VIRUSES-NEW LOOK-BLOCKING MECHANISM-2020 [RCV-2020]

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Part-1 : Introduction

Viruses have been challenging humans for the past 100 or more years. Tens of varieties of vaccines have been synthesized to eradicate many viruses (ex : Polio), yet, new types are evolving onto our globe and affecting our life style (ex : Covid-19). Though different scientists have been viewing these microbes in different platforms, yet, no specific concept or attempt successfully explained origin of viruses, their growth, life cycle, adverse effects and exact way of eradication of all types of viruses existing as on today or which may evolve in future.

A unified research may be essential to fight against all types of viruses for which ***universal vaccine*** may be needed keeping in view of all known possibilities of replication, transcription & translation processes taking place in different types of viruses. Our present concepts explain the mechanism of these three processes in every known living system (from single cell to trillion cell) and also isolated different types of enzymes or bio-chemicals which promote these. In this present worst scenario (thousands affected by covid-19 despite rocket level speed technology)

I would like to put my own concept "***Ramachandran Concept of Virus-2020***" which focuses mainly on "**chemical integrity chemical disintegrity**", which in turn, based on "**structure-nature-kinetics" (**of α-amino acids, nucleic acids and synthesis of RNA and proteins)

Part-2 : Salient features of RCV-2020

1] All types of viruses are originated either from plant kingdom, bacteria family or animal kingdom.

2] Any type of virus is created for the first time by a process called ***misfiring of replication or even transcription***.

3] In all living systems, ***replication* (*or*) *transcription*** takes place with lowest possible error (less than 0.1%). However, if ***unwinding of DNA strand*** is interrupted by any external factor such as sudden change in pH or non-availability of significant amount of enzyme or change in osmotic pressure or even temperature (due to any health ailment), the strand produces a **number of *fragments*** in the form of replication ***misfiring*** *of product.*

4] The **misfiring replication products** are mostly degraded by the system itself by its usual course (in Liver, Kidney etc.,), but, if the **rate** of such a degradation process is **not** equal to (or) less than **rate of formation of misfiring replication product**, it leads to a new minor DNA strand with fewer (or) quite lesser bases than parent DNA, which gets coagulated in the Liver/Intestine/Pancreas. This size increases slowly but *exponentially* with time.

5] The base sequence in any such **misfiring replication** product need not be the same as a small fragment of parent DNA. This itself is the ***origin of new DNA strand called VIRUS.***

6] If base sequence in this new DNA (or Virus) is same as base sequence in the fragment of parent DNA, then, such VIRUS remains ineffective, if not effective.

7] The shape (macroscopic) of any such Virus is either ***fibrous or slightly ellipsoid or spheroid or spherical*** which solely depends on number of hydrophobic or/and hydrophilic α-amino acids (residue) that can be utilized by m-RNA which in turn, produced from new DNA.

So, all ineffective viruses are more or less behave like normal RNA (or DNA).

8] The effective Virus (having different base sequence) however mostly **spherical** (spherical shape allows them to have minimum surfacial contact among themselves, but more speed in moving from one part to other through blood stream). The protective protein layer that surrounds this effective virus has highest percentage (by number) of ***hydrophobic type α-***

amino acids, hence it always ***targets the fragment of host m-RNA which is also rich in hydrophobic nature.*** Thus host m-RNA fails to bring more number of α-amino acids to form usual proteins to drive all those usual ***metabolic processes*** in the ***host body***. Thus effective virus gets a sort of domination over host cells hence number of ***α-amino acids forming protein capsule around virus starts increasing*** which ultimately results in a condition called "***dormant m-RNA*** of ***host cell***".

9] The living systems where rate of ***misfiring of replication (or even transcription)*** is more than expected level will behave either like "primary carriers" or "primarily affected hosts". This type unusual increase in rate of misfiring of replication (or transcription) is more apparent in those animal species which consume foods that are so rich in proteins having higher percentage (by number) of ***higher hydrophobic α-amino acids*** (ex: Valine, Isoleucine, Leucine etc.,).

10] Hydrophobic nature of α-AA follows the order (highest to lowest) as shown below :

[Except Proline, all other α-AA are shown as derivatives of Glycine as NH_2-CH(R)-COOH where R is the substituent which may be either aliphatic, aromatic or other group].

Hydrophobic Index Number [HIN]:

[HIN] indicates extent of hydrophobic nature of α-amino acid. As HIN decreases, hydrophobic nature decreases hence lesser the probability that effective virus can select it in forming ***protein capsule*** that protects it from any drug/chemical/anti-body within ***host cell***. (+) and (-) represent nature of α-amino acid (optical activity) and IEP represents ***Isoelectric Point***. Glycine assigned **HIN** as **1** (reference frame). To calculate HIN, the following formula has been proposed :

HIN (α-AA) = HIN (of Gly) + $\log_{10}$ [(constant-K) x 10^{20}] ----(1) where $\log_{10}$K may be negative or positive. However, only magnitude is to be considered in calculating HIN value (Equation-2) *The magnitude of K : CH_2 part (0.25), CH_3 part (0.30), C_6H_5 part (0.75), COOH group (1.25),NH_2 group (0.50), $CONH_2$ group (0.40), Pyrrole ring (0.75), Pyrrolidine ring (1.0), OH part (0.6), SH part (0.7), Thio ether part (-S-) (0.50).

Here, K (overall) = sum of the product of all contributions from various parts/groups. [Note : CH part ≈ CH_2 part]. In case, groups/parts having both positive and negative values of K are present, then,

HIN (α-AA) = HIN (Gly) + $\log_{10}$ [K x 10^{20}] – $\log_{10}$ [K* x 10^{20}] -----(2) [K > 0, K* < 0]

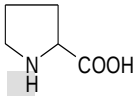
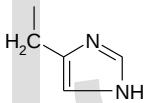
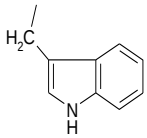
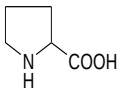
Illustrated Examples

Ex-1 : HIN (Phe) = 1 + $\log_{10}$ (0.25 x 0.75 x 10^{20}) = 1 + $\log_{10}$ (25 x 75 x 10^{16}) ≈ 20.28

Ex-2 : HIN (Leu) = 1 + $\log_{10}$ (0.30 x 0.30 x 0.25 x 0.25 x 10^{20}) = 1 + $\log_{10}$ (3 x 3 x 25 x 25 x 10^{14}) ≈ 18.76

Ex-3 : HIN (Trp) = 1 + $\log_{10}$ (0.25 x 0.75) – $\log_{10}$ (0.75 x 10^{20}) = 1 + $\log_{10}$ (25 x 75 x 10^{16}) – $\log_{10}$ (75 x 10^{20}) = 19.28 – 21.88 = – 2.60

Table showing α-AA with HIN value (as per RCV-2020)

Name	Symbol	Structure [R], (IEP)	HIN	MW g/mol
Alanine	Ala, (+)	CH_3-, (6.02)	20.48	89.0
Phenyl alanine	Phe, (-)	C_6H_5-CH_2-, (5.48)	20.28	165.0
Valine	Val, (+)	$(CH_3)_2$-CH-, (5.97)	19.36	117.0
Leucine	Leu, (-)	$(CH_3)_2$-CH-CH_2-, (5.98)	18.76	131.0
Isoleucine	Ile, (+)	CH_3-CH-CH_2-CH_3, (6.02)	18.76	131.0
Glycine	***Gly,***	***R = H, (5.76)***	***1.0***	***75.0***
Asparagine	Asn, (-)	NH_2-CO-CH_2-, (5.41)	0.80	132.0
Serine	Ser, (-)	HO-CH_2-, (5.68)	0.62	105.0
Cysteine	Cys, (-)	HS-CH_2-, (5.02)	0.55	121.0
Tyrosine	Tyr, (-)	 , (5.65)	0.50	189.0
Histidine	His, (-)	 , (7.58)	0.40	155.0
Aspartic acid	Asp, (+)	HOOC-CH_2-, (2.76)	0.30	133.0
Glutamine	Gln, (+)	NH_2-CO-CH_2-CH_2-, (5.65)	0.20	146.0
Threonine	Thr, (-)	-CH(OH)-CH_3, (5.16)	0.10	119.0
Glutamic acid	Glu, (+)	HOOC$(CH_2)_2$ (3.24)	–0.30	147.0
Arginine	Arg, (+)	HN=C(NH_2)-NH$(CH_2)_3$-, (10.76)	–0.50	174.0
Lysine	Lys, (+)	$NH_2(CH_2)_4$- (9.82)	–1.3	146.0
Methionine	Met, (-)	$CH_3S(CH_2)_2$ -(5.75)	–1.42	149.0
Tryptophan	Trp, (-)	 , (5.88)	– 2.60	204.0
Proline	Pro, (-)	 , (6.10) [Isolated structure]	– 19.7	115.0

11] When a peptide is formed, hydrophobic nature of such peptide increases with increase in number of α-AA having HIN > 0 i.e any peptide having more number of α-AA with HIN > 0 will usually adopt ***fibrous*** structure and any peptide having more number of α-AA having HIN < 0 (-ve) usually adopt ***globular*** structure. Most of viruses whose genome is constructed from r-RNA (abstracting from host) have protein envelope with HIN > 0 and those which adopt DNA (from host) have protein envelope with HIN < 0. This later type is more influential than former hence their interaction with r-RNA of host leads to more adverse effects. HIV, Flu, Hepatitis-B, Polio, Corona-19 (*which is now shaking entire human beings) etc., belong to this type-2.

12] So far, eradication of specific type of virus is based on specific type of vaccine only but, new ***universal protein*** however protects all hosts from the attack of viruses. A universal protein forms an envelope around each host cell which readily permeable for other cells of same body but not any ***pathogenic body*** such as ***virus***.

13] The ***universal protein*** is prepared in laboratory in specific way as described below:

Step-1 : 20 samples of aqueous solutions need to be prepared where each sample contains specific α-AA as major component (by mole or number) and all other 19 α-AA as minor, but in equi-molar amounts.

Step-2 : Mixing up of equal volumes of all 20 samples [say 10 mL each] to get sample-U

Step-3 : Adding suitable polymerase to sample-U that facilitates synthesis of protein-[RCUP]

Step-4 : Freezing RCUP or keeping RCUP at sufficiently cool & dark place.

Illustration :

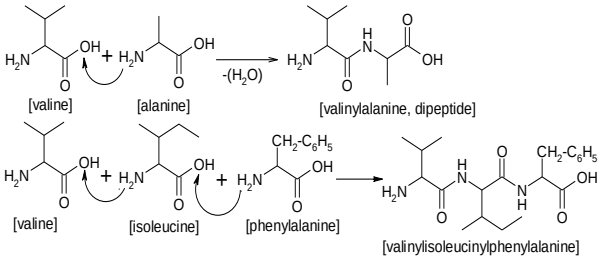
Preparation of individual samples :-
Sample-[a] : 0.2 mol mixture of all α-AA in 10.0 dm^3 aqueous solution (using DM-water). In this sample-[a], 50% (by mol) contribution from Alanine i.e 0.1 mol Alanine (8.90 g) & 50% (by mol) from all other 19 members in 1:1 molar ratio i.e (0.1/19) mol each
[ex: 8.9 g Ala + 0.8684 g Phe + 0.6158 g Val + 0.6895 g Leu + 0.6895 g Ile + 0.3947 g Gly + 0.6947 g Asn + 0.5526 g Ser + 0.6368 g Cys + 0.9947 g Tyr + 0.8158 g His + 0.7000 g Asp + 0.7684 g Gln + 0.6263 g Thr + 0.7737 g Glu + 0.9158 g Arg + 0.7684 g Lys + 0.7842 g Met + 10.7368 g Trp + 0.6053 g Pro = Sample-[a]}. This sample-[a] contains nearly ***6.022 x 10^{22}*** "**Ala"** units and "***3.1694 x 10^{21}*** (formula) units" of each of other members. As number of **Ala** units is nearly 19 times each other member, probability of **Ala** to involve in polypeptide (s) formation too, nearly 19 times more than each other member. As number of **Ala** units in this polypeptide chain (say PPC-1) is maximum, its HIN too maximum (positive value). So, PPC-1 ultimately possesses highest % of hydrophobic nature or highest number of hydrophobic fragments in the whole PPC-1. This PPC-1 may be expected to have one ***-NH-C=O*** link between Ala unit and each of all other 19 members. So, PPC-1 may have 38 α-AA residues or even more.
Sample-[b] : 0.2 mol mixture of all α-AA in 10.0 dm^3 aqueous solution (using DM-water). In this sample-[b], 50% (by mol) contribution from Val i.e 0.1 mol Val (16.50 g) & 50% (by mol) from all other 19 members in 1:1 molar ratio i.e (0.1/19) mol each. {See above example regarding composition of mixture or sample-[b]}
Sample-[c] : 0.2 mol mixture of all α-AA in 10.0 dm^3 aqueous solution (using DM-water). In this sample-[c], 50% (by mol) contribution from Phe i.e 0.1 mol Phe (11.70 g) & 50% (by mol) from all other 19 members in 1:1 molar ratio i.e (0.1/19) mol each.
{See the above example regarding composition of mixture or sample-[c]}

Like this, sample-[d], sample-[e], sample-[f] etc., [total 20 samples] are to be prepared. In each sample, there exists only one amino acid residue in highest percentage (by number) and all other remaining members are equal in quantity (by mol or number). PPC-20 (the one that has highest % of Proline) will have most negative HIN value hence PPC-20 is the most hydrophilic type.

14] Among all twenty PPC, 14 are hydrophobic dominant and just 6, hydrophilic dominant. So mixture of all these twenty PPC will be hydrophobic dominant. This mixture is called ***RCUP*** (***Rama Chandran Universal Protein***). If RCUP is injected into a host body, it tries to envelope all T-cells to prevent them attacking from viruses. This RCUP repels the protein envelope of virus thus serves as typical ***protective film***.

15] Ability of an α-AA to form a peptide link depends on whether its COOH group is stronger or NH_2 group is stronger. Though NH_2 is basic by nature, yet it behaves like acid while COOH (acidic by nature) behaves like base. Also, whether NH_2 or COOH part participates in holding another α-AA too, depends on relative strengths only.

Consider alanine where CH_3 acts as +I group (at C-2 with respect to COOH), alanine has weaker COOH group (acidic strength), so alanine behaves like weaker acid or its conjugate base is very strong (or more reactive). When COOH part of alanine contributes OH part, the resulting NH_2-$CH(CH_3)$-^+C=O (ion) is less stabilized by α-Hydrogen atom. But, when NH_2 part of alanine contributes H^+, resulting $^{(-)}NH_2$-$CH(CH_3)$-COOH (ion) which is highly reactive than NH_2-$CH(CH_3)$-^+C=O. So, alanine prefers to interact with other α-AA preferably from its COOH end. So, first 5 α-AA with larger HIN (+ve) values usually interact from their COOH end. However among these first five α-AA, interacting ability with respect to COOH part : Valine > Leucine > Isoleucine > Alanine > Phenyl alanine.
Ex-1: Valine + Alanine → Dipeptide where Valine contributes OH (from COOH) and Alanine′s H-atom (from NH_2). Observe the following illustrated examples (formation of peptide bond): Also see the two possibilities of each amino acid to form a O=C-NH- bond. If two α-AA unite to give two types of dipeptides, both peptides have same molar mass but, structurally different.



16] If PPC-1 is considered, possible polypeptide may be represented as :

[Ala→Leu][Ala→Ile][Ala→Val][Ala→Phe][Ala→Gly][Ala→Asn][Ala→Ser][Ala→Cys]

[Ala→Tyr][Ala→His][Ala→Asp][Ala→Gln][Ala→Thr][Ala→Glu][Ala→Arg][Ala→Lys]

[Ala→Met] [Ala→Trp][Ala →Pro] (reading from N-end to C-end) [Peptide links = 37].

Like this, other 19 PPC can be shown. The corresponding t-RNA (or m-RNA or DNA strand can be easily predicted based on standard rules*. [*refer codons]

For example, in case of PPC-1, POSSIBLE* complimentary strand of RNA is shown below:

S.No	α-AA	Codon	S.No	α-AA	Codon
1	Ala	GCA	20	His	CAU
2	Leu	UUG	21	Ala	GCC
3	Ala	GCC	22	Asp	GAC
4	Ile	AUA	23	Ala	GCC
5	Ala	GCG	24	Gln	CAA
6	Val	GUA	25	Ala	GCG
7	Ala	GCU	26	Thr	ACC
8	Phe	UUC	27	Ala	GCG
9	Ala	GCC	28	Glu	GAG
10	Gly	GGA	29	Ala	GCA
11	Ala	GCC	30	Arg	AGG
12	Asn	AAU	31	Ala	GCU
13	Ala	GCG	32	Lys	AAG
14	Ser	AGC	33	Ala	GCG
15	Ala	GCG	34	Met	AUG
16	Cys	UGC	35	Ala	GCG
17	Ala	GCU	36	Trp	UGG
18	Tyr	UAU	37	Ala	GCA
19	Ala	GCA	38	Pro	CCA

17] In RCUP, all twenty PPC are present whose 3D-packing leads to a protein or even an enzyme or structural part or conjugated protein (along with a metal ion such as Zn^{+2}, Cu^{+2}, Mo^{+2}, Co^{+3}, Fe^{+2} etc.,)

How to test this RCUP?

If this RCUP happens to exist in reality, let virologists or biochemists or pharmacists conduct experiments on various living systems (including plants).

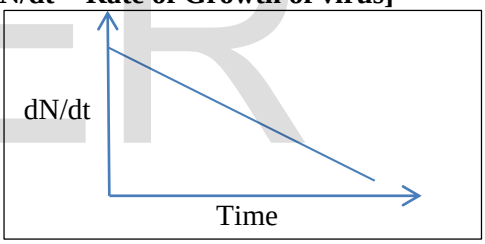
Let two living samples (tissue or part of body) to be selected (say A & B). Each of A & B are stained with any given and well-known virus (say Flu, Covid-19 if available) and check for the growth of virus in stipulated time interval (say 10 min). Then, RCUP is added to A or B and again check after few minutes to ensure whether growth of virus shows any reduction in ***rate of growth***.

Or alternatively, let sample-A is added with RCUP and sample-B left without RCUP. Now any well-known virus to be induced into both A & B and check about the growth of virus (Rate, in min^{-1}, usually $N = N_0e^{-kt}$ holds good for virus growth) in both samples. If RCUP is a real protector of host cells, there should be **sharp decline** in growth of virus in sample-A and shows its usual trend in B.

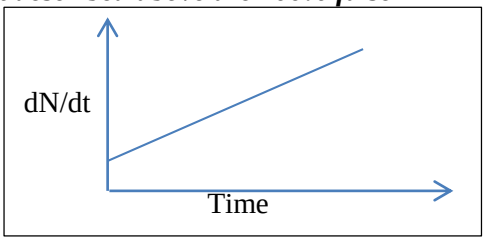
Graphical Representation:

Case-1: If RCUP works as per views what described above :

[dN/dt = Rate of Growth of virus]



Case-2 : If RCUP does not work or if views what described above are 100% false



Merits

1] This article is all new to modern technology or modern world.

2] This concept is based on utilization of all naturally existing α-AA in preparing RCUP, so, the creator of this article hopes that, there exists NO significant side effects on host cells.

3] A clear cut explanation has been provided regarding ability of specific α-AA to pair with another α-AA.

4] A clear cut procedure has been provided to synthesize ***RCUP*** in laboratory and its use.

Demerits

1] The creator assumed that every α-AA has both hydrophilic and hydrophobic characters and a new index (HIN) has been introduced just to give a rationalistic explanation for this.

2] The new mathematical expression to calculate HIN is purely hypothetical and so far, it has NO experimental evidence or support.

3] The specific shape of virus is based on HIN, which is also hypothetical and so far, there exists NO experiment to confirm this.

4] The creator has not provided any extra information about correct sequence of α-AA in any given PPC (i.e PPC-1 to PPC-20).

5] The contribution of every group/part/radical to HIN is shown by specific value. There is no specific explanation offered by the creator for these assigned values.

6] The creator has not provided any information, how does RCUP really protect host cells from virus and also no explanation being provided why virus is impermeable to host cells after being enclosed by RCUP.

7] The creator of this article has no clear cut idea whether all 20 amino acids are available in the synthetic form (or) can be produced in laboratory by simplest possible method.

Humble Message From creator of this article!

1] This article is purely the brain child of creator [***Rama Chandran V.S***]

2] The concept is purely hypothetical and never tested earlier anywhere across the globe.

3] The creator does not know whether similar concept already exists or proposed by some other person or such a typical universal protein had already in use or synthesized.

4] The creator requests real aspirants (from virology/pharmaceutical industry) to think about positive (if any) and negative aspects (if all) associated with this new concept. I hope, virologists/pharmacists/biologists/biochemists /doctors/botanists etc., may give their valuable comments and marvelous critics on this ***RCV-2020***. I request all top intellectuals to send their valuable critics/suggestions/comments if any to my *e-mail ID*.[vsrc280667@gmail.com]