
	C. neoformans	Mouse	neutropenic
Chronic Sepsis	C. albicans	Mouse	competent
Brain	C. neoformans	Mouse	neutropenic
Dialli	C. albicans	Mouse	neutropenic
GI tract	C. albicans	Mouse	competent
Griaci	C. albicans	Rat	competent
Skin	M. pachydermatis	Guinea pig	competent
SKIII	T. mentagrophytes	Guinea pig	competent
Vaginal	C. albicans	Mouse	competent
Vaginal	C. albicans	Rat	competent
Lung	A. fumigatus, A. flavus, A. terreus	Mouse	neutropenic
Lung aerosolised	A. fumigatus	Mouse	neutropenic
Oropharyngeal	C. albicans	Mouse	neutropenic

Neutropenic murine model of *A. fumigatus* lung infection. Survival and lung burden as endpoints:

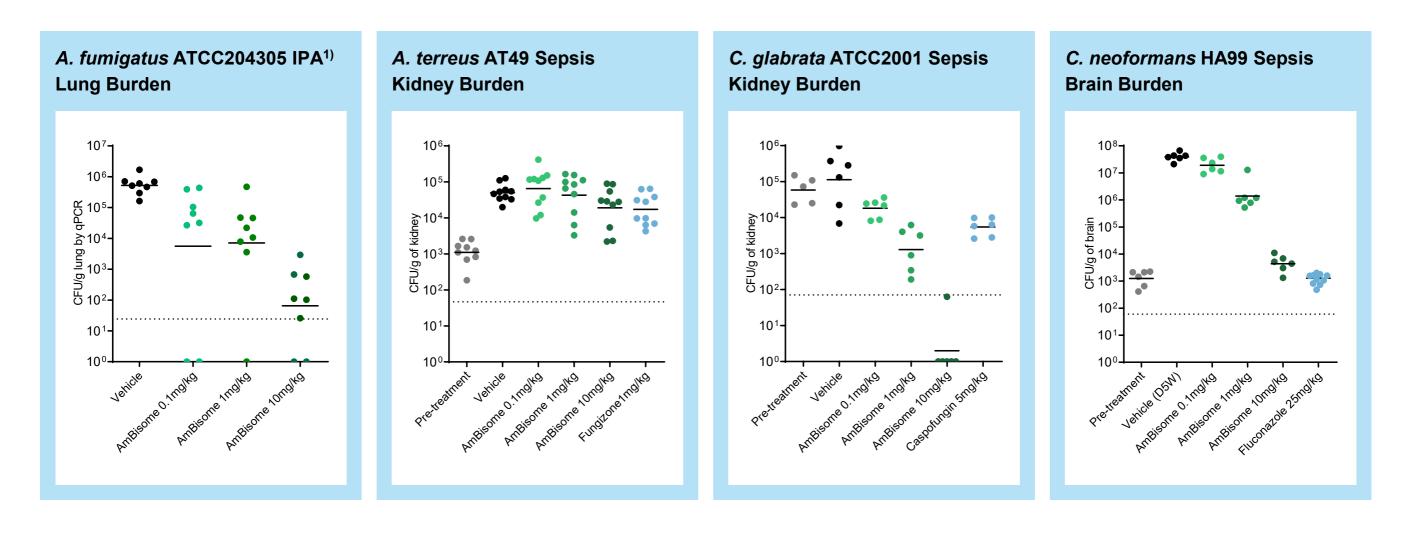


Additional endpoints: cytokines, cellular response, galactomannan, β glucan, histopathology



In vivo pharmacology – fungal infection models

Example Data^{2, 3}



¹⁾ IPA= Invasive pulmonary *Aspergillosis*, preferred measure of burden for IPA model is qPCR due to known difficulties recovering *Aspergillus* from lung tissues using standard microbiological culture ²⁾ Extended duration models are available to determine survival

³⁾ Additional types of models including vaginal and oral candidiasis, gastrointestinal tract infection and dermatophyte skin infection models are also available

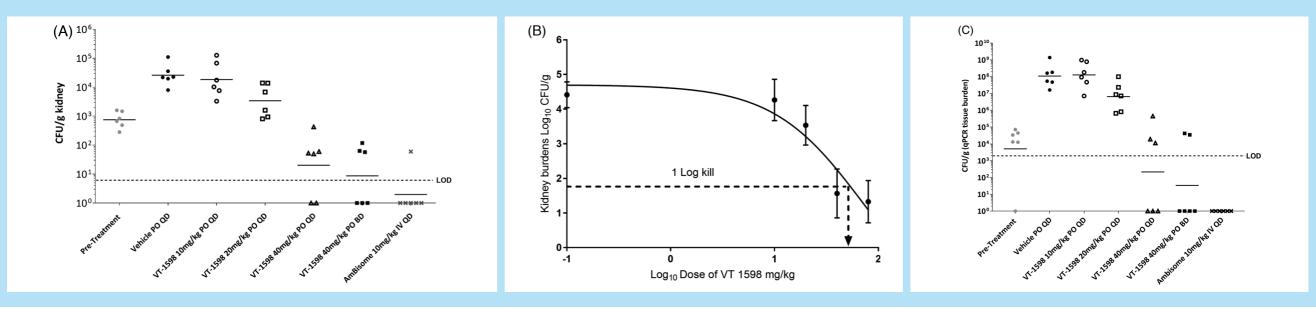


Aspergillosis model

Case study

VT-1598 dose-dependent reductions in fungal burdens in a neutropenic mouse acute model of disseminated invasive aspergillosis using *Aspergillus fumigatus* ATCC 204305 to infect

- A. Fungal burdens were determined by quantitative culture of kidney samples collected 1 day after the last treatment
- B. Kidney burden/dose response relationship to determine 1-log killing dose (i.e., the dose that would reduce fungal burden prior to treatment by 1-log)
- C. Fungal burdens were determined by measuring fungal DNA by qPCR in kidney samples collected 1 day after the last treatment. For each dose group shown in panels A and B, solid bar within each data set represents mean value. Dashed lines represent limit of detection (LOD).

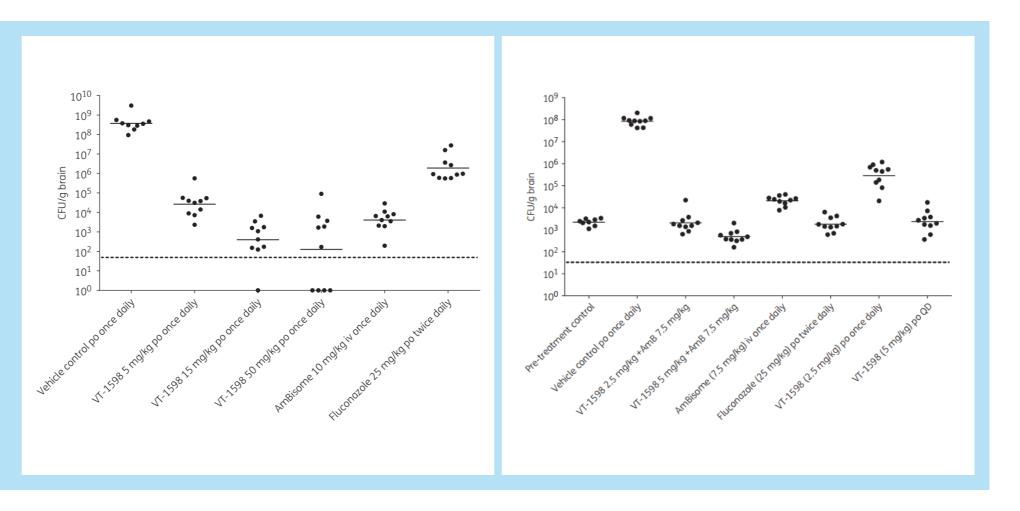




Cryptococcal meningitis model

Case study

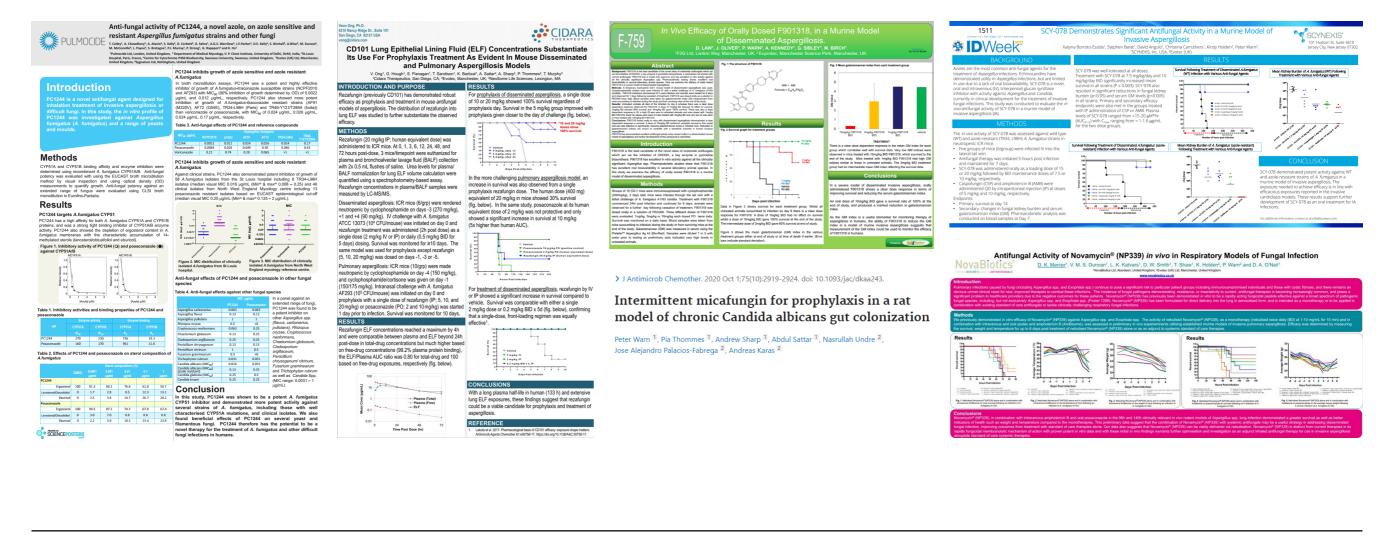
- VT-1598 maintains dosedependent reduction in brain fungal burden in treating murine cryptococcal meningitis after a 6 day drug washout
- VT-1598/AmBisome combination increases antifungal efficacy of both monotherapies in treating murine cryptococcal meningitis
- Treatment began 1 day after inoculation of *C. neoformans* H99 and lasted for 14 days, with brain samples collected 6 days after the last dose





Fungal disease models at Evotec

Publications





#RESEARCHNEVERSTOPS

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