The Origin of Extra Teeth in Mammals

POCHODZENIE DODATKOWYCH ZĘBÓW U SSAKÓW

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The occurrence of extra teeth in mammals is reviewed. It is suggested that most of the extra teeth may be interpreted either (1) as the effect of additional creation and development of a tooth germ, caused by the influence of genes which are rare but still present in the gene pool of a given species and which occurred much more frequently in those of its ancestral species, or (2) as the effect of development of a supernumerary tooth germ originated as a result of complete splitting of a tooth germ, which may be inherited or due to a mutation or a disturbance or change in the genetic control of tooth development. Supporting evidence for this hypothesis is presented.

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The presence of extra teeth has been reported for nearly all orders of recent mammals, i.e. for the *Marsupialia* (e.g. Bateson, 1892; Peyer, 1968; Archer, 1975), *Insectivora* (e.g. Stein, 1963; Ruprecht, 1965a; Choate, 1968), *Chiroptera* (e.g. Eisentraut, 1956; Phillips & Jones, 1969; Phillips, 1971), *Primates* (e.g. Saarenmaa, 1951; Hooijer, 1952; Järvinen & Lehtinen, 1981), *Lagomorpha* (e.g. Darwin, 1868; Dawson, 1956; Hochstrasser, 1969), *Rodentia* (e.g. Johnson, 1952; Sheppe, 1964; Sofaer & Shaw, 1971), *Cetacea* (e.g. Ritchie & Edwards, 1913; Bourdelle & Grassé, 1955; Best, 1981). *Carnivora* (e.g. Long & Long, 1965; Kratochvíl, 1971; Wolsan, 1984), *Pinnipedia* (e.g. Bateson, 1892; Degerbøl, 1930; Caldwell, 1964), *Proboscidea* (e.g. Weber, 1904; Morrison-Scott, 1939; Frade, 1955), *Perissodactyla* (e.g. Bradley, 1903; Cook, 1929; Nieberle & Cohrs, 1970), and *Artiodactyla* (e.g. Neal & Kirkpatrick, 1957; Żurowski, 1970; Steele & Parama, 1981). In addition, mammalian remains with extra teeth have been found both in archaeological sites (e.g. Wing, 1965; Guilday & Parmalee, 1966; Taylor, 1971) and among fossils (e.g. McKenna, 1960; Fine, 1964; Fordyce, 1982). These extra teeth have occurred both in wild and reared mammals of both sexes, in all four tooth classes and two tooth generations, both in the upper and lower jaw, and both bilaterally and unilaterally, in the right or left jaw half. They are situated either within a tooth row, as peripheral or intercalary teeth, or outside it, internally or externally.

Many varying hypotheses have so far been presented to explain the origin of extra teeth in mammals. In my opinion, however, most of the extra teeth hitherto described in mammalian dentitions may be interpreted either

(1) as the effect of additional creation and development of a tooth germ, caused by the influence of genes which are rare but still present in the gene pool of a given species and which occurred much more frequently in those of its ancestral species (see Wolsan, 1983), or

(2) as the effect of development of a supernumerary tooth germ originated as a result of complete splitting of a tooth germ; the ability

for such a splitting may be inherited or due to a mutation or a disturbance or change in the genetic control of tooth development; such factors as, for instance, trauma, infection, and diet deficiencies may be regarded as sources of interference with the mechanism of this genetic control (cf. Hitchin, 1971).

(1)

The first interpretation applies to most of the extra teeth appearing in positions occupied in the ancestors of a given species by teeth lost in the course of subsequent evolution (e.g. Paradiso, 1966; Miller & Tessier, 1971; Neuenschwander & Lüps, 1975). The paleontological, ontogenetical, and morphological evidence indicates that such a loss in therian mammals has generally proceeded anteroposteriorly for the premolars and posteroanteriorly for the molars (Ziegler, 1971). It seems that both these directions have been involved in the incisor loss but the latter has undoubtedly been a dominant direction (e.g. Ziegler, 1971; Schwartz, 1974; Wolsan, 1984). In early therian mammals there was only one canine in each jaw quadrant (Ziegler, 1971; Bown & Kraus, 1979), which has been lost in many descendant groups. The progressive simplification in shape and simultaneous reduction in size of a tooth have clearly preceded its loss (e.g. Kurtén, 1953; Ziegler, 1971; Hendey, 1980). This process has been related to gradients of tooth shape and size, which are to be found in nearly all mammalian dentitions. Two theories have been proposed to explain the presence of these gradients, i.e. the Field Theory (Butler, 1939) and the Clone Theory (Osborn, 1978). In the terms of both these theories it is impossible for a tooth developed individually from its own germ not to form in accordance with such a gradient. Therefore, only those mammalian extra teeth can be under consideration in the terms of my first interpretation, which, firstly, occur as a canine in those dentitions which are typically devoid of the tooth, or as the peripheral teeth in the incisor and cheek dentitions, or exceptionally, in some mammals, in other positions (e.g. Ziegler, 1971), however only those which have clearly been affected by the phylogenetic tooth loss, secondly, are both small and simple in shape, the smallest and simplest among the teeth of their tooth classes, and thirdly (only for the extra teeth occurring in dentitions with gradients of tooth shape and size), are formed in accordance with the gradients in their tooth classes.

If all living mammalian populations were to be gathered together, it would be possible to arrange them in increasing sequence according to the frequencies of phenotypes with extra teeth complying with the above-mentioned requirements. Thus, for instance, the occurrence of the upper canine was observed, among other frequencies, in $0^0/_0$ (0 of 7, 0 of 10, 0 of 15, and 0 of 16), $2.0^0/_0$ (1 of 50), $5.9^0/_0$ (1 of 17), and $16.7^0/_0$ (3 of 18) of the specimens of *Capreolus capreolus* from seven various areas of England and Scotland (Chaplin & Atkinson, 1968), and in $17.9^0/_0$ (29 of 162) of a sample of *Odocoileus virginianus* from San Patricio County, Texas (Knowlton & Glazener, 1965), while the second lower molar was found, for example, in $6.5^0/_0$ (2 of 31) and $13.6^0/_0$ (3 of 22) of samples of *Lynx lynx* from Sweden and Finland respectively

(Kurtén, 1963). Matyushkin (1979) claims that the second lower molar occurs in *Lynx lynx* in not less than 3—5⁰/o of the specimens, and in some populations its frequency exceeds 20—30⁰/o. Furthermore, there are mammalian populations in which the teeth, developed in accordance with the requirements mentioned above, are present approximately as often as absent (e.g. second premolars in some subspecies of *Mustela frenata;* Hall, 1951). There are, finally, those in which the frequency of the phenotype with such a tooth exceeds that with the tooth lost, reaching 100⁰/o in some populations. For instance, the second upper premolar was found in 78.1⁰/o (125 of 160) of a sample of *Felis bengalensis,* occurring with different frequencies in various populations of the sample (Glass & Todd, 1975, 1977), and, among other frequencies, in 71.6⁰/o (48 of 67), 88.3⁰/o (227 of 257), and 90.3⁰/o (131 of 145) of the specimens of *Felis catus* from the Kerguelen Archipelago, the Bern region, and Geneva respectively (Lüps, 1980).

Such a presence-absence tooth polymorphism has also been discovered in fossil mammals and, in addition, gradual changes in the frequencies of phenotypes with a tooth presence have been traced in successive species of an evolving lineage (e.g. Simpson, 1946; Kurtén, 1953, 1956). It is generally agreed that shape, size, and presence or absence of a tooth are under a strong genetic control and that a group of genes rather than a single gene is responsible for this. Thus, it seems very probable that the genes of such a group have been present in genotypes in qualitatively different compositions, resulting in phenotypes differing from each other in shape, size, and presence or absence of a given tooth, and that their frequencies have gradually changed with time in the gene pool of a population, resulting in different frequencies of the phenotypes in that population.

(2)

The second interpretation may apply to supernumerary teeth appearing in any position. Such teeth are usually very similar in shape to an adjacent one in a tooth row (e.g. Ruprecht, 1965b; Berkovitz & Musgrave, 1971; Wolsan, 1984), which suggests their common origin from one tooth germ. Moreover, they are often formed in unconformity to gradients of tooth shape and size in their tooth classes (e.g. Dolgov & Rossolimo, 1964: Fig. 2; Lüps, 1977: Fig. 1a; Buchalczyk *et al.,* 1981: Fig. 3), which, in terms of the Field and Clone Theories, excludes the possibility of their origin from individual tooth germs. Mammalian dentitions provide many examples which illustrate the successive stages in the process of tooth splitting. Hence, many mammalian teeth with signs of incomplete splitting, varying in degree of expression, have so far been described (e.g. Agduhr, 1921; Pavlinov, 1975; Wolsan, 1984). Furthermore, supernumerary teeth having an alveolus either partly or entirely united with that of an adjacent tooth have also been observed in mammals (Dolgov & Rossolimo, 1964; Bateman, 1970). Histological studies of the development of supernumerary teeth and teeth with signs of incomplete splitting have shown that such teeth in mammals may originate respectively as a result of complete or incomplete splitting of a tooth germ (e.g. Hitchin & Morris, 1966; Hitchin, 1971; Berkovitz & Thomson, 1973).

Considerable evidence has so far been accumulated to prove that such teeth may be inherited or due to a mutation (e.g. Miles, 1954; Hitchin, 1970; Kalter, 1980). Glasstone (1952) demonstrated that each part of a tooth germ cut in half may develop into a complete tooth, and Hitchin & Naylor (1964) showed that an infection may lead to the splitting of a tooth germ. Finally, Burn *et. al.*, (1937) have described supernumerary teeth whose occurrence may be caused by a deficiency of vitamin A in the diet.

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Possibility of Freemartinism in Roe Deer [1]

MOŻLIWOŚĆ WYSTĘPOWANIA FRYMARTYNIZMU U SARNY

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Sysa P. S. & Kałuziński J., 1984: Possibility of freemartinism in roe deer. Acta theriol., 29, 10: 133—137 [With Plate I]

Cytogenetic analysis was made in female roe deer, *Capreolus capreolus* (Linnaeus, 1758), belonging to members of heterosexual triplets. Lymphocytic chimerism was not discovered, the karyotype being defined as 70,XX. The result obtained justifies the assumption that in cases of twin or multiple pregnancy of unlike sexes in the roe deer there is no development of infertility in the females etiologically similar to the freemartinism syndrome in domestic cattle.

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