



Genome of Plasmodium

Plasmodium Genome :

- •. 20-25 Megabases
- •. 14 Chromosomes
- •. Haploïd
- •. ~5500 Genes

•. 60% with no orthologue in databases (hypothetical genes)

- •. Most genes 1-2 kb
- •. 50% genes have more than one exon

•. Genomes of rodent malaria parasites are homologous to those of human malaria parasites (except from subtelomeric regions).



Reverse Genetics : Site-directed Mutagenesis

(From Genotype to Phenotype, Gene Characterization)

Homologous Recombination 'Constant' Mutagenesis 'Conditional' Mutagenesis RNA Interference

Forward Genetics: Random Mutagenesis (From Phenotype to Genotype, Gene Identification)

Transposition Non Homologous Recombination

Systematic Mutagenesis: Pool, Gene-by-Gene Mutagenesis

Homologous Recombination or RNAi...



Transfection of *Plasmodium*



- P. falciparum : in vitro selection
- *P. berghei* : in vivo selection

TRANSFECTION

	Stage	Linear DNA	SCO	DCO	Selection
P. berghei	Extra	+	+	+	7-10 days
P. falciparum	Intra	-	+	+	Months

P. yoelii, P. knowlesi



1995:

Episomal transfection of *P. berghei* RBC stages (van Dijk et al, 1995, Science 268, 1358-62)

P. falciparum RBC stages (Wu et al, 1995, PNAS 92, 973-7)

1996:

Integrative transfection of *P. berghei* RBC stages (van Dijk et al, 1996, Science 271, 662-5)

P. falciparum RBC stages (Wu et al, 1996, PNAS 93, 1130-4)

100% homologous recombination (HR)

1997:

Gene Inactivation in *P. berghei* mosquito stages (Menard et al, 1997, Nature 385, 336-40) *P. falciparum* RBC stages (Crabb et al, 1997, Cell 89, 287-296)



Homologous recombination



For genome modifications

Need markers





Manipulating the *Plasmodium* Genome

Positive Selectable Markers

Example: hDHFR (human Dihydrofolate-reductase)



pyrimethamine



Negative Selectable Markers

Example: *yFCU* (yeast cytosine deaminase-uridyl phosphoribosyl transferase): 5-FC^S



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5-FC(ytosine) → 5-FU(racil) : TOXIC !!
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Transfection efficiency





Gene Inactivation

Gene Knock Out



Inactivation by Insertion (Pb & Pf)



CDS interrupted, mutation unstable



Inactivation by Replacement (Linear DNA, Pb)



CDS deleted, mutation stable



Inactivation by Replacement (Pf, No linear DNA)





Inactivation by Replacement (Pf, No linear DNA)





Gene Modification

Structure-Function Analysis Function of individual domains of a protein



Gene Modification by Replacement (Pb)





Gene Modification by Insertion (Pb & Pf)



Nunes et al., 1999, Mol Cell Biol 19, 2895-902



Transfection and phenotyping





Phenotype: what to conclude?

Phenotype can be due to mutation in locus Y unrelated to gene X KO Characterize 2 (independent) clones

Phenotype can be due to distance/polar effect on another gene than gene X All clones have the same defective phenotype

Phenotype is indeed due to the lack of protein X



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KO Complementation

Complementation (restoration of WT phenotype upon reintroduction of the targeted gene) is the only way to demonstrate that the phenotype of the KO is due to the inactivation of the targeted gene



Gene deletion (KO) using *DHFR-TS* (Pyr) and reintroduction of the gene (episomal or inserted) using *hDHFR* (WR).



WT phenotype?





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Three ways:

Level of Protein: Protein Destabilization

Level of RNA: Transcriptional Shut-down Level of DNA: Site-specific Excision





Amstrong and Golberg., 2007, Nat Methods Herm-Götz et al., 2007, Nat Methods



Conditional Protein Inactivation

Conditional Protein Inactivation using 'dd' System



Protein degraded via host cell proteasome

If only Episomal Expression : Conditional expression of dominant-negative (DN) constructs (- then +)

If replacement of WT copy possible : Conditional protein depletion (+ then -) !!





Amstrong and Golberg., 2007, Nat Methods 4, 1007-1009



PIA – Protein Interference Assays



*A) Pf*AspAT is a dimer (individual monomers shown in yellow and blue), with the dimeric interface stabilize by a 13-residue "Arm" (red). B) The two active sites of *Pf*AspAT are formed by contributions from both of the monomers (Y72) from one monomer (yellow) and R257 (blue) from the other.

Meissner et al., 2017, Curr Drug Targets



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Meissner et al., 2017, Curr Drug Targets



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Conditional Protein Inactivation

Transcriptional Regulators (RNA)









Conditional Protein Inactivation

Tetracycline Transactivators



'Toxoplasma' tTA (TATi)

Meissner et al., 2002, Science 298, 837-840 Mital et al, 2005, Mol Biol Cell 16, 4341-4349





(Meissner et al. 2005, PNAS)

Tet- System in *P. falciparum*





Tet-OFF System in P. falciparum







(Prommana et al. 2013)

glmS system – ribozyme RNA degradation



The ribozyme efficiently cleaves the 3' end of the transcript when exposed to glucosamine





New kid on the block: inserting aptamer

Inserting aptamer sequences in 3^c UTR which lead to the sequestration of the transcript (Goldfless et al. 2016, Nat Comm.)



Binding site of aptamer and tetracyclin

RNA cannot be translated



New kid on the block: inserting aptamer





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Andenmatten et al., 2013, Nat Methods





Andenmatten et al., 2013, Nat Methods









Lacroix et al., 2011, Nature Protocols 6, 1412-1428



Conditional SSR in Pb



Lacroix et al., 2011, Nature Protocols 6, 1412-1428





Figure 1. The principle of CRISPR/Cas9-mediated gene disruption. A single guide RNA (sgRNA), consisting of a crRNA sequence that is specific to the DNA target, and a tracrRNA sequence that interacts with the Cas9 protein (1), binds to a recombinant form of Cas9 protein that has DNA endonuclease activity (2). The resulting complex will cause target-specific double-stranded DNA cleavage (3). The cleavage site will be repaired by the non-homologous end joining (NHEJ) DNA repair pathway, an error-prone process that may result in insertions/deletions (INDELs) that may disrupt gene function (4).





















Cellular Repair System:

Non-homologous end joining (**NHEJ**) is a pathway that repairs double-strand breaks in DNA. NHEJ is referred to as "non-homologous" because the break ends are directly ligated without the need for a homologous template. **GENE DELETION**

Homology directed repair (**HDR**) is a mechanism in cells to repair double strand DNA lesions. The most common form of HDR is homologous recombination. The HDR repair mechanism can only be used by the cell when there is a homologue piece of DNA present in the cell. **GENE INSERTION**