af#ALO41220-TASCV-S-K-1a, By Dr.Allen Lau, NYS-08A3668

Segment K-1a, Supplemental, ©
Page K-1 & 2,

Supplemental, Cover Page Letter to: Dr.Rochelle Walensky, Director,
Center for Disease Control and Prevention; (CDCP),

Dear Dr.Rochelle Walensky,

Enclosed for you are my Corona Virus Research Thesis Segments pages that were composed during April 2020. I felt will be helpful for You, the medical & scientific research community at large.

• This Supplemental Segment-K-1a,
Pertains for matters mentioned in all TASCV Segments Pages, including well meant suggestions at TASCV Segments, I & J, has useful content for your consideration to communicate to all your colleagues in Genomics, Medical and Pharmacological developmental research of medications / vaccines, that can greatly enhance longer term effectiveness of CV vaccines and complementing medications.

•My theorems are accurate that further investigational research shall display and identify genomic associations and congruency that can be affected by Corona virus strains throughout segments of the Taxonomy chain and web to all life on Earth.

•These further findings shall prove as mentioned in my other TASCV Segment pages that Cross spectrum interspecies lifeforms / organisms that may be in part immune at various levels to Corona virus strains can also act as mechanisms of viral transports.

•The Corona viruses has unique characteristics, that it has the abilities to adapt cross specturmally, to adopt cellular genomics multi-dimensionally across taxonomy of interspecies, to within shorten cycles of time frames to change its genomics structure, reappear and to replicate with new Codeons of Receptors from the genetics of its former hosts.
•Which in its mutated metamorphical form can render it resistant to present medications / vaccines in very brief time frames of less than 14 days and between 5 to 30 days;
• Dependent upon the particular CV strain which emerged from that particular host lifeform.

*In Other words, Certain CV Strains can with each replication cycle has ability to recode in adopting its Hemagglutinin receptors to the genetic code sequences of its most recent and previous host's cellular genomics.
•Therefore reappearing / emerging as a slightly genomically altered new strain of CV.
•The replication cycle is dependent upon the host cells half life of whichever interspecies organisms the CV has infiltrated to infect.

* As mentioned in TASCV-S-I & J, It is highly suggested to forming a unified Genomics Database that is Globally Cloud accessible by all researchers,
•This can greatly improve the monitoring of genomic changes to the Corona virus strains, by cross referencing any local areas associated taxonomy of lifeforms/organisms.
• Networked Cloud shared database that is programmed to Cross Reference by algorithms that can Identify cellular genomics changes at each level of taxonomy and host infections.

•My Multi Dimensional theorems is that New CV infections are also caused by each locals interconnected Bio-diversity of lifeforms at many possible levels by taxonomy.

•How we can discover, know and enhance identifying all genetic shifts is by setting up Local Micro Genomics Sequencing labs equipment with the correct unified database algorithms at any epicenter's hospital laboratory of major outbreaks; That then can autonomously upload data in real-time upon unified global cloud shared database.

*What this local sequencing of infected patients and lifeforms will show us are that the mutated and emerging strains of CV viruses also contains sub-categories of genetics Codeons sequencing materials that can be traced back upon of its former transport hosts before further infecting its human hosts.

*> I do have lots more research data that was not yet published in TASCV Segments.
My main barrier is due to circumstances that I work under when composing TASCV Segments research thesis.
Plus that I do not have access to computer wordprocessor and pertaining resources to of composed research pages as I would prefer.
•Meaning that due to limitations of equipment, resources and circumstances,
That It was all manually typewritten on my typewriter, Which has taken great efforts in time while living under very adversely hostile to me restrictive conditions. I had to omitted lots more content than preferred.

•If I am able to work under better ideal conditions and place,
I could have provide lots more information that is helpful for You and fellow scientist.

* All I ask is your confidence in what I've written,
That There are expanded contents and views to it all.

* I am among the world's best and finest Laboratory and Scientific Research Technician and,
Administrator for Management Information Systems Facility, Technology Systems Development.

•My Talents and esteem abilities to spot and analyze scientific and technical research data nuances that by no fault of anyone that was potentially overlooked or yet undiscovered.

*I do have positive potentials in knowledge for never before thought of solutions for assisting with scientific research for stopping the CV virus strains in the wild and from further infecting cross-specturm hosts.

* Upon your request, I can provide Dossier, History of Education, Employments and Life Experience Skills and Professional Career Resume,

*If incase you have any further questions.
I can be reached by contacting my attorneys,

• Mr.Steven Metcalf, ESQ., Telephone # 631 521-1499, email: Metcalflawnyc @ gmail.com
Metcalf & Metcalf law firm
99 Park Avenue, suite 2501, 25th floor
New York, N.Y., 10016

• Mr.Sing Yee, (718) 921-9378, email: ysy3749 @ gmail.com
72 Bay Ridge Parkway,
Brooklyn, N.Y., 11209

Sincerely Yours,

Dr.Allen Lau,

Cc/;

Mr.Steven Metcalf, ESQ.,;
Mr.Sing Yee;

File, af# AL041220-S-K-1a, Supplemental

af#AL041220-TASCV-S-A-1,

by, Dr.Allen Lau, NYS-08A3668,
April 12, 2020 ©

Segment Part-A-1,
Page-1-A,

RE, Thesis Topics, Abstract & Technical, Summaries; Corona Virus,

All Pages are well meant suggestions presented to assist Scientific research for developing the best possible Antidote / Remedies to Corona virus strains,

•Genesis Theorem for Corona virus RNA Specific strains, Genomics
•Transient Convergent Gene Shifts Genomic Codes,
•CV-Divergent Convergent InterSpecies migrations,
•State of Corona Virus;(CV-I); & Corona Virus;(CV-II-X+), Strains,
•Introduction & Concept to My Scientific Theorem Of Duality-Dualities; Progressions via Dualities,
•Applied Enhanced Quantitative results for Scientific Research & Development Medications;
That will not cause longterm genetic maladies,
*Enhanced Research & Development to Diverse MultiDimenional, MultiGenomitariously;
Effective Antiviral CV19 Antidote solution(s);
•Medication for a complete Medical Cure to the Corona Virus;
•That Shall Work Universally for All People;
•That is unlike any presently in experimental testing use.
•Molecular compounds to elements & protiens in species of Myceilium Mychorrizals;
That couteracts CV19 & its variant strains from cellular infiltration, migration and,
counteracts after effects of CV Phases II & III; To protect CV Positive infected patients from CVA-DIC

* Abstract Summary,

Natures of Corona Virus strains,
Are highly interspersive interspecies adaptive parasitic microorganisms,
Are multidimensional aspects to many interrelated segments which must be further investigated
in genomics research.

•Potentially unintentionally overlooked by Geneticists and Genomics Researchers and Pharmaceutical developmental medication manufacturers,

•Are the longterm adverse genetics changes by certain experimental medications, serums, vaccines;
That transverses by hereditary upon future generations;
•By Duality Theorem, Potentially as genetic defects or other forms of mysterious illnesses.
*Duality-Dualities Theorem, Are other reasons why some vaccines are not administered during pregnancy nor to children under 6 months of age;
•Can potentially alter or interfere chromosomes genes structures during Fetus & infant child development.

*There are genetic codes sequences to biomolecular chemistry multi-aspect gene sequence compendiums interactions at multidimensional genomic levels potentially overlooked by researchers;
That requires further research.
•That shall greatly improve developments to manufacturing a medication,
•That will stop the Corona virus pandemic.
•That will cure in saving the lives to not just some, but for everyone!
Even those within varying stages infected!

*My Theorem, About common transient Gene Codes divergences convergent interspecies migrations,

* Since Archean Eon, when basic lifeforms appeared as simple microbial life on our Earth;
•Viruses & Bacteriums were the Earth's original Archaea-Prokaryotes; RNA,
single cell lifeforms that appeared long before Eurkarya/Eurkaryotes lifeforms appeared.

*RNA, Ribonucleic Acid, organisms existed long before increased complex atmospheric gases and oxygen levels rose over Eons to evolved DNA;(DeOxyribonucleic Acid), Organisms.

*All Life on Earth has always been in progressive transitions,
Where one/groups of species transitions over time to evolve or becomes extinct;
Other new or preexistent competing lifeforms appears in succession.

*However, Never before in the history of all life on Earth,
Since during the past 100 years has so many extreme changes happen to our environment ecosystems.
So many Species of lifeforms become extinguished and extinct forever!

Although Human Beings at our present state of existence may only see some of those newly appearing lifeforms as microbial organisms.

*Viruses, RNA Specific Species, by interspersive migrations between many lifeforms & species,
been nature's indirect Inter-Species & Trans Species evolutionary attributors.
That influenced Genetic-Genomics changes over billions of Eons.

*However are infact much in common Genetic Codes Sequences that exists within all Lifeforms natural to Earth.
Are by categories gene sequences common from Human Beings down to known microbial organisms.

***That researchers might be overlooking are the unified common genetic cross species segments to all life forms cross specturmally that interconnects our present "Glovessphere";
Where common interspecies Genetic Genomic codes exists.

*Genesis Theorem for Corona virus, RNA Specific strains, Genomics,
Although News media alleged CV unconfirmed migrated interspecies from Bats to Humans,
*There are potentially 3 or more overlooked hereditary CV Genesis not investigated by geneticist & genomics researchers,
That is vital for further investigational research,
1) The molecular genomics from alleged Bats; Fecal matter;
2) Fungi-Molds, at Genesis from Bat Fecal matter;
3) CV source adaptation genesis from source Fungi-Mold, to,
4) CV migration phases, Bats to other lifeforms; Animalia to Humans.

*What results by researching these 3-4 genomics genesises shall teach us are the elemental biochemical compositions, protein molecules, biomolecular genomics connections at each genesis phase;
That evolved the CV into its present forms CV-I & CV-II-X+.
•Will provide us history molecular chemistry & protein molecules, exospecies genomics transition records that evolved the CV strains.

•What doing so will further yield us in research data are the antigens;
Theorem of Dualities Receptorial ionic polarities at the subatomic & molecular levels.
This will teach us how to construct CV antidote remedies for immunity without host organelle genetic chromosome genes alterations.

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by, Dr.Allen Lau, NYS-08A3668,
April 12, 2020 ©

Segment-B-1,
Page-1-B,

Conventional Terminology Summary Overview,

Viruses are categories of Archaea single cell RNA interim Lifeforms without an inter cell nucleus, has an indifferent genealogy that has genetonoumously co-existed in nature with other lifeforms.

Viruses utilizes other lifeforms that has cell organelle structures with DNA,
to Replicate and has influenced genomilogical changes over protracted periods of time, across generations hereditary; (in certain respects over millions & billions of Eons);
To whichever host organisms that these viruses has divergent to convergenced upon.

*In Otherwords, Meaning that viruses has evolved conjointly over Eons to contain or possess in part some to similar gene codes sequences within its microbiolic-molecular genomic codes sequence(s);
That permits the Corona virus to infiltrate intercede convergence upon host bodies;(cells);
organisms with DNA to utilize in replication symbosistically.
And like most virus strains has its further potential ability to alter the hosts future genetic genealogy.

*By natural microbiology mutations happens by many potential causational categories,
from preexistent or changing environmental influences.

*In terms of Genetics-Genomics, Molecular Biology,
Contaminants including by environmental can be defined as any these potential Constants and known Random Variable Exponents:
Cellular replication distortions & mutations, Host body unique hereditary genealogy genetic anomalies/ distortions/ mutations.
At Chromatic developmental, transcription, replication phases.
Any particular host body's cellular genomics to preexistent uncommon mutated gene codes sequence(s);
•Including attributed potential factors, such as;
•Environmental Pollutants, Chemical, Radiation,
•Free-Radicals contamination or damage that are present within host body;
•Includes existent genomic changes from medications and defective vaccines,
•Hosts immunity/resistance & susceptibility by hereditary cellular biology.

*Corona viruses & its variant strains are living organisms,
Therefore like most living organisms,
Are several known ontogeny life cycle stages to COVID-19 & its variant strains;(CV-I,CV-II-X+ etc.);

*In nature that of "In The Wild", Are continuously naturally occurring Genetic Shifts & Transmutational species evolves. Includes many new strains of microbial organisms such as bacteria & especially viruses.

*The warmer Summer weather is soon to be upon us,
•When CV & Other virus conditions appears in remissions;
•Are CV *Gestational Incubational & Hibernative stages,
•Are further many random mutations in "Genetic Shifts to Trans-Species" Genomic Crossovers happening.

*These CV strains are highly adaptive, mutational,
Has ever abbreviated rapid cofactoring replicational cycles.
•Meaning that CV can during replications phases produce many newly mutated adaptive medication/vaccine resistant CV generation in very brief time frames;
•Between 5-15 days or less cycles by factors > 10X + numbers of hosts;
•Dependent CV gestational ability to compromise each host immunity;
•AVG Temperatures CV remains active at Human Body Temperature;(H.B.T.); 98.7°f & Betw, 85.5°f - 105°f, (29.7°C - 40.5°C).

*Soon shall, If already happening by genetic shifs crossover to other animal species, Mammals, Reptiles & Insects; includes most flying insects.

Potentially even by other microbial & Phylum;
Plant life species that can act as further forms of viral transport.

*This can include microbial particulate matter carried by water source & during atmospheric conditions in the air by wind; CV-infected organisms/allergens, such as bacterially attached air particulate matter, Mold; Pollen Spores & Sporrans.

•Facts, Are that Corona Viruses;(CV-I & CV-II-X+);
Are Air transportable not only by exudated sputum droplets during common human social contact.

*Airborne Dust, Organic Allergens & Bacteria are natural particulate matter in the air we breathe.
At present CV Are also air transported via many interrelated segments which by CV infected positive Microorganisms and common air particulate matter that are also acting as transport platforms substrates for vast array those microorganisms, allergens & viralgents;

•That by present Corona virus strains mutative transport can genetic codes shift,
Even on to such minute natural particulate matter in the air.

Which requires further investigational research to construct biomolecular models for beyond probablity and for genetic medications and remedies of greater quantitative coefficients.

*Having shared collaborative access to preexistent Gene Codes sequencing research data will save time to not replicate tasks to preexistent data.

*Data on genetic code listing of COVID-19's RNA & Gene sequences codes subdivision breakdown to the functional sequence to each of the virus's biomolecular chemistry at subatomic multidimensional aspects;
Proteins, Enzymic & Replication functions;
CV's separate individual genes codes; comparative to genomic host,
Changes occurred at Genomic levels.

*With this additional data,
There are several subcofactors where we can link in knowing the exact molecular byproducts produced & affected in multicontexts to Corona variants at very moments in contact to host body cells & stages thereafter.

The exact biomolecular chemical & biogenomic compounds & molecules released during each cofactoring stages.
*
*Note, That simply confronting matters by any linear single point aspect such as disabling CV M-RNA proteins to host body. May not solve to remedy CV Phase II & III, host body's, CVA-DIC immuno-response.

*By Theorem Of Duality-Dualities, disabling M-RNA can cause Catastrophic cascading effects.

* Theorem Of Counter Covalent Ionic Repulsion,
Are Several Methods that I can show you,
How to alter CV orbit of electrons at CV Hemagglutinin, to prevent CV from, host cell membrane Sialic Acid receptors infusions.

*Cont'd @ af#AL041220-TASCV-S-C-1; by, Dr.Allen Lau, NYS-08A3668,

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Segment-C-1,
Page-1-C,

Summary Discussion, Corona Virus, Research by MultiDimensional Aspects and Segments,

*Although, There are some commonly known biomedical & scientific data as pertains to Transitional Phases of Viruses and infected hosts Cells;
CV-RNA proteins, Sialic acid, Hemagglutinm, Neuraminidase,

* How Viruses Infects-Infiltrates, Replicates, Diappadecisis; Extravacions; Blastisporric Tranistions in Migration form host cells, to infect new hosts Cells and;
The Chemokines, Cytokines, Viriods, released when during host cells blastisporric tranistions,
That causes host body extreme Immunological Overreactions & Degradations.

*Further Investigational Genomic Research,
*Presently The actual data is potentially; Finite;

*Missing actual interactions Chemical Biomolecular proteins & submolecular ionic polarial changes to during cellular transitions;
*That there are 100s to 1000s of categories & types of chemical molecules, proteins, that can or may have immunological correlations during CV phases.

*Missing are Multi-level Comparitive Genomic code sequences, all effects to research data on Genetic shifts by CV Gestations/Gestated-Host Cells;
Chromosomes; Genes; Genetic structures, host cells Replicational Genomics;

*There remains much Genetic or Genomics codes and sequencing research that may not be totally unified to Central Source Databases;
*(It may require Researchers and Information Systems Development Programmers to develop several unified databases programming algorithms;
for multidimensional aspects data analysis);

*Where Research Data can be Collaboratively Accessed, Contributed upon and Comparitively shared from all posssible sources to CV genomics research Nationally and Worldwide.

•To be more precise, access for all researchers to Centralized Unified Distributed Computer DataCenter(s) facilities Networked Databases,
•To analyze, perform comparative / cross-referencing analysis at multidimensional levels and formulate consolidation reports to cellular changes, Chromosomes, the separate genomics codes analysis/ subdivisional breakdown to enzymic, purferins/grenzymic molecular proteins, cellular molecules & molecular level gene codes cofactorings by virus to host cells.

*That researchers potentially overlooking are the Unified Common Genetics-Genomics Cross Species;(UCGGCS);
Segments to all life forms cross specturmally that interconnects our present "Globvessphere";
Where common genetic-genomic codes exists.

•To further investigate by multidimensional genetic-genomic algorithmic comparative models any past/present/future changes and or damage to our intespecies biospheres-glovessphere.

•That by present Corona virus Type-I & Type-II-X+, New Corona Virus strains mutative transitions transport can genetic codes shift, Upon all Taxonomy levels of lifeforms on Earth.

However what more can be learned are further unknowns pertains to gene code keys to further potential variables in correlation to the genetic codes of CV-I & CV-II-X+ strains of viruses,
further potential effects to immunology;

*What else at the biomolecular, chemical & subatomic, correlations compendively by multidimensional aspects might been overlooked & can be further discovered as it pertains to;
•Thrombocytes, Erythrocytes, Mylocytes, Lymphocytes, the CV's effects upon all Lymph glands and, Lymphatic cells;
•Phagocytes, B-Lymphocytes; B-cells, Antigen cells, MHC-I Complexes, APC MHC-II Complexes,
T-cells/Helper T-cells, Cytotoxic cells; CD4+T-cells & CD8+T-cells, Immuno Synapse Receptors & molecular component protiens,
•Diappedicial Physio Inflammatory & Immuno Responses.

•Which requires further investigational research to construct multidimensional biomolecular genomic and potential non-genomic more conventional safe for longer term use on CV, Medications.

**That I'd like granted is physical collaborative participational research access to; Databases Libraries,
*The latest technical Genetic-Genomic codes Sequencing research data on Corona virus;
*Genetic-Genomics diagnostics research projects & reports from Infectious Diseases Medical, Scientific Research Facilities; Including National Institutes Of Health; Database Libraries.

*Having access will save time to not replicate tasks to preexistent data.

*Data on Genetic-Genomic codes listing of COVID-19's RNA & Gene sequences codes and Subsetting / subdivisions analytic breakdown to the Biomolecular Chemistry, functional sequence to each of the virus's elemental proteins enzymic & replication functions; those separate individual genes codes; by any reactive / interactions to Organelles & Hosts Cellular contexts.

*With this additional data,
There are several subcofactors where we can perform comparative cross links in knowing the exact molecular byproducts produced & affected in multicontexts by Corona variants at very moments in contact to host body cells;
•The exact biomolecular chemical & biogenetic compounds exchanged and released during cofactorings.

•The enzymic proteins correlations is amongst ways to how this virus penetrates human host cells,
to multiply by utilizing host cell's DNA replicatory genomics in mass replication;
•Is besides collateral damage to host body organs.

*We can directly disable, The CV strains from Adaptive proliferations at 2nd/3rd phase stages;
*(Ref'd @ af# AL041220-TASCV-S- -1).

*CFN: Further investigational Genomics research must be performed upon;

*Exist are Myceilium Mycorrhizal species which contains & produces biogenetic molecular elemental compounds that provides resistant immunity to & after effects of CV, without longterm genetic alterational damages & is non-toxic to internal cellular biosphere of humans.
*That can prevent CV from infecting Positive &
Alleviate those seriously ill CV infected Patients from CVA-DIC.

*Cont'd @ af#AL041220-TASCV-S-D-1, by, Dr.Allen Lau, NYS-08A3668,

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Segment D-1a,
Page-1-D

Topic About Mycelium/Myceilium, Mycorrhizals Species,

*Further investigational research should be performed upon;
•These Species of lifeforms are worthwhile for further investigational Genomics research;
•Because these are RNA Specific Species of Prokaryotes; Fugi & Fungus,
•That is Eon Genomic branched off relatives of viruses, the Eon branch offs;
•That Eventually became known as, the Corona virus strains,
•Myceliums/Myceiliums, Mycorrhizals, That has established genomic gene structures adaptively resistant to CV;
•That established genomic gene structures that are counter ionic polaritance, reversing-repelling to CV and it other relative viruses; the SARS and, MSRV; which in form nearly bacterium like.

*The molecular ionic arrangements and directional orbits of electrons at the subatomic levels can influence unique biomolecular behavior of similar appearing RNA; including that of M-RNA; Ribosomes,
Are many minute submolecular variants of M-RNAs;

•Is Dependent to Species and type of organisms are potentially 100s to 1000s of variants,
B-RNAs, M-RNAs, S-RNAs; to how each may react or interacts with other organisms cells.

*By Theorems of Duality-Dualities, $TSD^2=PD$,
Research for longterm progressionary genomics effects to test organism subjects is suggested.

*Myceliums/Myceiliums, Mycorrhizals;
Which contains utilizable extractable forms of Molecular products; B-RNAs, M-RNAs, S-RNAs Proteins and pertaining proteins molecular packages.

*So there exists in Mycelium/Myceilium, Mycorrhizal species that are distant genomic cousins from Eons, That evolved with viruses which contains the variant, B-RNA, M-RNA, S-RNA proteins molecules and products that produces biogenetic molecular elemental compounds that provides Immunity and Resistance to and after effects of Corona Viruses, without longterm genetic alterational damages to human genome, and is non-toxic to internal biosphere of humans.

*That can prevent CV from infecting Positive and;
•Alleviates those seriously ill CV infected Patients from CVA-DIC;
•(Corona Virus Attributed-Disseminated Intra-vascular Coagulations);
•Potentially many times better & safer than Aspirin;
•Which can cause ICH;(Intra-Cranial Hemorrhaging).

* The RNA Molecular chemistry of protiens can be dependent upon the species that it pertains to and how research chooses to perceive applications and utilizations of organism's contents;

•The M-RNA, Ribosomes Chemical Messenger Molecules on membranes of Corona viruses that interacts with Host Cells Membranes;

*To when Corona viruses begins to invade host cells;

•Should be given further investigational research to be sure that there are no adverse vaccines interactions with host organism's M-RNA which does exist during certain cellular functions in Human Beings.

•The B-RNA, are what I call the "Branch away" gene sequences in viruses and by that of Myceliums/Myceiliums, Mycorrhizals Species that works with;

• S-RNA, "The Separator" Gene Sequences; are a form of genomic "Check-Sum"; Error correcting code sequences that prevents other RNA specific Species from intercession upon its genomic sequences and future generations.

*The Scientific BioMechanics, How and Why this works,
Are two separate Basic Dimensional Aspects,

*1) There exist elemental molecules to chemical compounds that can both reduces and further prevents CVA-DIC.

*When CV invades host cells and progresses to vascular the Endothelial cells, activates immuno responses:

•The M-M components, limits & inhibits the M-Molecular protein molecules packages in Endothelial Cells and Platelets from Primary & Secondary Hemostasis by delimiting activation;
•Endothelial cells release of Endothenlin 3 Hormones to Fibrin in Platelets from becoming Fibringen;
•Which during Secondary Phases of Hemostasis is what Forms & Solidifies the Blood Clots;
•M-M factors assist maintaining Blood Plasma balance of Nitric Oxide;(NO2) & Prosecyclin;
•Hence preventing and reducing effects of CVA-DIC.

*2) Are protein molecule substance that has reversing effects to polar attraction that delimits and repels the M-RNA on Corona Virus strains, no matter mutational progressions, from attacking human host cells.

•And there are several methods to adjust the molecular structures of component products found in Mycelium/ Myceilium, Mycoorhizal species, to be greater functional in applicability for intended purposes.

*Your Genomics Research Scientist will have better more direct access to research reference libraries data;
*That will identify & verify substances contained within species of Myceliums/Myceiliums, Mycorrhizals species.

*I apologize that my present highly encumbered circumstances does not permit me direct access to research references & better scientific data,

*Please be welcome to contact me and, or share data with me.

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Segment-E-1a,
Page-1-E

* Abstract Technical Summary,
About Primary & Secondary Phases Of Hemostasis;

*Hemostasis is an Immunological Process to form preliminary repair at location(s);
of damaged blood vessels to stop bleeding by forming a blood clot.

* The BioMolecular Mechanics to, How Hemostasis works,

•Is 2 Part process: Primary & Secondary Hemostasis,

* At Primary phases of Hemostasis,

•Is both Nerve Reflex and BioChemical process,

* Step 1) Vasoconstriction,

* a) Occurs, At the damaged blood vessel cellular area is an initial Nerve Reflex Response,
•Where Nerve Reflex signals smooth muscles that lines the outer portions of vascular vessels;
•Where damage has occurred at The Capillaries, Veins, Arteries; to Contract/Constrict;
•Is an Nerve Reflex immuno response in attempt to decrease blood flow & loss at the damaged Endothelial cells;
blood vessel location,

* b) Endothelin, Which is secreted by damaged Endothelial cells; Further promotes Vasoconstriction,

* c) During Normal Healthy vascular functions;
•Blood Plasma content of;(Endothelin, Nitric Oxide & Prosecyclin); Is Balanced,
•The NO2 + Prosecyclin together maintains dilation of blood vessels, to promote normal blood flow;
•Both of which when equally present in the Plasma works in unison as vascil dilators, Counteracts Endothelin.

* d) When Endothelial cells are damaged/injuried; added Endothelin is secreted by those damaged cells,
•During this Immunological process, No Nitric Oxide is secreted,
•Which Endothelin and Prosecyclin causes further Vascil Constriction.

* Secondary phase Hemostasis,

* Step 2) Platelet Adhesion,
•The damaged Endothelial cells secret platelet activating chemical molecules in to the Plasma,
•That summonses more Platelets to arrive at the area of damaged Endothelial cells,
•The Platelet Receptors that pertains for Hemostasis, Glyco proteins; GP I-B and GP IIB, IIIA;

* a) While Under Normal conditions,
•The Endothelial cells that lines blood vessels maintains a balance of,
•Nitric Oxide & Prosecyclin @ surface of Endothelial Cells;
•Which prevent platelets from sticking;(adhering); to blood vessel walls.
•Platelets do not normally adhere to Endothelial Cells;(blood vessel walls); nor,
•The layer of Collagen between Endothelial Cells to Dermis layers;(skin layers);

* b) When cellular injury occurs to Endothelial cells,
•The Platelets release chemicals & protein packets to produce Fibrinogen.
•Which combines with a molecular substance in Plasma called the "Von Willebrand Factor";(VWF);
•That becomes the binding factors adhesive;(glue); That binds the Platelets together and at damaged
Endothelial cells; blood vessel's walls, collagen and Dermis cell layers.

* Step 3) Platelets Activation & Degranulation, are 2 phases,

* 1st phase,

* Platelets has many types of Receptors,
•Receptors that pertains for Hemostsis are Receptors Glyco Protein; GP I-B, and, Receptors GP IIB, IIIA,
•Platelets has organelles;(vesicles & vaculoes);
•That contains molecular Chemical & Protein packets;
• Vital for Secondary Hemostasis are, 2 molecular Granules Packets,

* a) Platelets after activation releases, 2 molecular Granules Packets that further stimulates VWF,

1) Alpha packet contains Fibrinogen, a secondary binding agent,
2) Dense packet vaculoe that, contains 3 types of chemical compound molecules;
•Seritonin, a vasicconstrictor,
•ADP, That Activates Platelets and Promotes Aggregation
•Calcium, content released by platelets, Stabilizes the bonding of Platelets.

* 2nd phase,

* b) Platelet, Activation function,
•Are that platelets release a chemical called,
•Thromboxane A2, which is opposite to what prosecyclin chemically does; further promotes platelet aggregation.

* Which is also manufactured by the same sets of molecular enzymes in Endothelial Cells that cause vascular constriction and sends chemical signatures that activates the Platelets to change shape and Clump together via Platelets cellular aggregation;

* c) By molecular stimulation of Glyco Protein IB,and Glyco Protein IIB-3a Receptors on Platelets and Fibrinogen Receptors to bind;
•(Pull-Together & Clump);

* d) The Final Blood Clot, forming stages,
• Includes phases 1 and 2 above, Plus;

•Coagulation Cascade, via Coagulation protein factors,
•SubEndothelin Collagen via Intrinsic Pathway;
•Tissue Factor, ThromboPlastin via Extrinsic Pathway,
•Phospolipid surface provided by Platelets,

•However, It is not until activated Platelets changes shape,
•Where they can bind with Fibrinogen.
•Where GP IIB, IIIA Receptors changes shape for its receptors binding actions,
•The calcium released by those activated Platelets solidifies the bonding process,

* e) Platelets now binds together and adheres to the damaged Endothelial Cells;(blood vessel walls); and Collagen located at the damaged sublayers of Dermis cells.

* f) The final product is the Stable Blood Clot.

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by, Dr.Allen Lau, NYS-08A3668,

April 12, 2020

Segment-F-1,
Page-1-F-1

*Abstract Review of Hemostasis,

* The Biomechanics How and Why Blood Clots Happens,
•As Referenced in af#AL041220-TASCV-E-1a, Technical Summary of Hemostasis.

*During normal healthy body functions,
Hemostasis is the body's immunological response to stop bleeding of damaged blood vessels,

•Either internally and or at the dermis layers;(skin layers);
•Where All vascular vessels;(Capillaries, Arteries, Veins);
•Are of a category of body cells called; Endothelial Cells;

* When Endothelial cells are damaged by any form of injuries,

* Those damaged cells secret, molecules of chemical messenger proteins compounds into the vascular system.
•Which signals immunological responses that summons more to a type of cell in the intersitial fluid and Plasma, called Platelets;(Thrombocytes);
•To arrive at the damaged Endothelial Cells area(s).

* Platelets, are the body's "cellular bandages";
•The platelets when activated releases a substance called Fibrin;

* Which during Secondary Phases of Hemostasis,
•The activated Platelets, further forms Fibrinogen,
•Its receptors GP II-B, IIIA changes shape,
•When Coupled with molecular protein that exist in plasma,
•Called the Von Willebrand Factor;(VWF);

•Which becomes the biomolecular adhesive; binding factors;
•That forms strands of proteins cross-links to each platelet & Cells within the proximity of that damaged cellular area to clump and pull together, That strengthens and promotes bonding of platelets and adhesion to damaged Endothelial cells; to the Collagen and to Dermis cells layers at those damaged cellular areas that;

* Eventually forms the Blood Clot(s).

af# AL041220-TASCV-S-G-1a, by, Dr.Allen Lau, NYS-08A3668

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Segment G-1a,
Page-1-G,

* Abstract Corona Virus Ontogency, Immunology, Immunogenicity Case Summary,

A mutual friend of my attorney & I;
Whom contracted the Corona virus was hospitalized a month in intensive care unit on ventilator.
After apparently survived his initial Seriously ill near death hospitalization,
Recovered but not long after being released from the hospital;
Suffered a heart attack, was rehospitalized, Released;
Then 2 weeks after that suffered a major stroke!

* As I explained the CV Ontogenic Progressionary process and Phases,
•To help him understand that happened to our mutual Friend,
• Corona Virus Ontogency, Immunology, Immunogenicity Protractions, transitional Phases.
* The Biochemical Molecular Attributive Correlational Hemodynamics Factors;(BMACHF);
Influenced via Corona Virus Strains Ontogency post Secondary Gestational Migrational Transitional phases from infected humoral host cells to;
• Corona Virus Attributed - Disseminated Intra-Vascular Coagulation;(CVA-DIC),

*(Expanded Technical Reference for this Segment in, af# AL041220-TASCV-S-H-1a)

* It is known that although varying degrees of immunity is developed by Corona virus positive survivors.
* There are also varying degrees of Primary & Post infection Ontogency phases to Corona virus;(CV),
•That aside from variables attributed to Environment and Lifestyle.
•Immunity is Dependent upon the Biogenomic Physiology Immunogenicity of CV infected persons;
•Every person has unique immunity by Genetic heredity.

* Pre-Ontogency Cellular Infiltration infection Phase,
•PreOntogency begins at initial Viral Exposure and Cellular infiltration infection,
•When inadvertent direct exposure to CV Spores/Sporrans,
•Which initially infects the cells throughout the Respiratory tract & Pulmonary system;
• Cilia cells and the lungs air-sacs;(Alveoli / Alveolus).

* This initial CV exposure has little to no symptoms; during the 1st few days to a week.
•At this stage are still low levels of Antibodies or Immunoglobulin activity.
•The infected person, thereafter between 3 - 15 days time frame progressively experiences diminished ability of smell & taste; this due to CV infiltrating & damaging mucous membrane and other cells that are interconnected with pertaining Nerve cells that are eventually CV infiltrated,
•Head and Chest Cold to Flu like symptoms progressively worsens.

* Inter-Meta Phase,
Is the Intercellular Ontogency post Gestational migration Transitional stages,

•Severity of CV Infection is also Dependent upon initial amounts of CV Sporrans exposure,
•Where CV has completed its initial Ontogency in Replication cycle after invaded its initial groups of host cells throughout the Respiratory tract and Pulmonary system in bronchial passages; brochioles and Alveoli,
•Utilizing the replication genomics of host Epithelial cells for multiple self replications.
•It is at this inital Ontogenic Diappadecisis Extravacionary Transitional Migratory stage,
•When millions/ billions/ trillions of new CV Spores/Sporrans, enters the vascular system;(blood stream);
•The host body becomes flooded with high levels of Cytotoxic Chemokines, viroids and, chemical-protein messenger molecules that are released by CV damaged cells,
•Signals initial Cascades Immunological responses at cellular levels.

* Post CV Ontogenicity, Ana-Phase and Post CV Secondary Tele-Phase,

• CV diappardecisis/Extravacions, inter-cellular migrations,
* At this stage is where the most vulnerable health categories patients are affected,
•Prevalent acute flu like symptoms manifests moderate to high fever,
* Respiratory system is in Acute immunno-inflammatory Response;(AiiR);

* The combination of Physio-Immuno activity,
•Severe Pulmonary congestive conditions result from body's over reactive AiiR,
•The CV destroys pertaining Cilia cells throughout Respiratory-Pulmonary tract rendering them non-functional to Exudate congestive Sputum,
• Excess build up of fluids in lungs diminishes patients ability to breathe; Respiratory Distress Syndrome,
•Further potential for Bacterial infections,
• Glandular over production of mucous and residual formations from over immuno response;(AiiR); Of antibodies,
•Results in Stagnant accumulations of Puss from antibodies;(white blood cells); and Alveolus cellular and vascular hemorraging, hemotomas causes Extreme Hypoxica,

*The humoral cells at pulmonary circulatory system & organs throughout the patients body are overwhelmed with CV virods, cytotoxic cell matter.
•CV further infects and Diminishes Organ function. Difficulty breathing and Extreme Hypoxica respiratory distress and potential organ failure; that requires intensive hospitalized care treatment,
•Requiring patients to be placed on supplemental oxygen and or assistive breathing with a mechanical Pulmonary Ventilator.

* Recovery or Septicemia/Sepsis,

* Post Diappadecisis are massive amounts of molecular proteins,
* Wherever damaged cells secreted proteins matter throughout vascular system,
•Those millions/ billions/ trillions of cells also have released Chemokines & Viroids particulate matter and, molecular proteins which causes Hemostasis response by Thrombocytes;(Platelets);
•Which activates deviated Coagulation Cascades,
•Thus activating Massive amounts of Platelets to bind with Fibrinogen;
•To form Blood Clots throughout the circulatory vascular system;
•That causes vast arrays of Auto-Immuno complex syndromes such as,
* Corona Virus Attributed - Disseminated Intra-Vascular Coagulations;(CVA - DIC)

* The larger clotted blood particules travels into the heart;
Causing Myocardial infractions,(Heart Attacks); Thrombosis Embolus.

* While Other Blood Clots throughout vascular system that travels into the brain causes Cerebral Infractions:
•Iscemic Infractions, Cerebal Embolism, Thrombosis-Embolus, Hemorrhagic Strokes,;
* Heart attacks and or Strokes.

* In review certain more seriously ill Corona virus infected cases,
What post CV infection can eventually leads to are,
•A vast array of Auto-Immuno Complex Syndromes,
•Alveoli Fibrinoid-Necrosis, Vasculitis,
•Sepsis attributed organ failures,
•Plasma Dyscrasias
•Acute Chronic Respiratory Hypoxica; Acute Repiratory Distress Syndrome;(ARDS),
•Requiring patients to be administered supplemental Oxygen,
•In most seriously ill CV cases due to acute lung and Alveoli damage;
•Requires patients to be placed on Mechanical Pulmonary Ventilator.

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Segment H-1,
Page-1-H,

* The Abstract Technical BioMechanics Of,
Corona Virus Attributed - Disseminated Intra-Vascular Coagulations;(CVA - DIC),
•How & Why some post Corona Virus infected survivors, Suffered Heart attacks and or Strokes,

* Definition of Terminologies for the scope of this segment:
•Corona Virus Strains, CV-1, CV-II, III-X+, Abbreviated as (CV).
•Spores/Sporran(s); Denotes when Viruses are in transport migration mediums,
•When CV is inter-host body or during trans-cellular migrations to infect/invade new host cells.

* Pertaining References in Segments af# AL041220-TASCV-S-A-1; S-B-1; S-C-1; S-D-1a; S-E-1a; S-F-1; S-G-1,
* CV infections can happen by,
•Direct contact exposure with CV Postive infected persons body fluids,
•Such as by Sputum "droplets", Coughing, Sneezing, Spitting.
•Direct contact exposure with any numbers of CV Cross Infected Trans-migrated InterSpecies,
•CV Particulate matter, Transported by MicroOrganisms in air particulate matter,
•CV infected surfaces

* It is known that even though some degree of immunity is developed by Corona virus positive survivors.
•There are varying degrees of Primary and Post Secondary Corona virus infection stages,
•Mutated forms of CV remains active within some infected hosts bodies.

*Facts are that exposure to Corona Virus, or any viral organisms are rarely by single Sporran.
•Usually by Millions of CV Sporrans per single particulate matter by any CV infected transport mediums.
*CV Sporrans are invasive will seek to infiltrate all cells of any host organisms.

* When CV sporrans are inadvertently inhaled,
•The Airborne CV Particulate matter enters the Respiratory Tract infiltrates cells in the Nasal & Oral cavity passages, Pharynx, Trachea, Esophagus and Pulmonary system; Bronchial passages & Bronchioles in the lungs.
•Which branches off into clusters of Alveoli and individual Air Sacs of the lungs;(Alveolus).

*CfN: Each lung has millions of Alveoli;(each between 200 - 300 microns, in size;(1/5 mm),
•The surface area if spread out covers an area 75 square meters);

* Within each Alveolus, Is where the gas exchange occurs from the air we breath when inhaling or exhaling.
• Oxygen in gas form by osmosis,
•Transverses via interstitial fluid layer that surrounds each Alveolus through cellular cascade of basement connective tissue layers into Endotheial cells of veins, arteries & capillaries,
Where Red Blood cells Hemoglobin absorbs Oxygen from the blood's Plasma.
•When plasma has higher Carbon Dioxide;(CO2); content it diffuses out each Alveolus;
•Which has lower ratios of CO2; Completes the Respiration Process.

*The Corona virus Sporrans, first attacks-infiltrates the cells throughout the Respiratory Tract,
•The cells in the lungs and Alveoli clusters of Alveolus;
•The CV damages large amounts of cell within Pulmonary system.
•Especially in most serious CV cases, vast majority of Epithelial Cells in Alevoili are infected & damaged.
•Which causes massive immunological response by antibodies;(white blood cells);
•That eventually these millions of dead white blood cells forms excessive build-ups of Puss throughout the respiratory tract, Bronchioles and Alveoli clusters in the lungs.
•Curtailing Respiration process, Which further exposes patients to Bacteriological infections.

* CV after penetrating the lung to blood barrier, invades Endothelial cells of veins, arteries & capillaries throughout vascular system.

* When each CV infected cells replications process matures by;(Millions to trillions of host Cells);

*It Blastisporically rupture out of each infected host cells,
•Where many millions to trillions of new CV Spores/Sporrans, enters the vascular system;(blood stream);
• In search of host cells to invade.
• The matured migrating CV further attacks most all cells in host body.

* While entered the Circulatory system;(blood stream),
•Many millions-trillions of CV Sporrans are transported to areas throughtout the host body's vascular system.
•Some CV Sporrans via blood vessels enters the Bone Marrow;
•Where Red blood cells and Platelets;(Thrombocytes) are produced;
•Each developing Red blood cell;(Erythrocytes); has Nucleus & DNA.

*CfN: In the average human body, Are between 20-30 trillion Red blood cells.
•Where each Red blood cell has 270 million Hemoglobin proteins, for attaching Oxygen atoms for eventual transport throughout all parts of the vascular system.
•When developing Red Blood Cells mature, in order to make more room for Hemoglobin,
•They are genetically programmed to commonly shed their Nucleus prior to release from Bone Marrow;
•Do not have nucleus.

*However, dependent upon severity level & phase of host body CV infections.
•Exist potential that great majority Red blood cell became infected during Bone Marrow developmental stages.
•Therefore when release from bone marrow developmental stages,
•These preinfected Red blood Cells;(Erythrocytes);
•Further exasperates damage & infection upon other host body organs.

* During CV Diappadicisis Blastisporic migration process from many millions of pre-infected host cells,
•Secreted-Released by each cellular blastisporisis are massive amounts of Endothelin, Toxic CV infected cell waste matter called Chemokiness & viroids, are released into blood stream;(circulatory system).

* Those millions/trillions Chemokines & Viroids particulate matter, has molecular proteins which activates Hemostasis response by Thrombocytes;(Platelets);
To where damaged cells secreted proteins matter throughout vascular system.
•Thus activating Massive amounts of Platelets to bind Fibrinogen;
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•Iscemic Infractions, Cerebal Embolism, Thrombosis-Embolus, Hemorrhagic Strokes,

* In certain Corona virus infected cases, What post CV infection can eventually lead to is,
•Massive Auto-Immuno Endothelin Complex,
•Fibrinoid-Necrosis and Vasculitis,

* Attributing problems that results by deviated Immuno-Response,
• The CV infected host cells, mass release of Endothelin, cellular proteins, Chemokines & Viroids,
This deviated Immuno Response by antibodies in white blood cells, Platelets and Fibrinogen binds in mass Hemostasis of Blood Clots, throughout the CV infected Host body.
•Flows downstream in turn causes auto-immuno complex syndromes such as,
* Corona Virus Attributed - Disseminated Intra-Vascular Coagulations;(CVA - DIC).

by, Dr.Allen Lau, NYS-08A3668

April 12, 2020

Segment H-1a,
Page-1-H,

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(Circulatory Vascular system).

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•Those millions/trillions of cells also have released Chemokines & Viroids particulate matter and, molecular proteins which causes Hemostasis response by Thrombocytes;(Platelets); activates deviated;
•Coagulation Cascades
•Thus activating Massive amounts of Platelets to bind with Fibrinogen;
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Segment I-1,
Page-1-I,

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Theorem About Virus Influenced Genetic-Genomics Changes and Shifts to InterSpecies Taxonomy Of All Lifeforms on Earth

* Segments I & J, Presents Multi-Faceted and Multi-Dimensional aspects intended for recommending further research in gauging changes affected by Corona Virus strains to our Earth's Globevessphere's Bio-Genomics and present states of interspecies genetic-genomic sequences for if any potential longterm changes are forthcoming that can affect the future well being of our human genome's genomics.

* Since Hadean, Archean Eons to Cenozoic-Plesitocene Geological Periods,
•With Exceptions to non-virus Genetic Mutations that transitioned via Heredity / Hereditary Genealogy.

* In many respects over Eons, Viruses were directly influential for Cross-Specturm Genomic Biodiversity.
That influenced evolutionary changes over Eons in binomial Eukaryotic Species.
The occurrence over Eons by viruses adopting and transporting genetic information To/From InterSpecies and InterOrganisms.
Occurrences Which eventually attributed for cross-specturm Genomic Biodiversity over Eons. Transmuted Throughout all geological time periods to the majority if all evolutionary InterSpecies genomics Biodiversity Developments and Genetic Shifts to all known life on Earth. Including into present day time periods.

•RNA;(Ribonucleic Acid), specific species,
•Viruses are among the Earth's earliest original monomial Archaea lifeforms,
•Which Evolved Many Eons before, Eukaryotic multi cellular lifeforms Species genesis first appeared as simple microbial life in our Earth's oceans.
*Archaeaic Monomial, to mean single cell organism without defined Nucleus as compared to Binomial Eukaryotic Membrane bound Nucleus Organisms and Multi cell lifeforms that later evolved thereafter Archean Eon Periods.

*RNA; Specific Archaea Species,
Are among our Earth's earliest lifeforms that appeared in our Earth's Oceans. Long before the Earth's Geological and Atmospheric changes over Archiepiscopate Eons. Influenced increases of Oxygen percentage levels in Oceanic and Ambient Atmospheric Air Gases levels over Eons to risen enough to Influenced DNA; (DeOxyribonuceic Acid); Organisms to Evolved into forming Archaea-Prokaryotic & Eukaryotic life forms.

* Present degrees/phases of Corona Virus Cellular Infiltrations to InterSpecies Genomic Taxonomy Genes Sequences, •Potentially upon (All lifeforms on Earth).

* Further research should be conducted upon, How / What amounts genomic Changes and Shifts has occurred to each categories/ compendiums to Eukaryote species as result infestations by Corona virus and related CV Strains.
• If exists attributive genetic influences to Transmutational Divergence and Convergence Interspecies Genetic shifts to Genomic codes sequences and Codeons.

* Research Project of this magnitude Requires Joint National and Global participational efforts by Researchers Globally whom focused research Genetic-Genomic Coders and Genomics Libraians,
• For Assemblage of a Unified National and Global Cloud Shared Research Database for Networked Collaborations. Cloud shared research Data Exchange for Unified Source accessible to Global Medical, Scientific and University Research Communities;
• Contributing DATA for Comparitive Genomic Sequences, Identifying & Categorizing New Discoveries Genomics sequences and for Enhancing Preexisting Data for Cloud Shared Genomics libraries.
Which DATA sets are Openly Accessible to and for all Researchers Globally.
* COMPARATIVE COMPUTER DATABASE CONSOLIDATIONS DEVELOPMENT CROSS REFERENCINGS for Cross Matching and Referencing Gene Codes Sequences; The Before & After Comparative by taxonomy.

* An Example Overview Outline @ af# AL041220-TASCV-S-J-1&2;

Theorem of Convergence & Divergence by Corona Virus,
To InterSpecies Genes Tranistionary Changes and Shifts

• Unified Cloud Shared Database Libraries, for Comparative Genomics Compendium Research by Taxonomy,

•Having Cloud Shared Global Database access to contributing for New and Updating Preexisting Genomic Codes sequencing research data will save time to not replicate tasks to preexistent data by others.

* Common Cross Species Genetics-Genomics Codes Sequences for Unified Globally Networked Cloud Shared Research Databases search criterias,

* This Global Taxonomy Outline,
For our Genomics Librarians, Scientist and Cloud Shared Database Programmers as an Illustrative Example Overview Outline:

*> The database search criterias By Taxonomy,

•Prexistent Common sequences,
•Cross Spectrum interspecies common matching Comparative Codeons and Genetic-Genomic Sequences:
•Preexistent cross spectrum gene sequences, before & after CV infiltrations;
•Categories of Intercellular Genomics Changes that Occurred,

Category 1) Animalia Eukarotes, Homosapiens
Human Genome Subsets: HSXYXXYY-X TAATGGCAAACTA
Prexistent common sequences:
HSAYYXXXY1000X/TAATGGCAAAGTA;
HSABXXYYXY0010X/TAATGGCAAAGTA,

Category 2) Animalia Eukaryotes, Spectrum, Other than Homosapiens,
Subspecies, Mammals,
Subsets: MSHABXYXXS-X

Category 3) SubSpecies, Animalia Eukaryotes Reptiles,
Subsets: RHABXYS-X

Category 4) SubSpecies, Insects-DNA
Subsets: IHDAXYS-X

Category 5) SubSpecies, Microbial-DNA,
Subsets: MDNAXYS-X

Category 6) Plantea / Vegetation,
Subspecies X, Subsets: VPABXY1-X

Category 7) Protista
SubSpecies, Fugi-X, Myceilium/Mycelium, Mycorrhizal,
Subsets: MYFHABXY-X,
•Common Denominator Codeons, MYFHABXY-X
SubSpecies Genomic Alpha, Beta & Delta Inhibitors Disables CV from Replication;
•Invitro in the wild and Ensitu at host organisms.

Category 7a) Protista, Subspecies, Fungi,
SubSets: PFHABXY-X, Common Denominator Codeons, PFHABXY-X

Category 9-X, Archaea, Prokaryotes,
SubSets: Neutral Single cell Organisms

**Category 10-X, SARS-CV-, Archaea, Prokaryotes
Subsets: CVSARSXX-X, Common Denominators Gene Codeons Sequences CV-Strains

*Category 11-X, VRNA-X, Archaea, Prokaryotes Gene Codeons; Virus Strains,
SubSets VRNA-XHMRIVM-X,
Common Denominators (X=?)

* The Scope to Objectives for Segments I & J, Are Multi-Faceted and Multi-Dimensional,
That the Bio-Genesis mediums from where the Corona virus strains originated. Also infact has Countering and Oppositionary lifeforms within that interconnected associated communal web of Bio-Diversity.
Lifeforms / Micro-Organisms that are resistant to Corona Virus strains; That of which has valuable Genomics Codes / Codeons Data for further Studies.

Inclusively with all possible sectors of medical scientific Bio-Genomics research communities are intended for recommending further research in gauging changes to our Earth's Globevessphere's
Bio-Genomics and present states of interspecies genetic-genomics sequences for if any potential longterm changes are forthcoming or has already occurred that can affect the future well being of our human genome's genomics and associations to our Globevessphere's entire Bio-Spectrums of Bio-Diversity.

*The Unified Global Genomics Data Repository Cloud Shared Network Globally Accessible by all researchers.

•Criteria's for database algorithm programmers;
•Comparative Compatable gene sequences and Codeons molecularity Sequences to;
SARS-CV-RNA;(Corona Virus Strains).

* The Pre and Post, Genomics from Post CV Interspecies infiltrations, Inter-Host Genetic Changes and Shifts.

*I wish to be granted freedoms for scientific access to Information Systems facilities with cooperative assigned staff of scientist and systems programmers to formulate DATABASE CONSOLIDATIONS CROSS REFERENCING OF Genomics Codes-Codeons Sequences. Physical Access to Genomics libraries Data. To Formulate New genomics sequencing of binomial interspecies gene patterns; That are Open-Source Cloud Shared Databases available globally.

*> The Beneficial assets that will be gained by This added Research data will benefit the greater good of all in society globally.

af#AL041220-ATCVD-Cc/;

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af#AL041220-TASCV-S-K-1a, By Dr.Allen Lau, NYS-08A3668

Segment K-1a, Supplemental, January 2, 2021 ©
Page K-1 & 2,

Supplemental, Cover Page Letter to: Dr.Anthony S. Fauci, M.D.,
National Institute of Allergy and Infectious Diseases,

Dear Dr.Fauci,

Enclosed for you are my Corona Virus Research Thesis Segments pages that were composed during April 2020. I felt will be helpful for You, the medical & scientific research community at large.

• This Supplemental Segment-K-1a,
Pertains for matters mentioned in all TASCV Segments Pages, including well meant suggestions at TASCV Segments, I & J, has useful content for your consideration to communicate to all your colleagues in Genomics, Medical and Pharmacological developmental research of medications / vaccines, that can greatly enhance longer term effectiveness of CV vaccines and complementing medications.

•My theorems are accurate that further investigational research shall display and identify genomic associations and congruency that can be affected by Corona virus strains throughout segments of the Taxonomy chain and web to all life on Earth.

•These further findings shall prove as mentioned in my other TASCV Segment pages that Cross spectrum interspecies lifeforms / organisms that may be in part immune at various levels to Corona virus strains can also act as mechanisms of viral transports.

•The Corona viruses has unique characteristics, that it has the abilities to adapt cross specturmally, to adopt cellular genomics multi-dimensionally across taxonomy of interspecies, to within shorten cycles of time frames to change its genomics structure, reappear and to replicate with new Codeons of Receptors from the genetics of its former hosts.
•Which in its mutated metamorphical form can render it resistant to present medications / vaccines in very brief time frames of less than 14 days and between 5 to 30 days;
• Dependent upon the particular CV strain which emerged from that particular host lifeform.

*In Other words, Certain CV Strains can with each replication cycle has ability to recode in adopting its Hemagglutinin receptors to the genetic code sequences of its most recent and previous host's cellular genomics.
•Therefore reappearing / emerging as a slightly genomically altered new strain of CV.
•The replication cycle is dependent upon the host cells half life of whichever interspecies organisms the CV has infiltrated to infect.

* As mentioned in TASCV-S-I & J, it is highly suggested to forming a unified Genomics Database that is Globally Cloud accessible by all researchers,
•This can greatly improve the monitoring of genomic changes to the Corona virus strains, by cross referencing any local areas associated taxonomy of lifeforms/organisms.
• Networked Cloud shared database that is programmed to Cross Reference by algorithms that can Identify cellular genomics changes at each level of taxonomy and host infections.

•My Multi Dimensional theorems is that New CV infections are also caused by each locals interconnected Bio-diversity of lifeforms at many possible levels by taxonomy.

•How we can discover, know and enhance identifying all genetic shifts is setting up Local Micro Genomics Sequencing labs equipment with the correct unified database algorithms at any epicenter's hospital laboratory of major outbreaks; That then can autonomously upload data in real-time upon unified global cloud shared database.

*What this local sequencing of infected patients and lifeforms will show us are that the mutated and emerging strains of CV viruses also contains sub-categories of genetics Codeons sequencing materials that can be traced back upon of its former transport hosts before further infecting its human hosts.

*> I do have lots more research data that was not yet published in TASCV Segments.
My main barrier is due to circumstances that I work under when composing TASCV Segments research thesis.
Plus that I do not have access to computer wordprocessor and pertaining resources to of compose research pages as I would prefer.
•Meaning that due to limitations of equipment, resources and circumstances,
That It was all manually typewritten on my typewriter, Which has taken great efforts in time while living under very adversely hostile to me restrictive conditions. I had to omitted lots more content than preferred.

•If I am able to work under better ideal conditions and place,
I could have provide lots more information that is helpful for You and fellow scientist.

* All I ask is your confidence in what I've written,
That There are expanded contents and views to it all.

* I am among the world's best and finest Laboratory and Scientific Research Technician and,
Administrator for Management Information Systems Facility, Technology Systems Development.

•My Talents and esteem abilities to spot and analyze scientific and technical research data nuances that by no fault of anyone that was potentially overlooked or yet undiscovered.

*I do have positive potentials in knowledge for never before thought of solutions for assisting with scientific research for stopping the CV virus strains in the wild and from further infecting cross-specturm hosts.

* Upon your request, I can provide Dossier, History of Education, Employments and Life Experience Skills and Professional Career Resume,

*If incase you have any further questions.
I can be reached by contacting my attorneys,

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Sincerely Yours,

Dr.Allen Lau,

Cc/;

Mr.Steven Metcalf, ESQ.,;
Mr.Sing Yee;

File, af# AL041220-S-K-1a, Supplemental