

4. Protein Engineering

Bi7430 Molecular Biotechnology

Outline

- □ Limitations of proteins in biotechnology processes
- Definition and aim of protein engineering
- □ Targeted properties of proteins
- □ Basic approaches in protein engineering
 - DIRECTED EVOLUTION
 - RATIONAL DESIGN
 - SEMI-RATIONAL DESIGN



Proteins in biotechnology

- availability of optimal protein for specific process
- traditional biotechnology adapt process
- modern biotechnology adapt protein



Proteins in biotechnology

classical screening

- screening culture collections
- polluted and extreme environment
- environmental gene libraries
 - metagenomic DNA
- data-base mining
 - gene databases
 - genome sequencing projects
 - numerous uncharacterised enzymes/proteins





- the process of constructing novel protein molecules by design first principles or altering existing structure
- use of genetic manipulations to alter the coding sequence of a gene and thus modify the properties of the protein
- AIMS AND APPLICATIONS
 - technological optimisation of the protein to be suitable in particular technology purpose
 - scientific desire to understand what elements of proteins contribute to folding, stability and function

Targeted properties of proteins

structural properties of proteins

- stability (temperature, solvents)
- tolerance to pH, salt
- resistance to oxidative stress

functional properties of proteins

- reaction type
- substrate specificity and selectivity
- kinetic properties (e.g., K_m, k_{cat}, K_i)
- cofactor selectivity
- protein-protein or protein-DNA interactions





Strategies in protein engineering

RATIONAL DESIGN

1. Computer aided design



2. Site-directed mutagenesis



- 3. Transformation
 - 4. Protein expression
 - 5. Protein purification
 - 6. not applied



Improved protein

7. Biochemical testing



Constructed mutant enzyme

DIRECTED EVOLUTION

1. not applied



Selected mutant enzymes

- □ directed evolution techniques emerged during mid-1990s
- inspired by natural evolution
- □ this form of "evolution" does not match what Darwin had envisioned
 - requires outside intelligence, not blind chance
 - does not create brand new species, macroevolution, but only improvements of molecules, molecular evolution
 - does not take millions of years, but happens rapidly

Directed evolution

evolution in test tube comprises two steps

- random mutagenesis
 mutant library building
- screening and selection identification of desired biocatalyst

prerequisites for directed evolution

- gene encoding protein of interest
- method to create mutant library
- suitable expression system
- screening or selection system



technology to generate large diversity

NON-RECOMBINING

one parent gene -> variants with point mutations



RECOMBINING

several parental homologous genes -> chimeras



Non-recombining mutagenesis

- UV irradiation or chemical mutagens (traditional)
- mutator strains lacks DNA repair mechanism mutations during replication (e.g., *Epicurian coli* XL1-Red)
- error-prone polymerase chain reaction (ep-PCR)
 - gene amplified in imperfect copying process

 (e.g., unbalanced deoxyribonucleotides concentrations,
 high Mg²⁺ concentration, Mn²⁺, low annealing temperatures)
 - 1 to 20 mutation per 1000 base pairs
- saturation mutagenesis
 - randomization of single or multiple codons
- other methods
 - gene site saturation mutagenesis
 - cassette mutagenesis (region mutagenesis)





Recombining mutagenesis

also referred to as "sexual mutagenesis"

DNA shuffling

- fragmentation step
- random reassembly of segments
- **StEP** staggered extension process
 - simpler then shuffling
 - random reannealing combined with limited primer extension

other methods

shuffling of genes with lower homology down to 70%

(e.g., RACHITT, ITCHY, SCRATCHY)



Screening and selection

- most critical step of direct evolution
- □ isolation of positive mutants hiding in library
 - HIGH THROUGHPUT SCREENING

individual assays of variants one by one

DIRECT SELECTION

display techniques (link between genotype and phenotype)



(Utra)High throughput screening

- common methods not applicable
- agar plate (pre)screening
- microtiter plates screening
 - 96-, 384- or 1536-well formate
 - robot assistance
 (colony picker, liquid handler)
 - 10⁴ libraries
 - volume 10 100 uL

microfluidic systems

- water in oil emulsions (up to 10 kHz)
- FACS sorting (10⁸ events/hour)
- 10⁹ libraries
- volume 1 10 pL













Direct selection

- not generally applicable (mutant libraries >10⁶ variants)
- Iink between genotype and phenotype
- display technologies
 - ribosome display
 - phage display

life-or-death assay

- auxotrophic strain
- toxicity based selection







- directed evolution of enantioselectivity
 - lipase from P. aeruginosa (E-value improved from 1.1 into 51)
 - spectrophotometric screening of (R)- and (S)-nitrophenyl esters
 - 40 000 variants screened
 - the best mutant contains six amino acid substitutions





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Selected mutant enzymes

- emerged around 1980s as the original protein engineering approach
- knowledge based combining theory and experiment
- protein engineering cycle:

"structure-theory-design-mutation-purification-analysis"

- **difficulty in prediction** of mutation effects on protein property
- de novo design

Principal of rational design

1. Computer aided design



2. Site-directed mutagenesis



Individual mutated gene

- 3. Transformation
 - 4. Protein expression
 - 5. Protein purification

6. not applied



Improved protein



Constructed mutant enzyme

7. Biochemical testing

a rational design comprises:

- design understanding of protein functionality
- experiment construction and testing of mutants

prerequisites for rational design:

- gene encoding protein of interest
- 3D structure (e.g., X-ray, NMR)
- structure-function relationship
- computational methods and capacity
- (multi)side directed mutagenesis techniques
- efficient expression system
- biochemical tests

Design

HOMOLOGY APPROACH

- homologous wild-type sequences are collected and compared
- identifying amino acid residues responsible for differences
- reconstruction transfer differences from one enzyme to another
- new design combination of possitive mutation from all parental proteins in one construct, new protein better than all parental

RLA0 DICDI	HSGAG	SKREKLFIEKATKL	FTTYDEMIVAEADFYGS	SQLOKIEKSIEGI-GAVLMGEKEMIREVI	EDLADSKPELD 75
Q54LP0 DICDI	MSG AG	-SKRENVFIEKATEL	FTTYDEMIVAEADFVGS	SOLOKIRKSIRGI-GAVLMGKKTMIRKVI	RDLADSKPELD 75
RLA0 PLAF8	MAKLS	KOOKKOMYIEKLSSL	IQQYSKILIVHVDNVGS	NOMASVEKSLEGK - ATILMGENTRIRTAL	KKNLOAVPOIE 76
RLA0 SULAC	MIGLAVTTTKK	LAKWEVDEVAELTEK	LKTHKTIIIANIEGFPA	DKLHEIRKKLEGK-ADIKVTKHNLFNIAL	KNAGYDTK 79
RLA0 SULTO	MRIMAVITQERK	IARWEIEEVKELEOK	LRE <mark>Y</mark> RTIIIANI <mark>EGFP</mark> A	DELED TREEMRGN- AF TEVTENTLEG TAA	KNAGLDVS 80
RLA0 SULSO	MKRLALALKORK	VASWELEEVKELTEL	IKNSNTILIGHLEGFPA	DKLHEIRKKLEGK-ATIKVTENTLEKIAA	KNAGIDIE 80
RLA0 AERPE	HS VVS LVGOMYKRE KP	IPEWETLMLRELEEL	FSKREVVLFADLTGTPT	FVVORVEKKLWKK-YPHMVAKKRIILEAM	KAAGLELDDN 86
RLA0 PYRAE	-HHLAIGKRRYVRTRO	PARKYKIVSEATEL	LOKYPYVFLFDLHGLSS	RILHE YRYR LERY-GVIKIIKPTLFKIAF	TKYYGGIPAE 05
RLA0 METAC	MAEERHHTEH	IPOWEKDE IEN IKEL	IOSHKVFGHVGIEGILA	TEMORIERDLEDV - AVLEVERNTLEERAL	NOLGETIP 78
RLAO HETHA	MAEERBHTEH	I I POWKKDE I EN IKEL	IQSHKYFGMVRIEGILA	TKICKIRRDLKDY-AVLKYSENTLTERAL	NQLGESIP 78
RLA0 ARCFU	MAAVRGS	PPEYEVRAVEEIKRM	ISSKPVVAIVSFRNVPA	GOMONIRRE FROM - AEIKVVKNTLLE RAL	DALGGDYL 75
RLAO METKA	MAYKAKGOPPSGYEPK	VAEWKRREVKELKEL	MDETENVELVOLEGIPA	POLOE IRAK LREEDTII BASRATLAR IAL	EEKLDERPELE 88
RLAO METTH	MAH	VAEWEKKEVOELHDL	IKGYEVVGIANLADIPA	ROLOKMBOT LEDS - ALTEMSKETLISLAL	EKAGRELENVD 74
RLAO METTL	H ITAESEHK	TAPWEIEEVNELEEL	LKNGOIVALVDMMEVPA	ROLOFIEDKIE-GTHTLEMSENTLIFEAI	REVALETGNPERA 82
RLAO METVA	MIDAKSEHK	IAPWKIEEVNALKEL	LKSANVIAL IDMMEVPA	VOLOFIEDKIE-DOMTLEMSENTLIKEAV	EEVAEETGNPEFA 82
RLAO METJA	METEVEAR	VAPWEIEEVETLEGL	IKSKPYVAIVDMMDVPA	POLOE IRDE IR-DEVELIMBENTLIIRAL	REAAEELNNPKLA 81
RLA0 PYRAB	MAH	VAEWERKEVEELANL	IKS PVIAL VDVSSMPA	YPLSOMERL IRENGELLEVERNTLIE LAI	KKAAGELGKPELE 77
RLA0 PYRHO	MAI	VAEWERREVEELARL	IKSYPVIAL VDVSSMPA	YPLSOMERL TRENGGLLEVERNTLIELAT	KKAAKELGKPELE 77
RLA0 PYRFU	MAH	VAEWKKKEVEELANL	IKS YPYYAL VDVSSMPA	YPLSOMERL IRENNGLLEVERNTLIELAI	
RLA0 PYRKO	MAR	VAEWERREVEELANI	IKSYPVIALVDVAGVPA	YPLSKMEDKLE-GKALLEVSENTLIELAI	KRAADELGOPELE 76
RLAO BALMA	MSAESERKTET	TPEWEGEEVDAIVEN	IES YESYGY VHIAGIPS	ROLODMERDLHOT - AELEVSENTLLE RAL	DDVDDGLE 79
RLAG HALVO	MSESEVROTEV	IPOWERE EVDELVDE	IES YES YES YEV YEVAGIPS	ROLOSMERE LEGS - AAVEMBERT LYN RAL	DEVNDGFE 79
RLAO HALSA	MSAEEORTTEE	VPEWERGEVAELVDL	LET YDS VGV VNVTGIPS	KOLODMERGLHGO-AALEMSENTLLVRAL	EEAGDGLD 79
RLAO THEAC	MKE	VSOOFFELVNE TTOP	TRASES VALVOTAGIET	ROIDDIRGENRGE-INLEVIERTLLFKAL	ENLODEKLS 72
RLAO THEVO				ROMODIRAKNEDK-VKIKVVKKTLLFKAL	
RLA0 PICTO				NEFORTENSTEDK-ARTEVERARLIELAT	
ruler				50	

Design

STRUCTURE-BASED APPROACH

- prediction of enzyme function from structure alone is challenging
- protein structure (X-ray crystallography, NMR, homology models)
- molecular modelling
 - o molecular docking
 - o molecular dynamics
 - quantum mechanics/molecular mechanics (QM/MM)



Construction

site-directed mutagenesis

- introducing point mutations
- multi site-directed mutagenesis
- **gene synthesis**
 - commercial service
 - codone optimisation







- **a** rational design of protein **stability**
 - stability to high temperature, extreme pH, proteases etc.
 - stabilizing mutations increase strength of weak interactions
 - salt bridges and H-bonds
 Eijsink et al., Biochem. J. 285: 625-628, 1992
 - S-S bonds
 Matsumura et al., Nature 342: 291-293, 1989
 - addition of prolines
 Watanabe et al., Eur. J. Biochem. 226: 277-283, 1994
 - less glycines
 Margarit et al., Protein Eng. 5: 543-550, 1992
 - oligomerisation
 Dalhus et al., J. Mol. Biol. 318: 707-721, 2002

engineering protein to resist boiling

- reduced rotational freedom Ser65Pro, Ala96Pro
- introduction of disulfide bridge Gly8Cys + Asn60Cys
- improved internal hydrogen bond Ala4Thr
- filling cavity Tyr63Phe



Half-lifes (min.)	80°C	100°C	
wild type	17.5	>0.5	
8-fold mutant	stable	170	

Burg, B., et al., 1998. PNAS 95: 2056-2060

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IMPROVED

ENZYME

DIRECTED EVOLUTION

SEMIRATIONAL DESIGN



- 3. Transformation
- 4. Protein expression
- 5. not applied
- 6. Screening and selection
 - stability - selectivity
 - affinity
 - activity





Selected mutant enzymes

conversion of 1,2,3-trichloropropane

by DhaA from *Rhodococcus erythropolis* Y2

DIRECTED EVOLUTION - importance of access pathways



Bosma, T., et al. 2002: AEM 68: 3582-87

Gray, K.A., et al. 2003: Adv. Appl. Microbiol. 52: 1-27

□ conversion of 1,2,3-trichloropropane

by DhaA from Rhodococcus erythropolis Y2

- **DIRECTED EVOLUTION** importance of access pathways
- SEMI-RATIONAL DESIGN hot spots in access tunels
- library of 5,300 clones screened



Pavlova, M., Klvana, M., Prokop, Z., et al. 2009: Nature Chem. Biol. 5: 727-733



Pavlova, M., Klvana, M., Prokop, Z., et al. 2009: Nature Chem. Biol. 5: 727-733