# 147. *Probabilities on Inheritance in Consanguineous Families.* XV

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(Comm. by T. FURUHATA, M.J.A., Oct. 12, 1956)

## XII. Generalization to the case of several ancestors

### 1. Ancestors-descendant combination

In the preceding chapter[1] we have dealt with a mother-descendants combination in a consanguineous lineage of general nature and further with some related combinations which result from the former by means of simple procedures of elimination. However, every combination considered there has concerned, in principle, only one distinguished ancestor, while the number of descendants has been supposed one or two. It seems now plausible that the results may be generalized to the case of several ancestors, which will be discussed in the present chapter.

For the sake of brevity, we confine ourselves throughout the present chapter to a supposition that every generation-number between two consecutive critical positions in a lineage is, in principle, greater than unity, unless a contrary is stated.

We now consider an ancestors-descendant combination in a non-consanguineous lineage with an assigned number of distinguished ancestors. All the possible types of ancestors-descendant combination which corresponds to a fixed number $D$ of distinguished ancestors will be classified into $\Phi(D)$ classes according to the topological structure of lineage.

Let a combination concerning a non-consanguineous lineage be given which consists of $D$ distinguished ancestors $\mathbf{0}_\delta\,(\delta=1,\cdots,D)$ and a common descendant $\mathbf{1}$. The set of these ancestors will be designated abbreviatedly by

$$\mathfrak{a}_D\equiv(\mathbf{0}_1,\cdots,\mathbf{0}_D),$$

the order of the constituents being a matter of indifference. It is shown that the reduced probability of the combination consisting of these $D+1$ individuals is given by the formula

$$K^F(\mathfrak{a}_D;\mathbf{1})=\bar{A}_1+2\sum_{\mathbf{0}_\delta\in\mathfrak{a}_D}2^{-\mathbf{1}(\mathbf{0}_\delta)}Q(\mathbf{0}_\delta;\mathbf{1})\qquad(F=\mathrm{I},\mathrm{II},\cdots,\Phi(D)).^{2)}$$

1) For previous part of the paper cf. Proc. Japan Acad. **31** (1955), 570–574. Details of the present paper will be published soon in Bull. Tokyo Inst. Tech.

2) We designate, as before, by $\mathbf{1}(\mathbf{0}_\delta)$ the length of the path from $\mathbf{0}_\delta$ to $\mathbf{1}$.

Though, among $\Phi(D)$ classes, the class containing the combination under consideration is once indicated by the index $F$, the values of the probability depend finally, besides of frequencies of genotypes of $D+1$ distinguished individuals, only on the length of the paths from the $\mathbf{0}$'s to $\mathbf{1}$ and not on the location of $D-1$ converging positions.

The last formula can be derived by induction with respect to $D$. For the lowest cases $D=1$ and $D=2$ the formulas have been established respectively in chapter I §1 and chapter II §2:

$$K^F(\mathfrak{a}_1;\mathbf{1})=\kappa_n(\mathbf{0}_1;\mathbf{1}),$$
$$K^F(\mathfrak{a}_2;\mathbf{1})=\varepsilon_{\mu\nu;n}(\mathbf{0}_1,\mathbf{0}_2;\mathbf{1}),$$

$\Phi(1)$ and $\Phi(2)$ being equal to unity.

## 2. Ancestors-descendants combination

We next consider an ancestors-descendants combination in a non-consanguineous lineage which consists of a certain number of ancestors and their two common descendants. Two systems are distinguished according whether, among distinguished ancestors, there exists a branching number or not.

We begin with the former system. Let the number of distinguished ancestors be equal to $D$. We designate by $\mathbf{0}$ the branching ancestor of such a lineage and further by

$$\mathbf{0}_u^1\ (u=1,\cdots,U) \quad \text{and} \quad \mathbf{0}_v^2\ (v=1,\cdots,V)$$

the ancestors of $\mathbf{1}$ alone and of $\mathbf{2}$ alone, respectively, so that $1+U+V=D$. Two sets of these ancestors will be designated by

$$\mathfrak{a}_U^1\equiv(\mathbf{0}_1^1,\cdots,\mathbf{0}_U^1) \quad \text{and} \quad \mathfrak{a}_V^2\equiv(\mathbf{0}_1^2,\cdots,\mathbf{0}_V^2).$$

The reduced probability of the combination for an arbitrary $D$ will be given by the formula

$$\begin{aligned}
&K_G(\mathbf{0},\mathfrak{a}_U^1,\mathfrak{a}_V^2;\mathbf{1},\mathbf{2})\\
&=\bar{A}_1\bar{A}_2+2\bar{A}_2\{2^{-1(\mathbf{0})}Q(\mathbf{0};\mathbf{1})+\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;\mathbf{1})\}\\
&\qquad+2\bar{A}_1\{2^{-2(\mathbf{0})}Q(\mathbf{0};\mathbf{2})+\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;\mathbf{2})\}+2\times2^{-1(\mathbf{0})-2(\mathbf{0})}T(\mathbf{0};\mathbf{1},\mathbf{2})\\
&+4\{2^{-2(\mathbf{0})}Q(\mathbf{0};\mathbf{2})\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;\mathbf{1})\\
&\quad+2^{-1(\mathbf{0})}Q(\mathbf{0};\mathbf{1})\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;\mathbf{2})+\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;\mathbf{1})\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;\mathbf{2})\}\\
&\qquad\qquad(G=\mathrm{I},\mathrm{II},\cdots,\Psi(D)).
\end{aligned}$$
[3]

We next proceed to the latter system. There exists a single intermediate branching position, which will be designated by $Z$. Any lineage of this system may be regarded as a composition of its sub-

3) We classify all the possible types of ancestors-descendants combination into $\Psi(D)$ classes according to the topological structure of lineage.

lineage corresponding to an ancestors-descendant combination

$$(\mathfrak{a}_W^{12};\zeta)^F \equiv (\mathbf{0}_1^{12},\cdots,\mathbf{0}_W^{12};\zeta)^F \qquad (W\geqq 1)$$

and an ancestors-descendants combination

$$(\zeta,\mathfrak{a}_U^1,\mathfrak{a}_V^2;\mathbf{1},\mathbf{2})_G \equiv (\zeta,\mathbf{0}_1^1,\cdots,\mathbf{0}_U^1,\mathbf{0}_1^2,\cdots,\mathbf{0}_V^2;\mathbf{1},\mathbf{2})_G$$

after connecting them at the branching position $Z$.

Consequently, we obtain the reduced probability of the ancestors-descendants combination under consideration in the form

$$\begin{aligned}
&K_G^F(\mathfrak{a}_W^{12},(Z),\mathfrak{a}_U^1,\mathfrak{a}_V^2;\mathbf{1},\mathbf{2})\\
&=\sum_{\zeta} K^F(\mathfrak{a}_W^{12};\zeta)K_G(\zeta,\mathfrak{a}_U^1,\mathfrak{a}_V^2;\mathbf{1},\mathbf{2})\\
&=\bar{A}_1\bar{A}_2+2\bar{A}_2\Big\{\sum_{\mathfrak{a}_W^{12}}2^{-1(\mathbf{0}_w^{12})}Q(\mathbf{0}_w^{12};1)+\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;1)\Big\}\\
&\quad+2\bar{A}_1\Big\{\sum_{\mathfrak{a}_W^{12}}2^{-2(\mathbf{0}_w^{12})}Q(\mathbf{0}_w^{12};2)+\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;2)\Big\}\\
&\quad+2\times 2^{-1(Z)-2(Z)}\Big\{\bar{A}_1Q(1;2)+\bar{A}_2Q(2;1)+2\sum_{\mathfrak{a}_W^{12}}2^{-Z(\mathbf{0}_w^{12})}S(\mathbf{0}_w^{12};1,2)\Big\}\\
&\quad+4\Big\{\sum_{\mathfrak{a}_W^{12}}2^{-2(\mathbf{0}_w^{12})}Q(\mathbf{0}_w^{12};2)\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;1)\\
&\qquad+\sum_{\mathfrak{a}_W^{12}}2^{-1(\mathbf{0}_w^{12})}Q(\mathbf{0}_w^{12};1)\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;2)\\
&\qquad+\sum_{\mathfrak{a}_U^1}2^{-1(\mathbf{0}_u^1)}Q(\mathbf{0}_u^1;1)\sum_{\mathfrak{a}_V^2}2^{-2(\mathbf{0}_v^2)}Q(\mathbf{0}_v^2;2)\Big\}.
\end{aligned}$$

### 3. Ancestors-descendants combination in a consanguineous lineage

We are now in position to attack our main problem on ancestors-descendants combination in a consanguineous lineage. We consider an ancestor-descendants combination $(\mathbf{0};\mathbf{1},\mathbf{2})_t^J$ of a lineage of the type considered in chapter XI §2, in which $\mathbf{0}$ is a branching member, $t$ designates the number of consanguineous marriages involved, and $J$ indicates a subclass among $M(t)$ possible subclasses. Such a lineage contains, besides of $\mathbf{0}$, $2t$ critical positions, namely $t$ intermediate branching positions $B_\tau$ $(\tau=1,\cdots,t)$ and $t$ converging positions $C_\tau$ $(\tau=1,\cdots,t)$. There are $3t$ intermediate critical members, namely $t$ branching members $b_\tau$ at $B_\tau$ and $2t$ converging members $c_\tau$, $d_\tau$ at $C_\tau$. We take such a lineage as a *trunk* of a more general lineage to be dealt with in the present section. A trunk consists of $3t+2$ maximal chains terminating at $3t$ intermediate critical members $b_\tau$, $c_\tau$, $d_\tau$ $(\tau=1,\cdots,t)$ and two descendants $\mathbf{1}$ and $\mathbf{2}$. A maximal chain which terminates at a position $Z$ bearing a member $\zeta$ will be designated, in general, by $\gamma_\zeta$. We now suppose that each maximal chain $\gamma_\zeta$ is replaced by a *twig* consisting of such an ancestors-descendant combination

$$(b, \mathfrak{a}^{\zeta}; \zeta) \quad \text{or} \quad (c, d, \mathfrak{a}^{\zeta}; \zeta), \qquad \mathfrak{a}^{\zeta} \equiv (\mathbf{0}_1^{\zeta}, \cdots, \mathbf{0}_{D(\zeta)}^{\zeta}),$$

with no interjacent consanguineous marriages as considered in §1, in which one ancestor $b$ or two ancestors $c$ and $d$ coincide with the initial member or members of $\gamma_\zeta$ and the descendant coincides just with $\zeta$ while $\mathfrak{a}^{\zeta}$ represents the set of inserted *twig-ancestors*. A lineage thus constructed is the object of our present consideration and may be designated by the symbol

$$(\mathbf{0}, \mathfrak{A}; \mathbf{1}, \mathbf{2})_{t|H}^{J}$$

in which $\mathfrak{A}$ denotes the whole set of the inserted twig-ancestors and indicates a subclass in the classification according to the topological structure of lineage.

It is shown that the reduced probability of a generalized ancestors-descendants combination of the type just introduced is given by

$$K_{t|H}^{J}(\mathbf{0}, \mathfrak{A}; \mathbf{1}, \mathbf{2}) = \sum_{b_\tau, c_\tau, d_\tau} K_{G_0}(\mathbf{0}, \mathfrak{a}^{h_0}, \mathfrak{a}^{k_0}; h_0, k_0) \times \prod_{1 \leq \tau \leq t} K_{G_\tau}(b_\tau, \mathfrak{a}^{h_\tau}, \mathfrak{a}^{k_\tau}; h_\tau, k_\tau) K^{F_\tau}(c_\tau, d_\tau, \mathfrak{a}^{g_\tau}; g_\tau)$$

$$= \bar{A}_1\bar{A}_2 + 2\bar{A}_2 \sum_{\mathbf{0}^1 \in \mathbf{0} \cup \mathfrak{A}} 2^{-\mathbf{1}(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) + 2\bar{A}_1 \sum_{\mathbf{0}^2 \in \mathbf{0} \cup \mathfrak{A}} 2^{-\mathbf{2}(\mathbf{0}^2)} Q(\mathbf{0}^2; \mathbf{2})$$
$$+ [\boldsymbol{T}]_t^J T(\mathbf{0}; \mathbf{1}, \mathbf{2}) + 4 \sum_{\Omega} \sum_{u,v} \sum_{\delta} 2^{-\Omega_{uv}(\mathbf{0}_\delta^{\Omega}) - \mathbf{1}_u(\Omega) - \mathbf{2}_v(\Omega)} S(\mathbf{0}_\delta^{\Omega}; \mathbf{1}, \mathbf{2})$$
$$+ [\boldsymbol{O}]_t^J \{\bar{A}_1 Q(\mathbf{1}; \mathbf{2}) + \bar{A}_2 Q(\mathbf{2}; \mathbf{1})\} + 4 \sum_{\substack{\mathbf{0}^1, \mathbf{0}^2 \in \mathbf{0} \cup \mathfrak{A} \\ \mathbf{1}(\mathbf{0}^1) \cap \mathbf{2}(\mathbf{0}^2) = 0}} Q(\mathbf{0}^1; \mathbf{1}) Q(\mathbf{0}^2; \mathbf{2}).$$

We next consider the case where it is also permitted to insert a twig of an ancestors-descendant combination terminating at $\mathbf{0}$. It is shown that, by means of readily comprehensible notations, the final result can be brought into the form

$$K_{t|H}^{J|F}(\mathfrak{a}, (Z), \mathfrak{A}; \mathbf{1}, \mathbf{2}) = \sum_{\zeta} K^F(\mathfrak{a}; \zeta) K_{t|H}^{J}(\zeta, \mathfrak{A}; \mathbf{1}, \mathbf{2})$$
$$= \bar{A}_1\bar{A}_2 + 2\bar{A}_2 \sum_{\mathbf{0}^1 \in \mathfrak{a} \cup \mathfrak{A}} 2^{-\mathbf{1}(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) + 2\bar{A}_1 \sum_{\mathbf{0}^2 \in \mathfrak{a} \cup \mathfrak{A}} 2^{-\mathbf{2}(\mathbf{0}^2)} Q(\mathbf{0}^2; \mathbf{2})$$
$$+ 4 \sum_{\Omega} \sum_{u,v} \sum_{\mathbf{0}^{\Omega} \in \mathfrak{a} \cup \mathfrak{A}} 2^{-\Omega_{uv}(\mathbf{0}^{\Omega}) - \mathbf{1}_u(\Omega) - \mathbf{2}_v(\Omega)} S(\mathbf{0}^{\Omega}; \mathbf{1}, \mathbf{2})$$
$$+ \{[\boldsymbol{T}]_t^J + [\boldsymbol{O}]_t^J\} \{\bar{A}_1 Q(\mathbf{1}; \mathbf{2}) + \bar{A}_2 Q(\mathbf{2}; \mathbf{1})\}$$
$$+ 4 \sum_{\substack{\mathbf{0}^1, \mathbf{0}^2 \in \mathfrak{a} \cup \mathfrak{A} \\ \mathbf{1}(\mathbf{0}^1) \cap \mathbf{2}(\mathbf{0}^2) = 0}} Q(\mathbf{0}^1; \mathbf{1}) Q(\mathbf{0}^2; \mathbf{2}).$$

## 4. Ancestors-descendant combination in a consanguineous lineage

Ancestors-descendants combinations yield, after convolution by $\varepsilon_n$ from below, the corresponding ancestors-descendant combinations, of which the reduced probabilities will be designated by

$$K_{t|H;n}^{J}(\mathbf{0}, \mathfrak{A}; \mathbf{1}) = \sum_{p,q} K_{t|H}^{J}(\mathbf{0}, \mathfrak{A}; p, q) \varepsilon_n(p, q; \mathbf{1}),$$
$$K_{t|H;n}^{J|F}(\mathfrak{a}, (Z), \mathfrak{A}; \mathbf{1}) = \sum_{p,q} K_{t|H}^{J|F}(\mathfrak{a}, (Z), \mathfrak{A}; p, q) \varepsilon_n(p, q; \mathbf{1}),$$

the number of interjacent consanguineous marriages being equal to $t+1$. The final results are expressed by the formulas

$$K^J_{t|H;1}(\mathbf{0}, \mathfrak{A}; \mathbf{1}) = \bar{A}_1 + 2 \sum_{\mathbf{0}^1 \in \mathbf{0} \cup \mathfrak{A}} 2^{-1(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) + [\boldsymbol{O}]^J_t R(\mathbf{1}) + [\boldsymbol{T}]^J_t T(\mathbf{0}; \mathbf{1})$$

$$+ 2 \sum_{\Omega} \sum_{u,v} \sum_{\mathbf{0}^\Omega \in \mathbf{0} \cup \mathfrak{A}} 2^{-\Omega_{uv}(\mathbf{0}^\Omega) - p_u(\Omega) - q_v(\Omega)} S(\mathbf{0}^\Omega; \mathbf{1}) + \sum_{\substack{\mathbf{0}', \mathbf{0}'' \in \mathbf{0} \cup \mathfrak{A} \\ p(\mathbf{0}') \cap q(\mathbf{0}'') = 0}} D_0(\mathbf{0}', \mathbf{0}''; \mathbf{1}),$$

$$K^J_{t|H;n}(\mathbf{0}, \mathfrak{A}; \mathbf{1}) = \bar{A}_1 + 2 \sum_{\mathbf{0}^1 \in \mathbf{0} \cup \mathfrak{A}} 2^{-1(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) \qquad (n > 1);$$

$$K^{J|F}_{t|H;1}(\mathfrak{a}, (Z), \mathfrak{A}; \mathbf{1}) = \bar{A}_1 + 2 \sum_{\mathbf{0}^1 \in \mathfrak{a} \cup \mathfrak{A}} 2^{-1(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) + \{[\boldsymbol{T}]^J_t + [\boldsymbol{O}]^J_t\} R(\mathbf{1})$$

$$+ 2 \sum_{\Omega} \sum_{u,v} \sum_{\mathbf{0}^\Omega \in \mathfrak{a} \cup \mathfrak{A}} 2^{-\Omega_{uv}(\mathbf{0}^\Omega) - p_u(\Omega) - q_v(\Omega)} S(\mathbf{0}^\Omega; \mathbf{1}) + \sum_{\substack{\mathbf{0}', \mathbf{0}'' \in \mathfrak{a} \cup \mathfrak{A} \\ p(\mathbf{0}') \cap q(\mathbf{0}'') = 0}} D_0(\mathbf{0}', \mathbf{0}''; \mathbf{1}),$$

$$K^{J|F}_{t|H;n}(\mathfrak{a}, (Z), \mathfrak{A}; \mathbf{1}) = \bar{A}_1 + 2 \sum_{\mathbf{0}^1 \in \mathfrak{a} \cup \mathfrak{A}} 2^{-1(\mathbf{0}^1)} Q(\mathbf{0}^1; \mathbf{1}) \qquad (n > 1),$$

where $p$ and $q$ denote the pair of the last converging members and $\Omega$ extends over all the branching positions.

## 5. Descendants combination and distribution of genotypes

The probability of a descendants combination or distribution of genotypes in a generation of descendant can be obtained by eliminating ancestors' genotypes from the corresponding ancestors-descendants combination or ancestors-descendant combination, respectively. By the elimination procedure the effect of inserted twigs is entirely removed away and the result depends on the trunk of lineage alone. Thus we get

$$\textstyle\sum^J_{t|H}(\mathbf{1}, \mathbf{2}) = \sum^J_t(\mathbf{1}, \mathbf{2})$$

$$= \bar{A}_1 \bar{A}_2 + \{[\boldsymbol{T}]^J_t + [\boldsymbol{O}]^J_t\} \{\bar{A}_1 Q(\mathbf{1}; \mathbf{2}) + \bar{A}_2 Q(\mathbf{2}; \mathbf{1})\};$$

$$\bar{A}^J_{t|H;n}(\mathbf{1}) = \bar{A}^J_{t;n}(\mathbf{1}) = \begin{cases} \bar{A}_1 + \{[\boldsymbol{T}]^J_t + [\boldsymbol{O}]^J_t\} R(\mathbf{1}) & (n=1), \\ \bar{A}_1 & (n>1). \end{cases}$$