

I-Abstract

The decoded information from the Hc-4 molar in *Equus stenonis* requires renewing the Linnaeus paradigm

A. RUIZ BUSTOS, Instituto Andaluz de Ciencias de la Tierra, CSIC-UGR, avenida de las palmeras, 4, 18100 Armilla, Granada, Spain, email: aruizb@ugr.es

Owing to the uncertainties and anomalies that are historically constants in the Linnaean paradigm, it happens that the phylogenetic data obtained from crown molars, although these morphologies are inherited, have a complementary scientific value with regard to the biochemical data.

The Hc-4 molar (Betic Cordillera, Spain) is analyzed in order to obtain new data using two techniques. Its crown wear section is a biomineralized embryonic morphology (retrogerminative technique), and its enamel line draws hexagonal marks (superimposition technique). These data are the foundations of the mitosis area loop development hypothesis during morphogenesis. The tooth structure is a germination process of the embryonic dermal masses (mitosis areas), and in relationship to (1) the moment they were born during loop process, (2) size, and (3) location when they constitute a specific cusps crown when they are petrified by an enamel mantle.

In conclusion, Linnaean characteristics (morphology) are associated with two parameters: frequency percentage with which the cusps are inherited and their functional role. This parameters group is called "Biological Nature".

The Reference Series in each molar is the biological nature values group positioned in linear order. The Reference Series of each linnaean holotype imply phylogenetic relationships using similarity percentages and the Linnaean uncertainties disappear from the phylogeny.

If I express phenotype with the reference series and also the genotype (DNA) is displayed with a numerical sequence, then it happens that we have two numerical sequences and between them exist cause and effect relationship.

II- Poster Presentations (next page)

The decoded information from the Hc-4 molar in *Equus stenonis* requires renewing the Linnaeus paradigm

The past, present and future of mammalian diversity
86th Annual Conference
German Society of Mammalogy
September 2012, Frankfurt (a.M.)

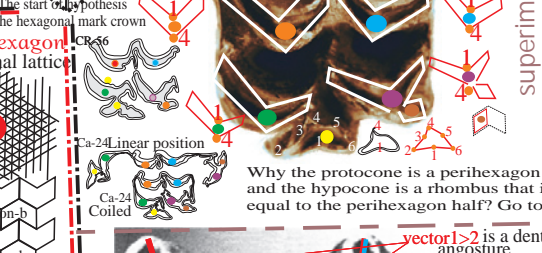
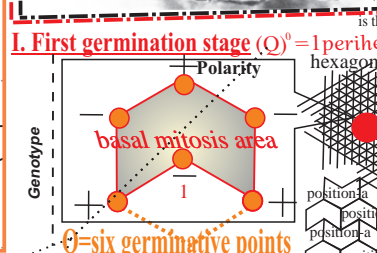
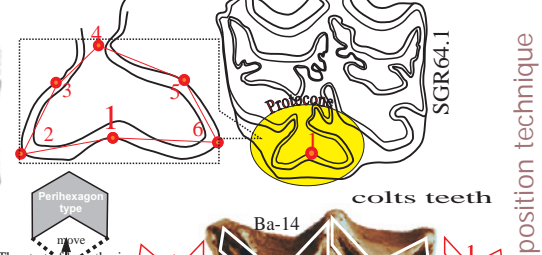
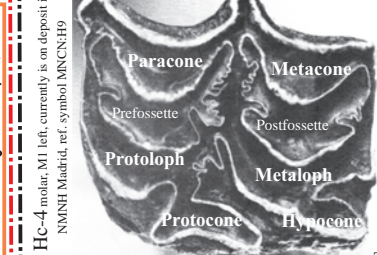
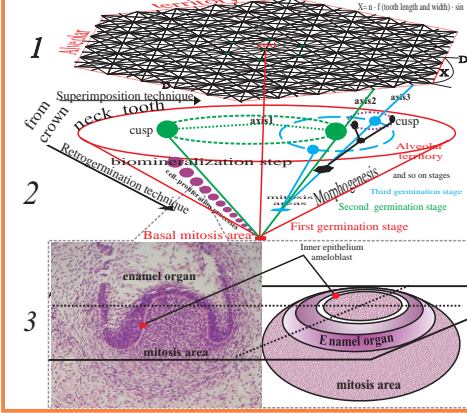
Antonio Ruiz Bustos Instituto Andaluz de Ciencias de la Tierra CSIC-UGR (Granada, Spain)

THE PROBLEM. Owing to the uncertainties and anomalies that are historically constants in the Linnaean paradigm, it happens that the phylogenetic data obtained from the crown molars, although these morphologies are inherited, have a complementary scientific value with regard to the biochemical data.

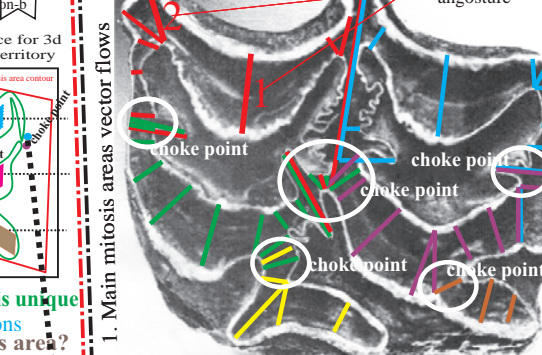
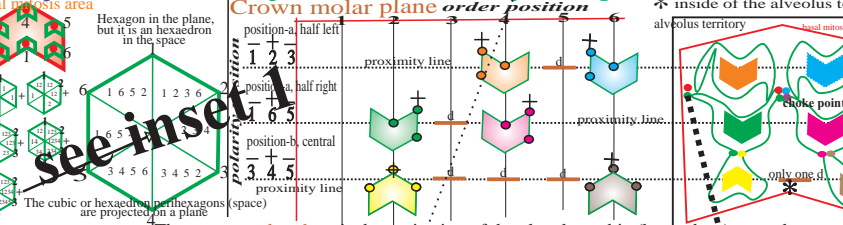
2-Hypothesis

1-Data

Hypothesis standard model
The data from the hexagonal lattice marks in molar cusp enamel line + embryo morphogenesis, they are the foundations of the mitosis area loop development hypothesis.



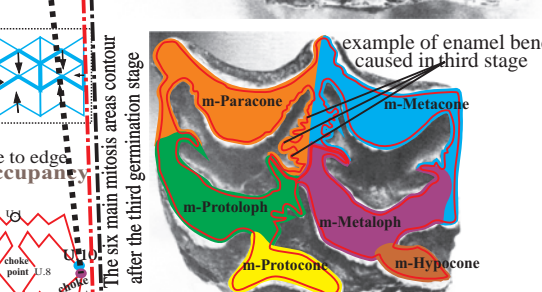
II. Second germination stage (Q^2) = 6 perihexagons
The question 1. What is the position of the six main perihexagon?



Answer 1. The perihexagons position of the second germination stage in the hexagonal lattice is unique

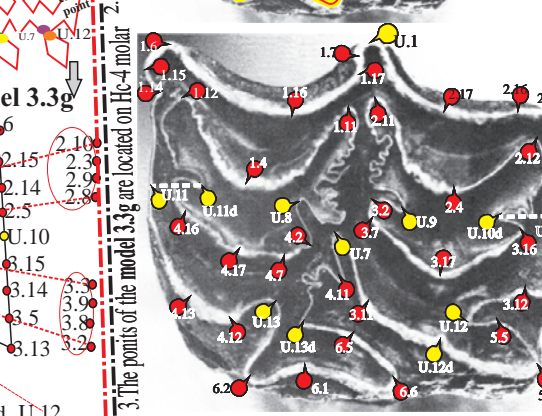
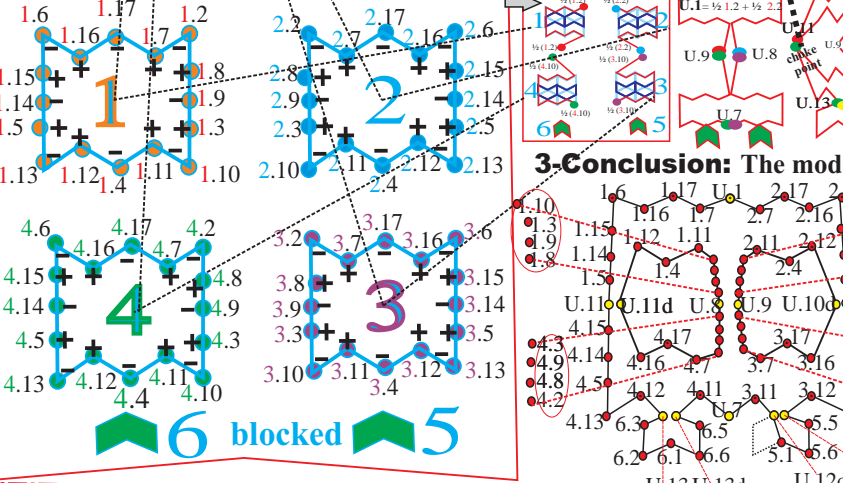
III. Third germination stage. (Q^3 - (2Q^1) + 2Q^2 = 36 - (2*6) + 2 = 26 Perihexagons

The question 2. How I know the position perihexagons into each one principal mitosis area?



Answer 2. The adjunct perohexagons have only one way of achieving the maximum occupancy

Adjustment of the perihexagons inside of alveolar territory during Third stage



4-Results in taxonomy: The Reference Series

- The biological nature of the Hc-4 molar characteristics is quantified with the associations of three parameters type: (1) Shape as linnean concept, (2) Genetic role by Hypothesis, and (3) funcional role by Plastic Evolution (Ruiz Bustos, 1994).
- The Reference Series (RS) of a molar represents the values of the biological nature of a set of crown characters that have a constant position and that are arranged in a linear order. This order is unique and unalterable forever, after having been published for the first time. S.RE1 (Ruiz Bustos, 2006) is a sequence integrate by 34 enamel line segments with biological nature, mathematically specified by factors and constant order.
- Factors of the S.RE1: l= occlusal length (mm); w= occlusal width (mm); PL=enamel length between two biological nature points; Theoretic comparison model (LMT) = $2\delta\sqrt{l^2+w^2}$; Parameter of the theoretic comparison model VPT = $(PL * 100)/LMT$; GNV= whole number evaluated group; Example: l° parameter = $PL * (VPT + GNV) =$ enamel length from 1.6 point to 1.17 point $7.95 * (3.67 + 1) = 45.50$
- S.RE1 of the molar Hc-4 (Ruiz Bustos 2006): 1°, 45.50; 2°, 56.02; 3°, 61.82; 4°, 40.01; 5°, 41.97; 6°, 19.16; 7°, 55.11; 8°, 71.31; 9°, 88.46; 10°, 113.32; 11°, 197.91; 12°, 41.04; 13°, 19.24; 14°, 17.13; 15°, 152.54; 16°, 28.05; 17°, 39.19; 18°, 88.62; 19°, 15.90; 20°, 121.94; 21°, 13.01; 22°, 34.64; 23°, 37.44; 24°, 63.05; 25°, 227.55; 26°, 73.36; 27°, 79.82; 28°, 88.18; 29°, 87.35; 30°, 66.21; 31°, 65.38; 32°, 67.60; 33°, 54.66; 34°, 67.81.

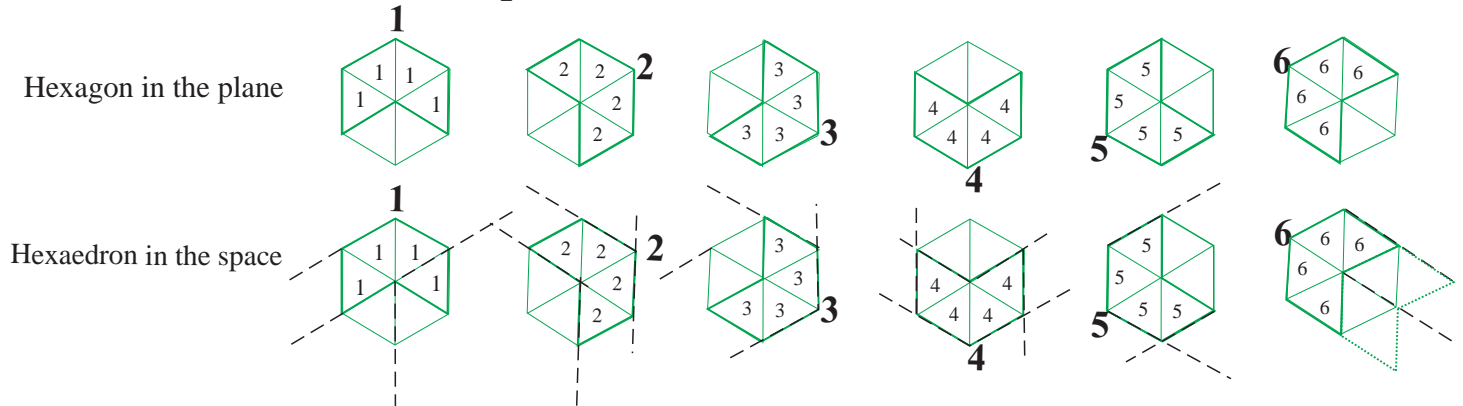
The added elucidation 1 on second germination stage

II. Second germination stage $(Q)^1 = 6$ perihexagons

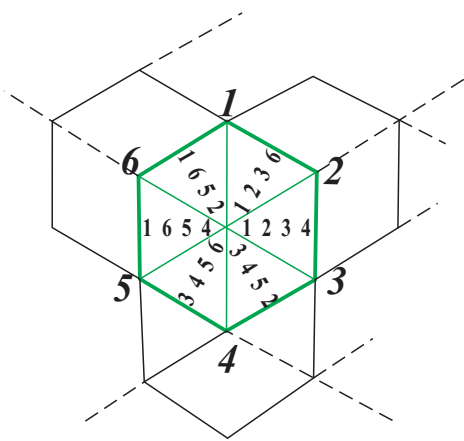


The question 1. What is the position of the six main perihexagon?

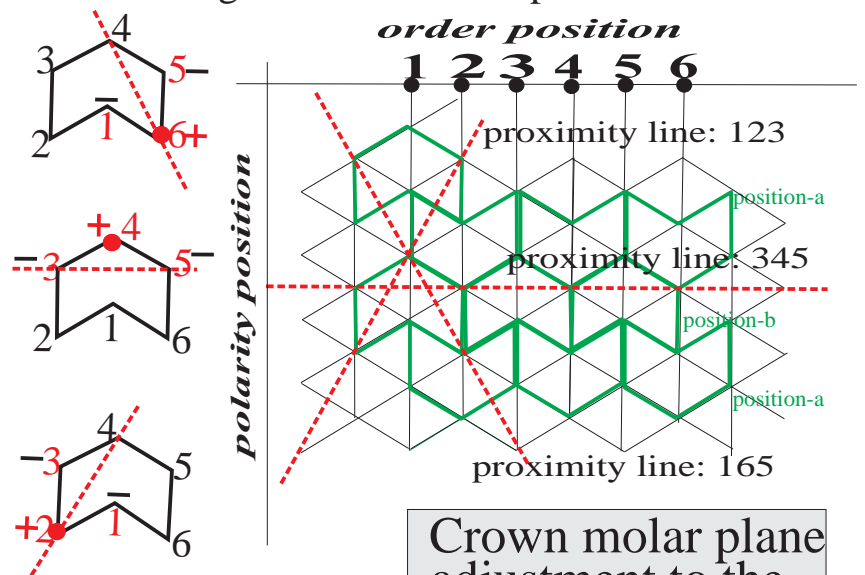
The molar crown is a plane, but the alveolus is a cubic (hexaedron)



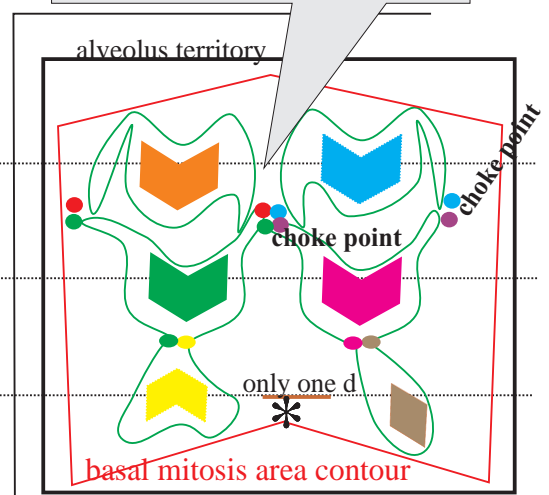
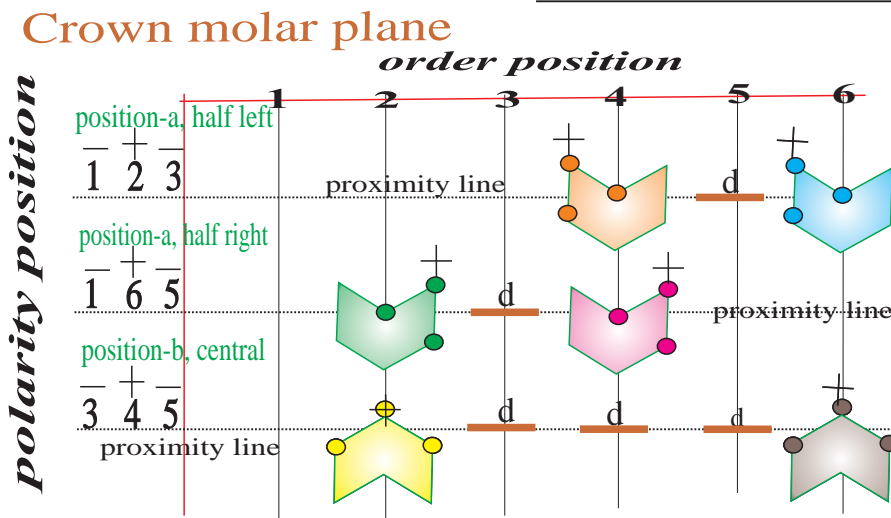
In the space



The perihexagons in the space are projected on a hexagonal lattice in the plane

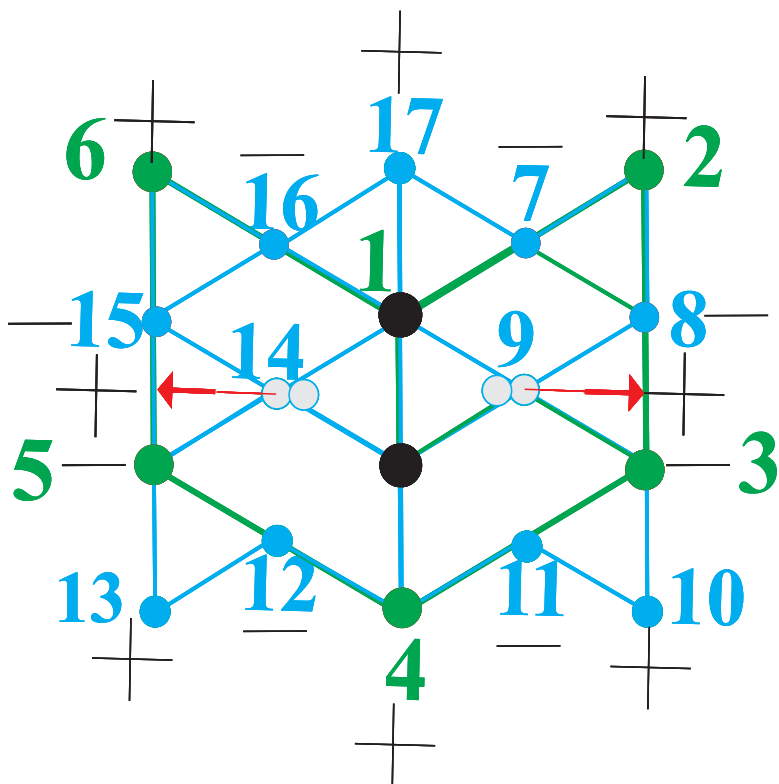
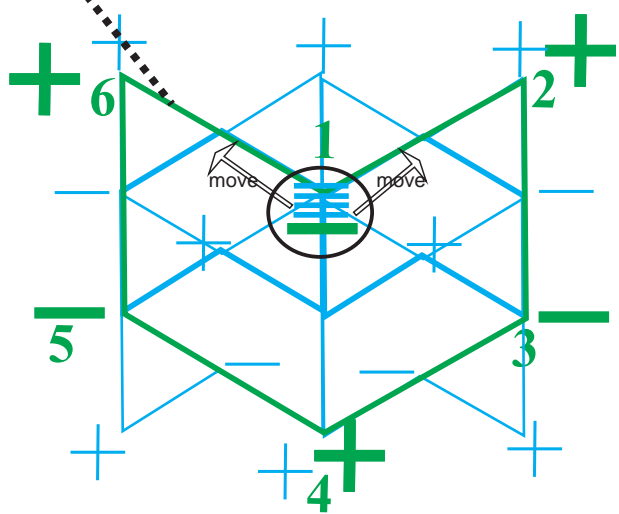
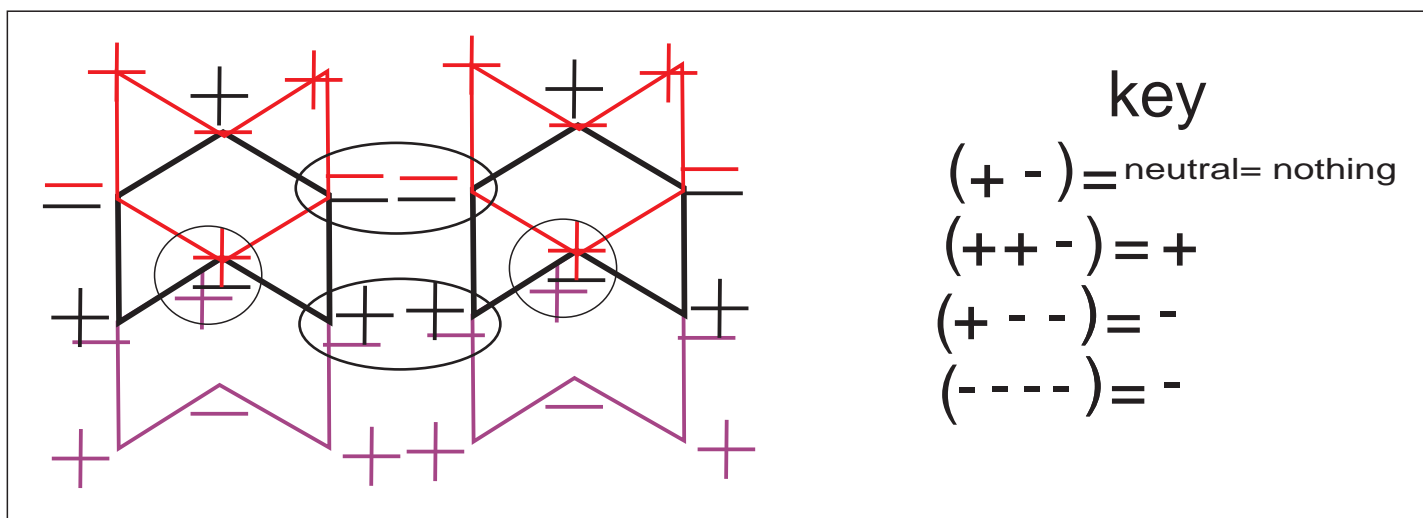
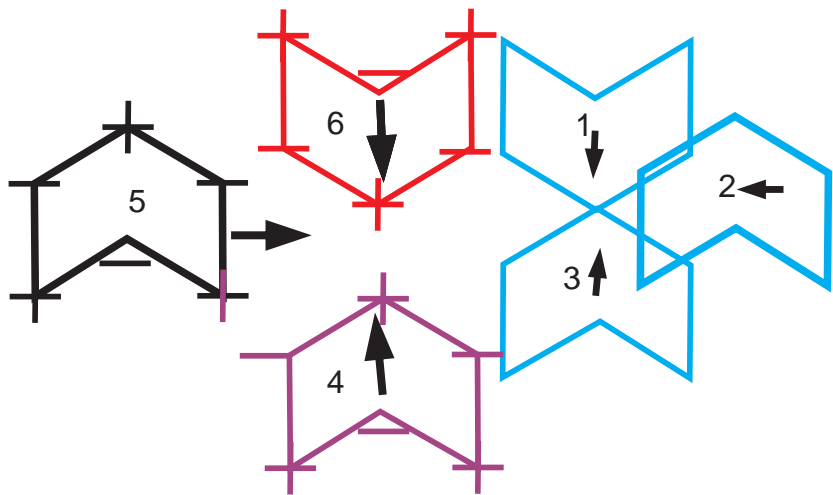
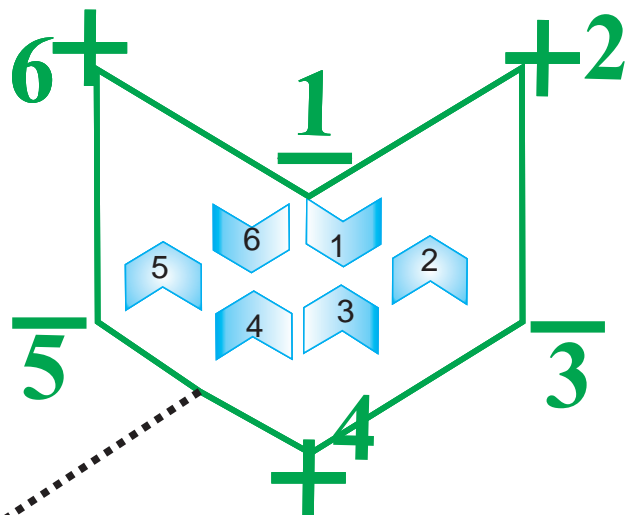


Crown molar plane adjustment to the alveolar territory



The crown molar plane is the results of the projection of the alveolus cubic (hexaedron) on a plane

The added elucidation 2 on orientations (Polarity) in the third germination stage



III - Comment to the poster

1. Data and techniques

Mammals have teeth to capture food and grind it (mechanical digestion). The environment imposes the characteristics of the food, where the energy is bottled. This makes teeth the inevitable material points for the circulation of energy within the ecosystem, i.e. bottlenecks.

Teeth bear a contradiction. They need to be strong (mineralized) during the lifespan of the individual, but because mammals face unpredictable changes in food as a consequence of the ecosystem, teeth must be morphologically malleable in order to adapt to the scale of environmental changes. The extinction of a mammal is inevitable when its teeth fail to resolve this contradiction.

Mammals use two common basic processes in any biomass to build the framework of their teeth during morphogenesis: (1) cell proliferation to form the cusp mass, and (2) biomineralization to produce dentin and the enamel mantel that petrifies the cusps.

Two techniques can be employed to analyse the morphology of teeth crowns: retrogermination and superimposition. The daily use of the molar causes sections of wear. These reveal the tooth structure from the highest points of the cusps to the neck of the tooth, reversing the order of what occurred during embryonic genesis. The retrogermination technique transforms successive sections of wear into contour lines of the embryonic geometry that results from the adaptation of its cell mass to the alveolar space. This technique reconstructs embryos from fossil and present-day molars without physically using embryos.

By reasoning that the occlusion is crucial to explain tooth morphology, and in order to use these data to complement the results found with the retrogermination technique, I define the superposition technique. This consists of superimposing a hexagonal lattice (specifically an equilateral triangular network) over images of molar-wear sections in order to find geometric correspondence between the enamel line and hexagonal symmetry.

This technique raises two questions: (1) Why is there geometry in molars? (2) Why is it hexagonal geometry? The answer to the first question is based on the fact that the occlusion of teeth is decisive in natural selection, since poor occlusion at weaning signifies a poor bite and thus a low possibility that the individual will produce offspring. For accurate functional occlusion with the least possible energy expenditure, mammal teeth require geometric construction. With regard to the second question, my experience analysing not only mouse teeth from successive laboratory litters but also mammal teeth from fossil populations, verifies that any specimen, in any cusp, always show some marks of hexagonal symmetry in their enamel line (Ruiz Bustos, 2011a). Another source of data are the dermoskeletal structures of vertebrates. These reflect hexagonal geometry codified in a genetic algorithm because they are inherited from parent to offspring. For example, the hypothesis concerning the evolution of teeth from dermal scales is based on the marks of hexagonal symmetry expressed during phylogeny (Ruiz Bustos, 2005).

The advantages of hexagonal symmetry are that: (a) no voids appear in the network and consequently the space is occupied with the minimum possible quantity of construction material; and (b) only reference points of the circumference and diameter are needed, these elements being geometrically easy for animal faculties to materialize with exactitude. These advantages obligate construction with hexagonal patterns in the animal kingdom, from mammal teeth to honeycomb. This odontohehexasyymetry provides the keys to the hexagonal marks on the mammal molar crown.

The material studied was the fossil horse molar Hc-4 (Fig. poster) from the Huelago site, in south-western Europe (Betic Cordillera, Spain), dating to 2.5 Ma. The site has been codified by biozonemark rules (Ruiz Bustos, 2011b) as: 2.5-1Hu. Currently this material is on deposit (ref. symbol MNCN:H9) in the National Museum of Natural History in Madrid.

2. The perihexagon

The first time that I applied the superimposition technique to the molar Hc-4, I found no evident marks of hexagons or hexagonal symmetry. Surprised, I searched for an explanation in museum collections, analysing horse molars one by one, but with monotonous and sterile repetition. However, I found a meaningful clue to the existence of hexagonal symmetry in the crown of colt molars. These show the fusion of six dentin surfaces, which occurs progressively with wear (Fig. poster), and this number coincides with the vertices of the hexagon, constituting the basis for hexagonal symmetry.

From this discovery, I pose the problem with different perspectives that I summarize in the question: What structural transformation did the contour of the enamel line undergo in horse teeth so that the hexagons are not obvious with the superimposition technique? I repeatedly review collections and plates looking for the possible transformations that could have occurred in the marks of hexagonal symmetry and that should be manifested in the enamel line.

With the superimposition technique, I recognized for the first time in the protocone of the left P3 tooth of the species *Equus caballus cf. gallicus*, discovered at the site of Saint-Germain-la-Rivière and figured by Dr. F. Prat in Plate 64.1 of his doctoral thesis (Prat, 1968), that the enamel line follows a modified hexagon. At that moment, the molar became a key testament, which I identify as SGR64.1.

The alteration of the hexagonal geometry consists of a hexagonal vertex shifting its two sides towards the centre of the hexagon. The new polygon preserves the perimeter of the hexagon, but reduces its surface area. In the literature, I have found no specific name for this type of polygon, which I call a perihexagon (Fig. poster). The observation of the first perihexagon makes it easy to identify the other hexagonal marks on the of the Hc-4 molar crown.

3. Molar Hc-4 morphological data

The crown of molar Hc-4 shows a wear section that is a constant in adult horse morphology (Fig. poster), consisting of the following data.

The first datum is an enamel line around the crown edge. This line constitutes a circuit that begins at one point and follows the entire edge of the crown to end at the same point. I identify this enamel line of the crown edge as an external closed curve and, simplifying its geometry, refer to it as circumference-1.

The second datum is two pits in the centre of the crown. The proximal pit is called a prefossette and the distal pit is referred to as a postfossette (Fig. poster). Each has its perimeter marked with a closed enamel line and, if I simplify its course, two circumferences result, which I call circumference 2 and 3. The topographical positions of the outer circuit of the enamel line appear to be outside the dentin mass (circumference-1), and the fossettes (circumferences 2 and 3) appear to lie inside the dentin mass. These three contours are in reality three stretches of a single contour of enamel line, because in the beginning of the embryological development, the histology shows the dental germ as a unique space surrounded by a membrane, inside of this one there are areas that it grow by cell proliferation until to form the cusps mass and other stable areas without growth, as for example, the background of the two pits. The fossettes guarantee that the dentin mass in its coiling has the plasticity necessary to occupy any square space in the maxilla. Maxillary space and the embryonic molar size are presumably condition each other during the embryonic development of the horse.

The histological analysis of the two pits of the crown specifies the sequence: dentin, enamel, and cement. This means that the pit bottom only has been able to build during morphogenesis, if there are specific points with cell proliferation around of the pit bottom that it is a point without cell proliferation. This confirms that the two pits are not simply open cracks in the dentin mass that they are external to the dentin mass.

The six dentin areas (cusps) observed in colts molar are the highest points of the growth areas and the points without growth are the background of the pits, and therefore parties lower.

The third morphological datum is the topographical crown map of the wear sections. This is the synthesis of the morphologies observed in molar crown Hc-4 and the wear sections of colts. The map shows the tooth neck surrounds a single plane, where the six cusps are represented by contour lines. These height rings around the six cusps determine the morphology of the enamel line of the tooth neck. The tritubercular theory (Cope, 1883 and Osborn, 1907) identifies the six dentin surfaces as the cusps called: protocone, protoloph, paracone, metacone, metaloph, and hypocone. The prefossette around are located the protocone, protoloph, and paracone, and the postfossette around: the metacone, metaloph, and hypocone. These are called the main or principal cusps.

The superimposition technique indicate that the protoloph, paracone, metacone, and metaloph have enamel line bend with marks that deformed their perihexagon, but the protocone and hypocone were blocked and its morphology is persistent, perhaps for a lack of space, and therefore the protocone enamel line is a perihexagon shape. This I identified in molar SGR64.1, and the hypocone forms a rhombus, which is half of a perihexagon (Fig. poster).

The fourth datum is the dentin mass. The wear sections in the molar crowns of colts reflects the progressive fusion of six dentin surfaces until forming the single, common dentin space. This is observed in wear section of molar Hc-4 where a single dentin mass is surrounded by a unique enamel contour. This is the result of the sum of three parts of the enamel line: the edge of the crown circumference-1 and two edges of the fossettes circumferences 2 and 3 (Fig. poster).

The fifth datum is the flow mark. The mitosis areas growing by a cell-proliferation process had to jostle to accommodate the alveolar space. Therefore, the geometry of the enamel line of the molar crown Hc-4 should bear testimonial marks from which I infer the data on the expansive flows of the mitosis areas during morphogenesis. How can the expansion flows of the mitosis areas during morphogenesis be identified? The method consists of drawing vectors between constriction points of the angostures belonging to each fossette (inner circumference 2 and 3) to the equivalent point on the contour (outer circumference 1). This defines the vectors (Fig. poster). The expansion flows are reconstructed joining the middle points of the vectors. In this way, I locate the six centres where the expansion flows of the main mitosis areas start (Fig. poster).

The choke points of the Hc-4 molar crown, where the mitosis areas collide, they show an overlap of the flow vectors (Fig. poster). In the choke points of the fossettes the enamel line bend (pli) observed (Fig. poster) they are mathematically defined and obtained experimentally by the crash of two and four viscous and immiscible masses, which they move slowly by almost horizontal planes to the choke point.

The sixth datum show marks in the fossettes that indicate a cusps number exceeding of the six main cusps, for example, the intensive folding of the fossettes (Fig. poster). These indicate the existence of new mitosis areas within the main cusps, which I call adjunct mitosis areas. These hexagonal marks on the adjunct cusps, they signal a third germination stage, which repeats the mechanisms of the germination that took place within the basal mitosis area to give rise to the main mitosis areas. In the tritubercular theory, the adjunct cusps have no specific name.

Finally the arranging of the six data involves that the morphology of molar Hc-4 displays the petrified marks of a loop process. This begins with the basal mitosis area that the histology shows the dental germ as a unique space surrounded by a membrane. Inside of the basal mitosis area continue the second loop, it is originated from six cells within the basal mitosis area, which constitute the six main mitosis areas. Only in four main mitosis areas the third loop start. This new loop implies against six mitosis areas inside of each one of the four main mitosis areas, because the protocone and hypocone were blocked and its morphology is persistent. The result produces 24 adjunct mitosis areas. All the mitosis areas from the basal to the adjunct cusps, they adapt progressively to the alveolar space, while there is free space available in the alveolus. *Universal rule for any tooth: if each cusp crown was embryonic space enough, it will try to reproduce in the adult crown the basal mitosis area hexagonal contour.* During biomineralization, the mitosis areas contour leave marks on the enamel mantle covering them.

The mitosis areas during morphogenesis never leave any available space unoccupied, and once occupied, the space is never abandoned. When the free space is filled, the cell-proliferation finish and the dental embryo is biomineralized.

4. The mitosis areas loop development hypothesis during morphogenesis

I) Basis of the hypothesis: data (1 to 8).

(1) In successive litters of mammals the same enamel-line morphology is passed from parent to offspring.

(2) The enamel line in the molars (1, 2, and 3) belonging to the same individual repeat the same morphology but each molar adapts its specific morphology to the corresponding alveolar space available in the maxillae. For example, the width limitation in jaw alveolus causes the different morphology observed among the molars of the maxilla and the lower jaw.

(3) The tooth architecture, from an inside view, displays a large cavity in its neck, which in turn connects with successively smaller and smaller cavities. The outside view of the tooth, reconstructed with the wear sections, confirms that the cavities are the internal gaps of the cusps. The cusps show the inner cavity surrounded by dentin which is in turn coated by an enamel layer. The enamel line in the wear sections of the molar crown, it follows circumferences, ellipses, and marks of hexagonal symmetry.

(4) The histology of the tooth indicates that the enamel is deposited exclusively over the exterior or the façade of a layer prior to the dentin. Never in phylogeny is enamel present without a prior underlying dentin layer.

(5) In crown sections, isolated cusps reveal surfaces of dentin ringed by the enamel line. From the geometric centre of the dentin the radii always reach all the points of the enamel line geometry of the cusp.

(6) The crown sections with cusps forming a group reveal a single space of dentin in their interior. This is outlined by a single enamel line, but each of the folds conforms to a specific geometry, which corresponds to the geometry of each individual cusp in the group. I verified this using Euclidean geometry to analyse the arches and hexagonal marks of the enamel line.

(7) The morphology of the enamel line viewed in crown wear sections is transformed into a mathematical model using the equations that describe the dynamics of immiscible viscous fluids, which occupy a horizontal surface with slow movement.

(8) The morphological data observed in the Hc-4 molar.

II) Hypothesis statement: premises (i to xiii) and their cause-and-effect relations.

These are inferred from the eight data that support the hypothesis.

(i) A genetic algorithm that is passed from parents to offspring. In each individual, this is identical for all their teeth, and the differences noted in their phenotypic expression (incisors, canines, and molars) are caused by the specific conditions in the maxillary space where the teeth develop during morphogenesis.

(ii) Cusp histology and morphology imply the existence of embryonic dermal masses that grow by cell proliferation during morphogenesis. In living embryos, I have identified dermal masses invariably associated with enamel organs, which I have stained with basic dyes because of the large number of cells in mitosis. These cell concentrations I call mitosis areas.

(iii) The tooth structure is explained by a process of loop development of the mitosis areas, which I infer in laboratory mouse embryos during morphogenesis, noting successive stains stained with basic dyes. The process is an initial stage consisting of the formation of a stain that I call the basal mitosis area. Then in few hours, I examine new stains within the basal mitosis area stains, clearly associated with the enamel organs (Vahtokari, et al, 1996), which I call principle or main mitosis areas. Occasionally appear again stains, which I call adjunct mitosis areas. My hypothesis is that, after biomineralization in the adult tooth the morphogenesis is petrified and the result are:

the tooth neck marks the space of the enamel crown (basal mitosis area), within this crown are the main cusps identified and named by the tritubercular theory, these are from stains (main mitosis areas), and around these appear small cusps that they are from of the last stains (adjunct mitosis areas).

Biotechnological studies showing gene families such as: BMP (Bone Morphogenetic Protein), FGF (Fibroblast Growth Factor), SHH (Sonic Hedgehog) and WNT (Wingless-Integrated) that in a loop process, repeatedly follows the same biochemical pathways throughout embryonic development, from the primordial layer stage to the final stage of embryonic morphogenesis of the tooth.

During the embryonic bud and cup stages, the recombinations of the mesenchyma and dental organ of the enamel indicate that the secretory potential of biochemical substances for inducing the morphogenesis of the tooth reside in mitosis areas of the dental dermal mesenchyma (Kollar, 1970; Osman and Ruch, 1976).

(iv) The degree of development attained by the embryonic framework at each point (space/time) during morphogenesis is determined by the free space available to the expanding mitosis areas. This implies that a factor determining the morphology of a given mitosis area is the point in time at which it is born during morphogenesis.

(v) The hexagonal marks in the enamel line imply the existence of a hexagonal lattice, located within the basal mitosis area, which determines the germination points and guides the loop development.

(vi) A break in the outline of the mitosis areas would cause disorderly cell expansion within the embryonic space, but this catastrophe never occurs. Therefore, the contour of the mitosis areas must be physically very elastic to surmount obstacles and withstand the physical pressure of cell proliferation without breaking.

(vii) What happens during morphogenesis that forms the façade or neck tooth where the outer section of each main mitosis area contour left its mark, and at the same time inside of main mitosis area each adjunct mitosis area left its mark? My hypothesis to explain this morphology is: (1) the dermal mass grows by cell proliferation, (2) the deformations marked on the contour of the basal mitosis area are testimony that within the contour grew other mitosis areas, identical to the basal mitosis area, which I call: main or principal mitosis areas and which are the origin of the main cusps in the crown, (3) the same happen with the main mitosis area and adjunct mitosis area. This implies that the basal mitosis area, main mitosis areas and adjunct grew by cell proliferation until filling the entire alveolar space available. The competition to occupy the alveolar space was so intense that the mitosis areas, in their effort to occupy maximum space, deformed the outline of the mitosis area where it grows. There is a unique way to place main mitosis area inside of the basal mitosis area, and adjunct inside of the main mitosis area, because they occupying the maximum space (Fig. poster).

(viii) In theory, the dentin mass of a mitosis area should be preserve the contour line of the other mitosis area inside of it as a division line, but this does not occur. In the dentin mass of the crown mitosis area contour disappears (presumably by reabsorption), forming a single dentin surface. The dentin space is unique and the marks of the cusps are preserved only in the enamel line of the molar. The simplest hypothesis is the contour is a membrane formed by proteins. This would explain the properties (characteristics) of the mitosis areas contour expressed in premises -vi- and -vii-. Other datum is gives for the starting organization of the immature enamel covering the dentin implies a protein between the two layers that would serve as a template.

The protein between the enamel and the dentin or between two dentine layers would be destroyed during the biomineralization process. The membrane-protein hypothesis is necessary to explain. (1) How the mitosis area movements occur (cell proliferation and accommodation to the alveolar spaces)? (2) How these movements can be transmitted to the prisms of the immature enamel organization. (3) How these movements determine the enamel framework? This explains

the diversity and evolution of Hunter-Schreger band configuration in tooth enamel of perissodactyl mammals (Koenigswald, et al, 2011).

(ix) The features of the contour of the mitosis areas imply that, for a mitosis area to occupy the alveolar area, the greatest obstacle and the greatest aid is another mitosis area. As a result of this interaction between mitosis areas, the folds in the enamel line in the molar crown are never random. Rather, they are governed by a particular factor (cells, polarity, or lack of space) that acts during morphogenesis, leaving an indelible mark in the molar crown.

(x) The hypothesis of loop development of the mitosis areas is equivalent to the integral self-control systems of computers. Therefore, the teeth of a mammal specimen constitute an integral intelligent system of dental self-control. The integral system is composed of a memory (in this case: biomemory), which is stored in the genes and which transmits a dental-algorithm pattern to the offspring. The dental algorithm codifies a programme of loop development of the mitosis areas (dermal masses), where each grows independently by cell proliferation. Other programmes codified in the dental algorithm are: (1) a hexagonal lattice, which guarantees molar occlusion, and (2) biomineralization, which at the proper moment for functionality petrifies the embryo tooth and transforms it into an adult tooth with dentin coated by enamel.

(xi) Environmental alterations in the ecosystem prompt changes in food characteristics, which are unpredictable for mammals. During phylogeny, these problems are resolved by mammals with a heritable dental-algorithm pattern (integral system) which is explained by the hypothesis of mitosis-area loop development during morphogenesis. This demonstrates Haeckel's Law (Haeckel, 1866) without using embryos, but rather only fossil teeth.

(xii) Mutations are vital to modify crown morphology. These are the most random point of the dental algorithm, since if they do not appear at the right moment, and then extinction is inevitable.

(xiii) Finally, the mitosis area loop development hypotheses is a method to mammal taxonomy and reconstruct the teeth morphogenesis of fossil and living mammals without using embryos.

5. Biological Nature

Taxonomic classification from Carl Nilsson Linæus, 1758 to the present is governed by the concepts of: (1) hierarchical ordering of characters according to criteria inferred by each specialist after analysing the greatest possible number of specimens; (2) the choice of a holotype that best represents the morphology, according to the criteria of the specialist who first defines the species; and (3) binomial nomenclature to (also called binary nomenclature) identify the animal. These concepts are meant to systematize the greatest possible number of clearly and frequently encountered traits in populations.

Nevertheless, the historical analysis of the taxonomical results with the Linnaean method meets with constant uncertainties. These arise even in phylogenies documented with the best collections of fossil and living specimens bearing the clearest and most frequent traits. This incongruity can be summarized by asking: If the parent-offspring lines are unique in time and form a unique family tree, how is it possible for mammal phylogenies (and those of any other organism), based on Linnaean principles, to be riddled by constant uncertainty, confusion, and contradiction? Taxonomic anomalies indicate that the Linnaean method, though necessary to unveil mammal taxonomy and phylogeny, is inadequate alone. Under these circumstances, I ask: What other data of phenotype, in addition to Linnaean principles, should be analysed and incorporated into taxonomy to solve the problem of uncertainty in phylogenies?

The mitosis area loop development hypothesis during morphogenesis is the solution that I propose to resolve Linnaean taxonomical anomalies. This defines the biological nature of each phenotypic character of the molar crown, associating three types of data: morphology of Linnaean characters, their heritability, and their function.

The biological nature of the characteristics of the molar crown Hc-4 is quantified with three parameters. (1) Shape. (2) Genetic role, defined as the heritability of the morphology of a cusp, and this in turn depends on its location within the group of cusps that constitutes the molar crown

and on the point in time that the morphology originates during morphogenesis. (3) Functional role to obtain food, which I define with the following criterion: the larger the cusp, the greater its participation in the mechanical preparation of the food.

The mitosis-area loop-development hypothesis during morphogenesis and the quantification of the biological nature of its characters implies a renewal of the Linnaean method and the beginning of a new paradigm. This is called: integral organic-morpho-functional self-control system, which I identify with the acronym SAIO (from its original name in Spanish, Sistema integral de Autocontrol Inteligente Orgánico-morfo-funcional; in preparation).

6. Reference Series

The Reference Series (RS) of a molar represents the values of the biological nature of a set of crown characters that have a constant position in the crown and that are arranged in a linear order. This order is unique and unalterable forever, after having been published for the first time.

The Enamel and Morphological Units method quantify the biological nature of the crown characters. The Morphological Unit quantifies: genesis sequences, cusp number in all or part of the crown, position and genesis cusps relationship (groups, isolated, etc.). The Enamel Unit is a segment of the enamel line able to identify at least one cusp.

The reference series (RS) of different populations of the same lineage, and therefore with the same parameters, can be compared by any mathematical calculation that expresses its similarity, such as, for example, the linear-regression coefficient. In this context, the choice of a reference series as point zero of reference (similar to point zero in a coordinate system) for the molar morphology of a mammal lineage implies percentages of similarity among all the reference series of all the populations known to belong to that lineage.

Each molar designated as a holotype in Linnaean taxonomy, has a reference series. This represents the species morphology, with the same advantages and restrictions as with the holotype. The phylogenetic tree bearing the holotypes, chosen with Linnaean criteria, is constructed with the information provided by the reference series of each molar, its chronology and location in an ecosystem. These data create phylogenetic maps that materialize the new paradigm (SAIO), which is based on the mitosis area loop development hypothesis during morphogenesis and the quantification of the biological nature of the characters.

The limitations of the holotype to represent the morphology of a species are avoided in the SAIO with the standard reference series. This integrates the holotype reference series into the reference-series data for 25 specimens of the type population. The need for a reference-series file requires the creation of a reference-series bank (SRBank), where these data are sent to be recognized, processed, and stored. This reference-series bank can be modelled on gene-sequence banks (GeneBank, EMBL, DDBJ).

The reference series, being immutable in the order and number of its parameters, demands a specific term to be identified always under any circumstance. For this, the reference series would have common abbreviations (RS). The mammal lineage is indicated with an upper-case letter of its taxonomic name, for example in equids, it would be RSE (Reference Series Equidae). The content in each lineage is specified by adding successive notations. For the upper molars, a dot is added (.) to form the abbreviation (R.S). For the lower molars, a comma is added (,), to form (R,S), and finally the number representing the order of the publication it is add. This number will be the next to the last number that I was ben published. For example in the case of the molar Hc-4, the denomination of its reference series is R.SE1-MNCN:H9/2006 (Ruiz Bustos, 2004).

One result of the organic-morpho-functional self-control integral system (SAIO) which is materialized by living organisms is the objective value of the reference series in the biogeological sciences. This is expressed with the concept of Biological Plasticity, which is based on the association of three factors: (1) the Reference Series of the phenotype, which expresses the biological nature of the molar-crown characteristics (phenotype), (2) the genetic code, and (3) each environment where the phenotype lived during its ontogeny.

The genetic code is shown by the Genic Series of Reference (GRS), which is the result of the translation of the DNA sequence into a numerical sequence, quantifying, for example, the positions of the nucleotides and their types of bases to provide a succession of numbers. The environmental conditions where the specimens live can be expressed in numerical values using the biocenogram (Ruiz Bustos, 2011b).

Biological Plasticity of mammals at the scale of individuals and populations can be calculated over long periods of time and across the different habitats used.

7. Conclusion

At the moment, characters and parameters of the molar crown (phenotype) constitute the paradigm of the Integral system of the self-control of organic-morpho-functional (SAIO). This implies that the geometry of the enamel line of molar Hc-4, preserved for 2.5 Ma in a fallow field of Granada displays specific data that have an objective meaning in the sciences that study: (1) adult morphology, (2) ecological function, (3) genetic code, and (4) embryo morphogenesis, which until now were secrets hidden in the enamel line of molar Hc-4.

To establish mammal phylogeny without the taxonomic anomalies and to identify the parameters capable of characterizing fossil and living ecosystems, and to quantify their state of vitality, I propose: (1) to construct in the coming years a Systematic Mammal-Tooth Table listing the basal mitosis areas in logical order, (2) to establish a Reference-Series Bank, and (3) to relate the molar-crown morphologies to the parameters of ecological preference in the biocenogram.

References

Cope, E. D. (1883). On the trituberculate type of molar teeth in the Mammalia. P. Am. Philos. Soc., 21: 324–326.

Haeckel, E. 1866. *Generelle Morphologie der Organismen: Allgemeine Grundzüge der organischen Formen-Wissenschaft, mechanisch begründet durch die von Charles Darwin reformirte Descendenz-Theorie*. 2 vols. Georg Reimer, Berlin.

Koenigswald, W., Holbrook, L. T. and Kenneth D.R. (2011). Diversity and evolution of Hunter-Schreger Band configuration in tooth enamel of perissodactyl mammals. Acta Palaeontol. Pol. 56(1):11-32.

Linnaeus, C. 1758. *Systema naturae per regna tria naturae: secundum classes, ordines, genera, species, cum characteribus, differentiis, synonymis, locis*. Stockholm: Laurentius Salvius. 10th edition ed. (in Latin)

Osborn, H.F. 1907. Evolution of mammalian molar teeth. New York: Macmillan, 250 pp.

Prat, F., 1968. Recherches sur les Equides pleistocenes en France. *Thèse Doct. Fac. Scienc. Univ. de Bordeaux*, n 226, 4t. 696 p.

Ruiz Bustos, A. 1994. La Evolución Plástica, Editorial Andalucía, Granada, pp 127.

Ruiz Bustos, A. 1995. Analysis of enamel-line length as a morphometric parameter and its application to Quaternary arvicolid. Lethaia, 28: 361-369.

Ruiz Bustos, A. (2002). Enamel line molar analysis in arvicolid rodents: its potential use in biostratigraphy and palaeoecology. Micromamíferos y Bioestratigrafía, 1: 1-24.

Ruiz Bustos, A. (2004a). Características paleoecológicas y bioestratigráficas del Cuaternario aportadas por el estudio de los mamíferos fósiles en la Cordillera Bética. El Valle del Guadalquivir como ámbito de las primitivas poblaciones humanas. In Zona Arqueológica, Miscelánea en homenaje a Emiliano Aguirre 4 (II) (paleontología) (Baquedano, E & Rubio Jara S., eds.). Museo Regional. Madrid. 488-504.

Ruiz Bustos, A. (2004b). Numerical coding of the molar morphology of the family Muridae Gray, 1821, (Rodentia) for its lineage knowledge and implications in: biostratigraphy, paleoecology and composition of a correlation language from the phenotype to the genotype. *Micromamíferos y Bioestratigrafía*, 2:1-141.

Ruiz Bustos, A. (2005). The framework of mammal dental morphology in ontogeny and phylogeny. *Micromamíferos y Bioestratigrafía*, 3: 1-47.

Ruiz Bustos, A. (2006). The hidden geometry in the enamel line of horse molars. *Micromamíferos y Bioestratigrafía*, 4:1-112.

Ruiz Bustos, A. (2007). The framework of the systematic table of the mammal teeth by means of the mitosis areas. *Micromamíferos y Bioestratigrafía*, 5: 1-31.

Ruiz Bustos, A. (2011a). The hexagonal lattice marks in the muroids rodent explain molar-cusp enamel line. *Estudios Geológicos*, 67(2): 505-521.

Ruiz Bustos, A., (2011b). Escala Bioestratigráfica y Cambio Climático en la Cordillera Bética / Biostratigraphic Scale and Climatic Change at Betic Cordillera. Bubok Publishing S.L. Madrid, Spain, pp. 1-412. Bilingual.

Vahtokari, A., T. Åberg, J. Jernvall, S. Keränen, & I. Thesleff. 1996. The enamel knot as a signaling center in the developing mouse tooth. *Mechanisms of Development*, 54:39-43.