

PROTEINE – Wozu ?

- „PROTEIN“: gr. “protos” bedeutet: ‘Erstes Element’
 - → Aufbau v. zell-eigenem Eiweiss – Strukturproteine: z.B. Kollagen (alpha-Helix)
 - → Aufbau von Enzymen und Hormonen z.B. Somatotropin, Insulin, Luteinisierendes H.
 - → Für die Reproduktion der Zellsubstanz Enzyme: DNA-Polymerase, RNA-Polymerase, ..
 - → Für Stütz- und Schutzfunktion Z.B.: Keratin (meist β -Faltblatt-Strukturen)
 - → Wasser-Bindung und Transport: durch Ladung, Aquaporine, ..
 - → Nährstofftransport - Alle Carrier, Ionen-Transport durch Membran
 - → Energiegewinnung, z.B. ATPase
- PEPTIDE:
 - 2 – 10 Aminosäuren: Oligopeptid
 - 11 – 100 Aminosäuren: Polypeptid
 - > 100 Aminosäuren: Protein
- Richtung der Aminosäurekette:
 - Aminoanfang (N-terminus)
 - und Carboxylende (C-terminus)
- Peptidbindungen:
 - Spaltung durch Hydrolyse
 - säure-katalytische oder
 - enzymatisch (vergleichbar m. Esterbindung).

8 essentielle Aminosäuren

Herkömmlich: „Biol. Wertigk.: BW“



Diese 8 AS sind für den Menschen essenziell, d.h. er muss sie über die Nahrung aufnehmen:

- → Valin
- → Isoleucin
- → Methionin
- → Phenylalanin
- → Leucin
- → Threonin
- → Lysin
- → Tryptophan

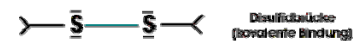
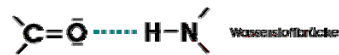
Alternative Methode: “Protein digestibility-corrected amino acid score (PDCAAS)”

Protein Quality Evaluation, Report of the Joint FAO/WHO Expert Consultation. Rome: FAO Food and Nutrition Paper No. 51, 1991.

Struktur der Proteine

- **Primärstruktur:** Reihenfolge der Aminosäuren (AS) in einem Protein (= AS-Sequenz)
z.B.: ...-Gly-Leu-Tyr-Ala-Pro-His-...
 - → Jedes Protein hat eine durch die DNA eindeutig festgelegte AS-Sequenz
- Bereits geringfügige Abweichungen können zum Verlust d. biolog. Aktivität führen
- Kombinationen der 20 AS → Nahezu unbegrenzt hohe Anzahl möglicher Proteine!
- Physikal-chem. Kräfte zwischen den Kettengliedern bedingen räumliche Anordnung der AS-Kette (Konformation):

- H⁺-Brückenbindung
- Kovalente Bindung (Disulfid-Brücken)
- Ionen-Bindung
- hydrophobe Wechselwirkungen



- **Sekundärstruktur:**

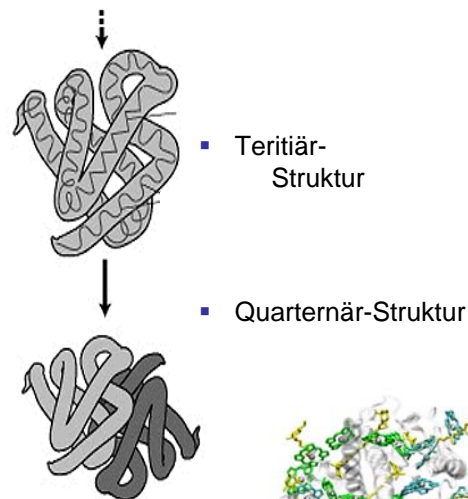
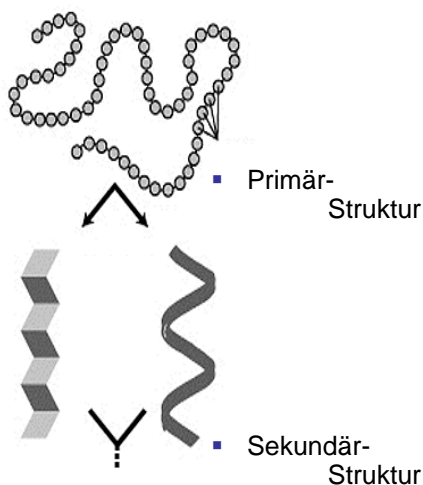
- Raumanordnung eines Proteins:

- α-Helix oder
- β-Faltblattstruktur
- durch Ausbildung von H-Brückenbindungen zw. Peptidbindungen (R-C=O...H-N-R')



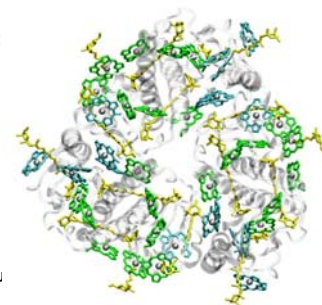
Hydrophobe Wechselwirkung zw. zwei hydrophoben (hier: aromatischen) Gruppen in wässrigem Milieu

Peptid – Protein - Struktur

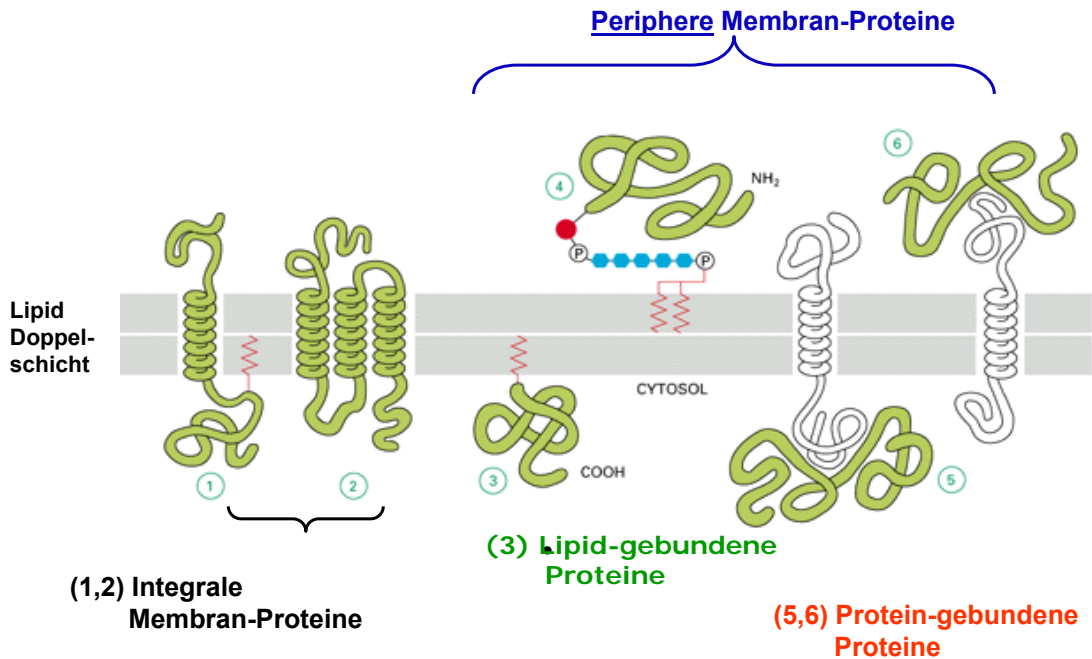


- Z.B. Light harvesting complex, LHC:

- Chlorophyll a (grün), Chlorophyll b (cyan) Carotinoide (gelb), Proteingerüst (grau)



Lage der Proteine



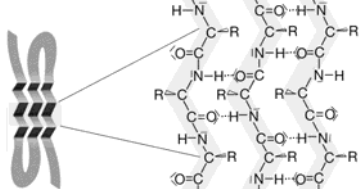
Funktionelle Eigenschaften der Proteine

Faserproteine

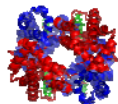
- V.a. Strukturelle Aufgaben:
- wiederholte Strukturelemente
- Z. B.: Kollagen (α -Helix),



Seidenfibrin (β -Faltblatt)



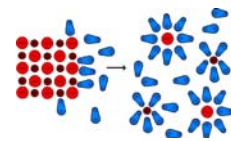
Globuläre Proteine



- Biol. wirksame Proteine
- Komplexe Tertiärstrukturen
- mehrere Arten v Sekundärstrukturen innerhalb derselben Polypeptidkette

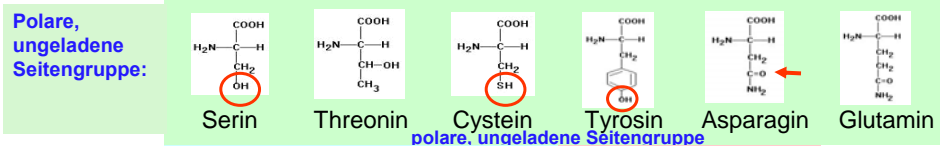
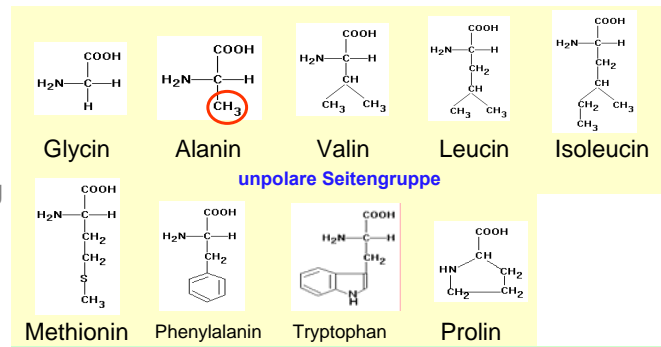
Proteine tragen also bei zu:

- Hydratation
- Löslichkeit
- Viskosität
- Gelbildung
- Texturierung
- → Teig-Stabilität (v.a. Glutene)
- → Schäumung
- → Aroma-Bindung (z.B. Butylamin)
- → Emulgation (z.B. Öl – H₂O)
- → Wechselwirkung mit anderen Lebensmittel-Bestandteilen

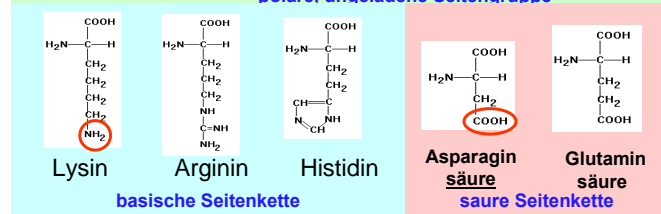


Aminosäuren

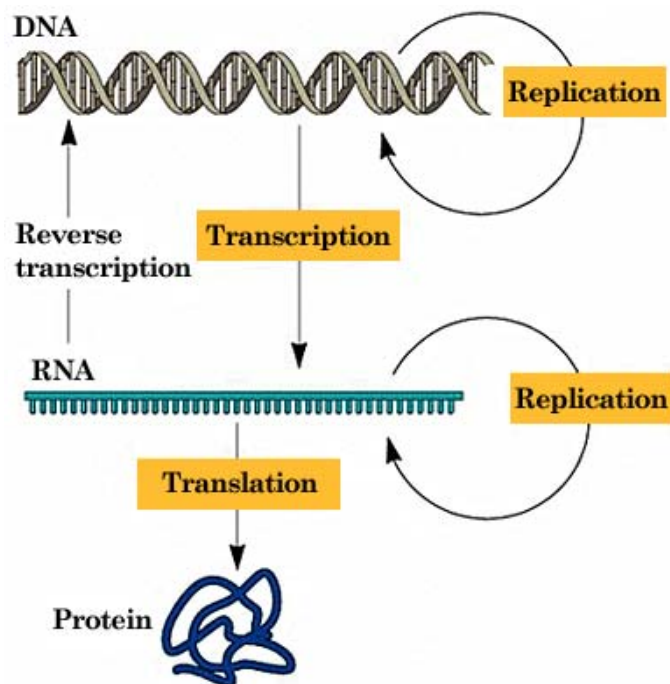
- Hydratation
- Löslichkeit
- Viskosität
- Gelbildung
- Texturierung



- Seitengruppen:
 - polar
 - unpolar
 - geladen
 - ungeladen
 - basisch
 - sauer



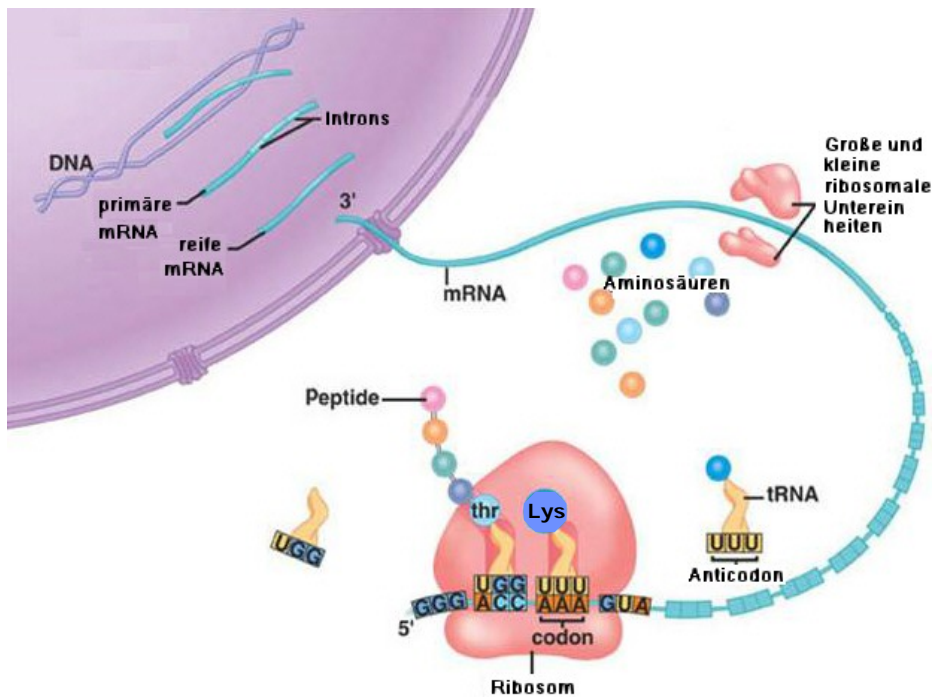
'Zentrales Dogma' der Molekularen Biologie



Der genetische Code - Wobble

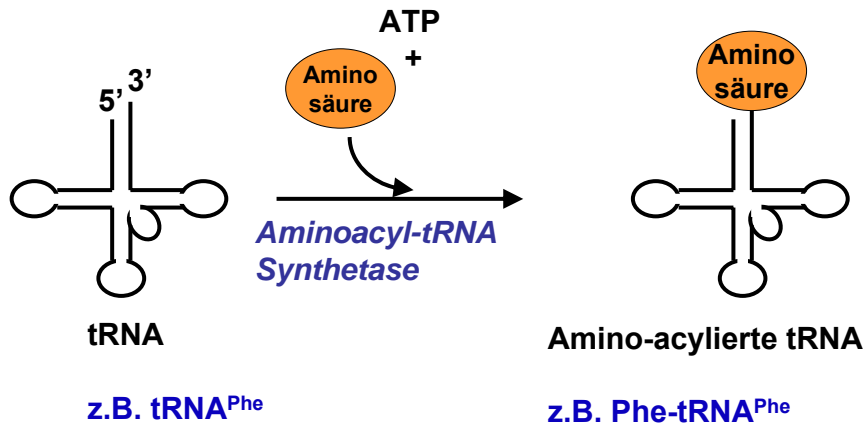
	U	C	A	G	
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	Zweite Position
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	
	UUA Leu	UCA Ser	UAA Stop	UGA Stop	
	UUG Leu	UCG Ser	UAG Stop	UGG Trp	
C	CUU Leu	CCU Pro	CAU His	CGU Arg	3. (Wobble) Position
	CUC Leu	CCC Pro	CAC His	CGC Arg	
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	Erste Position
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	
	AUG Met	ACG Thr	AAG Lys	AGG Arg	
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	
	GUC Val	GCC Ala	GAC Asp	GGC Gly	
	GUA Val	GCA Ala	GAA Glu	GGA Gly	
	GUG Val	GCG Ala	GAG Glu	GGG Gly	

Proteinbiosynthese: einfacher Überblick

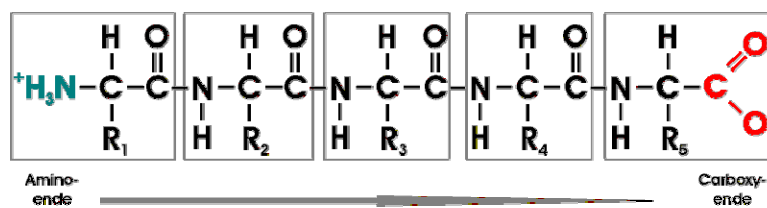
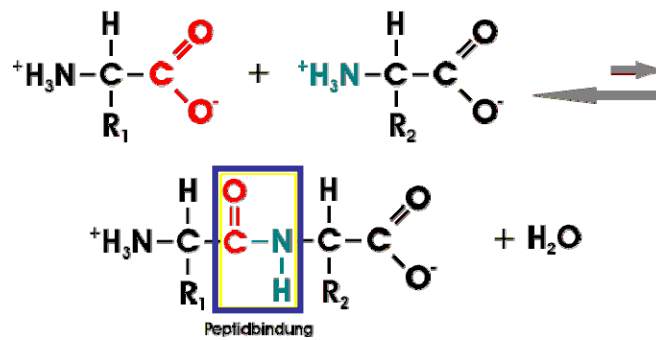


tRNAs: spezifische Träger der Aminosäuren

- **Aminoacyl-tRNA Synthetasen** transportieren die spezifischen Aminosäuren an die tRNA-Moleküle heran.



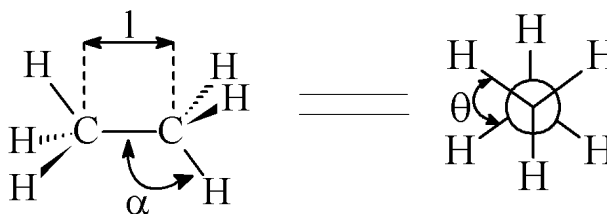
Peptidbindung



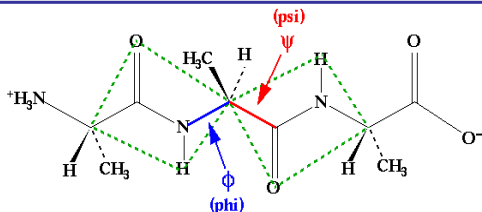
Molekulare Geometrie organischer Verbindungen

- Die molekulare Geometrie kann durch drei Angaben beschrieben werden:

- Bindungslänge (l)
- Bindungswinkel (α)
- "Diederwinkel" Theta (θ)



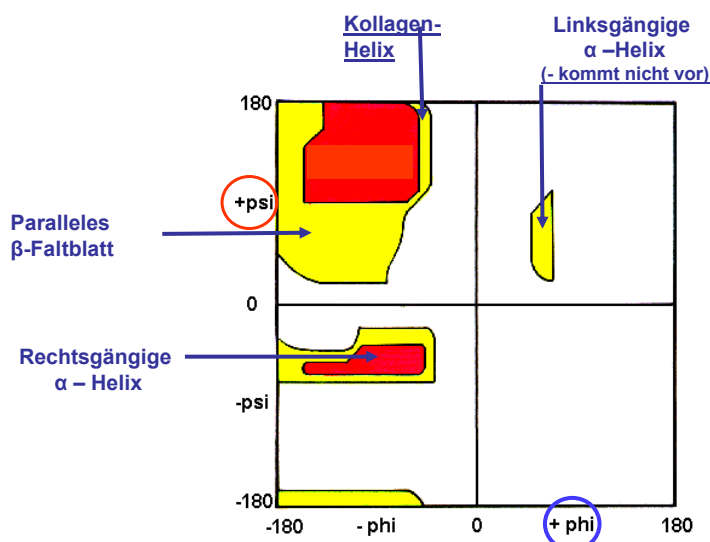
Verdrillung



G. N. Ramachandran and V. Sasiskharan (1968) *Adv. Protein Chem.* 23, 283-437

- Für jede Aminosäure sind nur zwei Diederwinkel (ϕ und ψ) frei rotierbar.
- Die Peptidbindung $\text{O}=\text{C}-\text{N}-\text{H}$ ist fast immer planar (gemeinsame Ebene).
- Daher kann man die Positionen jeder AS in dem sog. Ramachandran-Plot für die beiden Winkel ϕ und ψ eintragen...

Sasisekharan-Ramakrisnan-Ramachandran-Diagramm



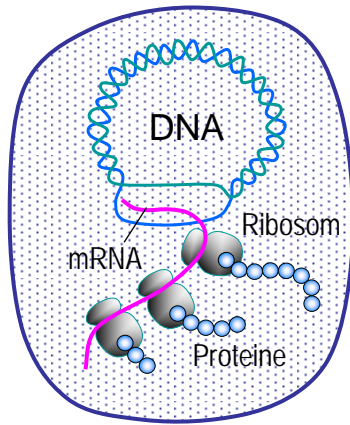
- Aus sterischen Gründen sind nur bestimmte Winkelkombinationen erlaubt, die im Ramachandran-Plot zu erkennen sind.
- Die Struktur einer Polypeptidkette kann durch die Winkel ϕ (ϕ) und ψ (ψ) beschrieben werden.

Ausstattung

Letzte Version der zellulären genetischen Mechanismen

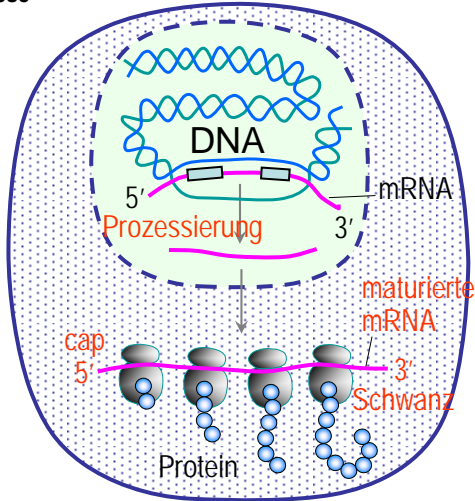
DNA ersetzt RNA und wurde zum Hauptträger der genetischen Information

Die Rolle der RNA wurde v.a. die Protein-Biosynthese



Prokaryont

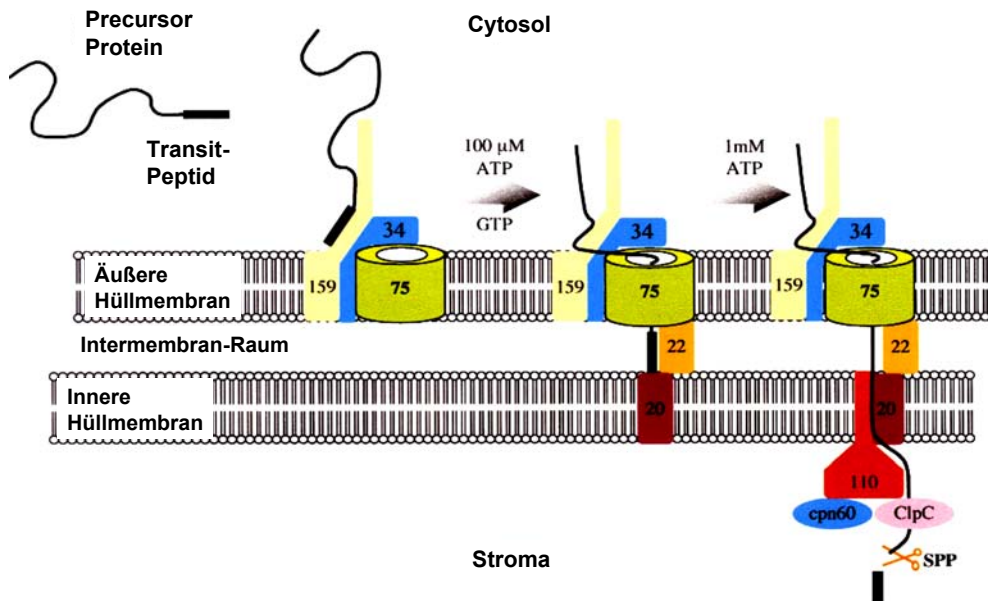
Studentenwohnheim



Eukaryont

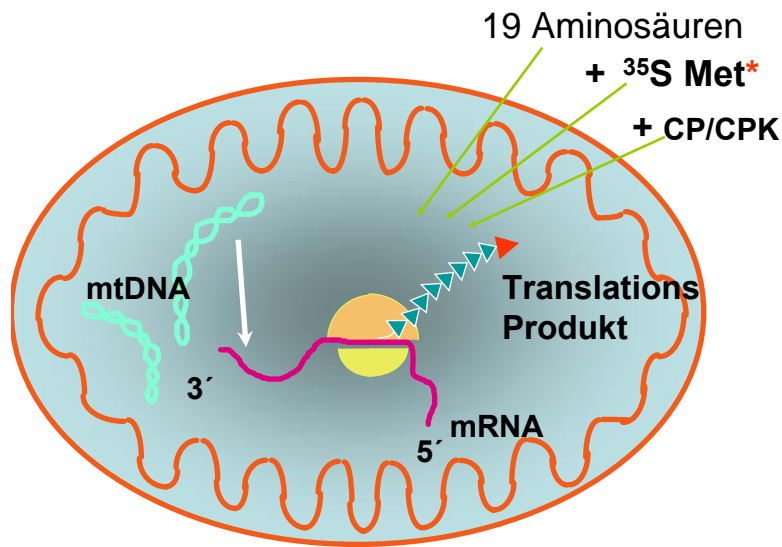
Möbliertes Apartment

Protein-Import -Apparat

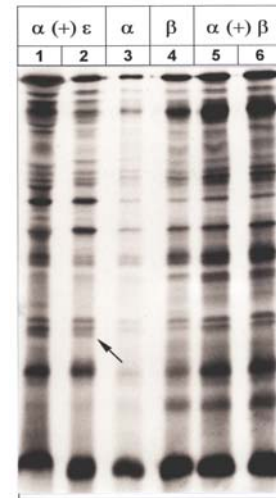


Hiltbrunner et al., 2001

In organello Translation



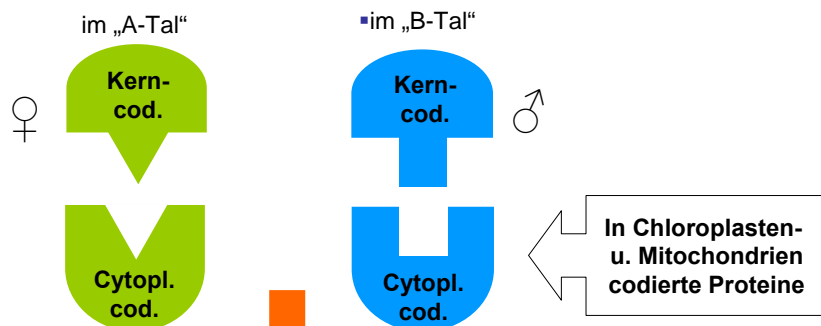
Variabilität zw. Mitochondrien



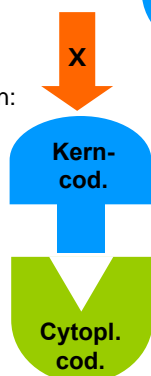
Am Beispiel der Kulturkartoffel:
PAGE nach in-organello-Translation

Kern-Cytoplasma-Kompatibilität

- 1.: Pflanze gleicher Art: Auseinander-Entwicklung im Laufe der Entwicklungsgeschichte



- 2.: Kreuzung der Pflanzen: „A-Tal“ X „B-Tal“



- CMS
- Chlorosen
- Verzweigung
- Sensitivität für Pilztoxine
- Energiehaushalt generell

Regulation von Transkription und Translation

Plant Cell Physiol. 46(9): 1462–1471 (2005)
doi:10.1093/pcp/pci157, available online at www.pcp.oupjournals.org
JSPF © 2005

Inducible Trans-activation of Plastid Transgenes: Expression of the *R. eutropha phb* Operon in Transplastomic Tobacco

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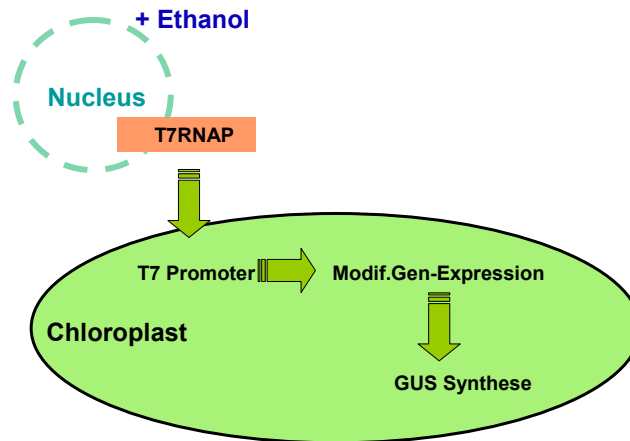
² Max-Planck-Institut für Molekulare Pflanzenphysiologie, Am Mühlenberg

³ Institut für Pflanzenbau und Pflanzenzüchtung, Christian-Albrechts-Universität

⁴ KCON Genetics AG, Research Centre Freising, Lise-Meitner-Str. 30, D-8

⁵ Ludwig-Maximilians-Universität, Faculty of Biology, Department 1, Bota

Deleterious effects of constitutive transgene expression can occur if gene products are harmful to the transformed plant. Constraints such as growth inhibition and male sterility have been observed in plastid transformants containing the *phb* operon encoding the genes required for the production of the polyester polyhydroxybutyric acid (PHB). In order to induce PHB synthesis in tobacco in a well-timed manner, we have constructed a trans-activation system to regulate transcription of the *phb* operon in plastids. This system consists of a nuclear-located, ethanol-inducible T7RNA polymerase (T7RNAP) which is targeted to plastids harboring the *phb* operon under control of T7 regulatory elements. Following treatment with 5% ethanol, moderate induction of PHB synthesis was found. PHB amounts reached 1,383 ppm in dry weight, and an overall background activity of 171 ppm was measured in uninduced tissues. On the transcriptional level, T7RNAP induction was proven and we found that the *phb* operon is transcribed into at least two mRNAs. Without ethanol induction, development of flowers and fertile seeds was possible. Thus, the main problem of inhibitory transgene expression was solved. Our results show that this inducible trans-activation system could serve as an alternative to constitutive expression of transgenes in the plastome.



Produktion neuer Proteine in Chloroplasten

Transgenic Res
DOI 10.1007/s11248-010-9415-4

ORIGINAL PAPER

Transplastomic expression of a modified human papillomavirus L1 protein leading to the assembly of capsomeres in tobacco: a step towards cost-effective second-generation vaccines

M. Tahir Waheed · Nadja Thönes · Martin Müller · S. Waqas Hassan · N. Mona Razavi · Elke Lössl · Hans-Peter Kaul · Andreas G. Lössl

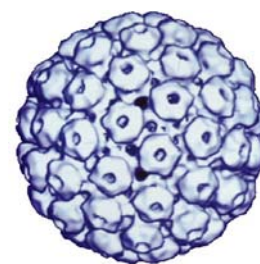
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Abstract Certain types of human papillomaviruses (HPV) are causatively associated with cervical carcinoma, the second most common cancer in women worldwide. Due to limitations in the availability of currently used virus-like particle (VLP)-based vaccines against HPV to women of developing countries, where most cases of cervical cancer occur, the development of a cost-effective second-generation vaccine is a necessity. Capsomeres have recently been demonstrated to be highly immunogenic and to have a number of advantages as a potential cost-effective alternative to VLP-based HPV vaccines. We have expressed a mutated HPV-16 L1 (L1_{2xCysM}) gene that retained the ability to assemble L1 protein to capsomeres in tobacco chloroplasts. The recombinant protein yielded up to 1.5% of total soluble protein. The assembly of capsomeres was examined and verified by

cesium chloride density gradient centrifugation and sucrose sedimentation analysis. An antigen capture enzyme-linked immunosorbent assay confirmed the formation of capsomeres by using a conformation-specific monoclonal antibody which recognized the conformational epitopes. Transplastomic tobacco plants exhibited normal growth and morphology, but all such lines showed male sterility in the T₀, T₁ and T₂ generations. Taken together, these results indicate the possibility of producing a low-cost capsomere-based vaccine by plastids.

Keywords HPV-16 · L1_{2xCysM} gene · Capsomeres · Plastids · ELISA · Male sterility

Introduction



▪ Z.B. Impfstoffe: