brachten Membranpumpe wurde jedes Becken durch einen Ausströmer durchlüftet.

Gewichtszunahmen dieses Ausmasses sind bisher in Aquarien noch nie erreicht worden. Besonders durch den Ausfall der Winterruhe erhoffen wir eine erheblich früher eintretende Geschlechtsreife der Karpfen.

In Verbindung mit der vollständig kontrollierbaren Aufzucht der Fische wird es das Bestreben sein, mit Hilfe der neuen Methode züchterische Arbeiten an Nutzfischen, wie die Auswahl grätenloser Mutanten, die Individualauslese schnellwüchsiger Exemplare sowie Probleme der Inzucht und der Heterosiszüchtung durchzuführen.

Summary. Keeping carps (*Cyprinus carpio*) according to a new method in plastic containers (40 l) in a closed water cycle with biological cleaning yielded a quick increase in weight at a water temperature of 25°C.

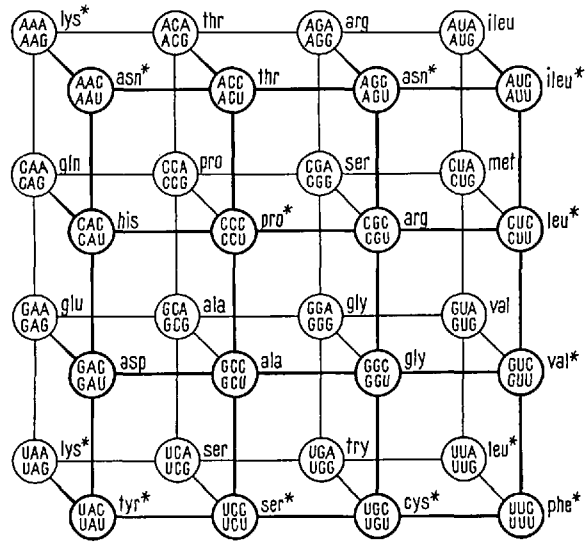
R. VON SENGBUSCH, CH. MESKE und W. SZABLEWSKI

Max-Planck-Institut für Kulturpflanzenzüchtung, Hamburg-Volksdorf (Deutschland), 1. Juni 1965.

COGITATIONES

A Spatial Depiction for the Systematically Degenerate Genetic Code

On the basis of their experiments with trinucleotides of defined base sequence, BERNFIELD and NIRENBERG[1], LEDER et al.[2], and TRUPIN et al.[3] proposed that the genetic code is degenerate according to a general pattern. In their view, the 64 possible code words are arranged in 32 pairs of triplets with identical bases in the first and second position of each pair. 16 of these pairs have either cytidine (C) or uridine (U) as 3′ terminal nucleosides, and the 16 other pairs have either adenosine (A) or guanosine (G) as 3′ terminal nucleosides. Both triplets of a codon-pair are coding for the same amino acid (compare the scheme of ECK[4]). We want to put forward a spatial depiction, in which the relations between these 32 triplet pairs are clearly visualized. The amino acids corresponding to the codes are included, so that the consequence of single base conversions in a codon, with respect to amino acid coding, can be read off on the three lines crossing the codon. Starting from the known data, which are summarized in the Table, we deduced the meaning in terms of amino acid of the 19 remaining codon-pairs. For this purpose we made use of the in vitro amino acid incorporation data of NIRENBERG and JONES[8], and of OCHOA[9]; amino acid replacements in the A protein of tryptophan synthetase of *E. coli* mutants[10,11]; and of amino acid substitutions in



Spatial depiction of the degenerate genetic code. * Literature data.

Amino acids	RNA codons	Literature
Asparagine	A_pG_pC; A_pG_pU	5
Asparagine	A_pA_pC; A_pA_pU	2, 3
Cysteine	U_pG_pU	1
Isoleucine	A_pU_pC; A_pU_pU	2, 3
Leucine	C_pU_pC; C_pU_pU	1, 7
Leucine	U_pU_pG	1, 6
Phenylalanine	U_pU_pC; U_pU_pU	1, 7
Proline	C_pC_pC; C_pC_pU	1, 7
Serine	U_pC_pC; U_pC_pU	1, 7
Tyrosine	U_pA_pC; U_pA_pU	2, 3
Valine	G_pU_pU	1
Lysine	A_pA_pA; A_pA_pG	2, 3
Lysine[a]	U_pA_pA	2

[a] uncertain

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abnormal hemoglobins[12]. We presumed the genetic code to be universal.

It is worth noting that our deductions have led to results which differ on several points from comparable predictions of YANOFSKI[11] and of TRUPIN et al.[3]. The scheme derived by OSGOOD[13] does not fit the present state of knowledge. The genetic code may be more complicated if 5′ terminal, 3′ terminal and internal codons are recognized in somewhat different ways[3], and if the code is not as consistently degenerate as supposed here[14].

Zusammenfassung. Auf Grund von Literaturangaben und durch Deduktion haben wir ein dreidimensionales Schema (oder Modell) des systematisch degenerierten genetischen Codes entworfen, aus dem man in einfacher Weise ablesen kann, welche Aminosäuresubstitutionen aus der Veränderung einer Base folgen.

D. H. G. VERSTEEG[15] and J. F. G. VLIEGENTHART

Laboratory of Organic Chemistry of the University of Utrecht (The Netherlands), May 31, 1965.

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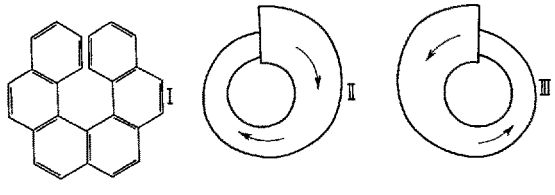
[14] Note added in proof: Compare the recent paper: M. NIRENBERG, P. LEDER, M. BERNFIELD, R. BRIMACOMBE, J. TRUPIN, F. ROTTMAN, and C. O'NEAL, Proc. nat. Acad. Sci. US *53*, 1161 (1965).
[15] Present address: Department of Pharmacology, University of Utrecht (The Netherlands).

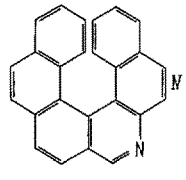
Adaptation of the CAHN-INGOLD-PRELOG System of Nomenclature to Hexahelicene

The CAHN-INGOLD-PRELOG system of nomenclature for optically active compounds[1,2] has been applied successfully to a wide variety of compounds. Present nomenclature rules, however, do not provide for an R (rectus) or S (sinister) assignment to the enantiomers of compounds such as hexahelicene (I). This compound exhibits optical activity because intramolecular crowding forces the molecule to twist into an asymmetric helix[3].

An extension of the CAHN-INGOLD-PRELOG system, allowing for an R or S assignment to the enantiomers of such compounds, would seem to be quite simple. If one observes this molecule as shown in I, one of the terminal rings would appear slightly above and overlapping the other, as shown schematically in II or III. Arrows drawn in the direction of the spiral, i.e. from the terminal ring nearest the observer to the other terminal ring, going around the molecule, will describe a clockwise rotation in one case (II), and a counter-clockwise rotation in the other (III).



It is proposed to assign the symbol R to the clockwise spiral and S to the counter-clockwise spiral. This assignment will remain unchanged, even if the molecule is flipped over or rotated. This method is applicable to other compounds derived from hexahelicene, such as IV, because assignment is dependent only on the direction of the spiral. For this reason, this method of assignment may also be applied to any other spiral or screw-shaped molecule, such as 4,5-dimethyl-substituted phenanthrene[4], starches and proteins.



Résumé. On propose une extension du système de CAHN-INGOLD-PRELOG pour nommer des enantiomers des composés en forme d'hélice tels que le hexahélicène.

J. P. JENDREK

Chemistry Department, Tulane University, New Orleans (Louisiana USA), March 8, 1965.

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